Highly-regulated, diversifying NTP-dependent biological conflict systems with implications for the emergence of multicellularity

SOURCE DATA

Gurmeet Kaur†, A. Maxwell Burroughs†, Lakshminarayan M. Iyer, L. Aravind*

Computational Biology Branch, National Center for Biotechnology Information, National Library of Medicine, National Institutes of Health, Bethesda, MD 20894, USA

†These authors contributed equally to the manuscript

Source Data

I. Source data - genome identifiers, multicellular status, and systems in genome
II. Source data - domain architectures, genome identifiers, gene neighborhoods
III. Source data - profile-profile comparisons
IV. Source data - pairwise systems comparison in same genomes
V. Source data - organisms with multiple systems in same genomes
VI. Source data - genome identifiers and systems for all EAD1-containing organisms
VII. Source data - organism abbreviations
VIII. Source data - multiple sequence alignments

I. Source data - genome identifiers, multicellular status, and systems in genome

VMAP systems

- **GCA_000349325.1; Streptomyces davawensis JCM 4913; counts= 6; multicellularity status: TRUE**
  - AB_hydrolase->CASPASE+VMAP-M0+VMAP-C->MoxR->vWA+STAND_NTPase+Trypsin+CASPASE+S1COLD*->
  - AB_hydrolase->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-CASPASE+EAD2
  - CASPASE+VMAP-M0+VMAP-C->vWA+HTH*->
  - EAD2+VMAP-M0+VMAP-C->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like<-Trypsin+EAD2||FXSXX-COOH-like->METALLOPROTEASE+TPRs->
  - Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD*->
  - Trypco1->Trypsin+VMAP-M7+VMAP-C->MoxR->vWA+EAD2+VMAP-M0+VMAP-C*->
- **GCA_000014265.1; Trichodesmium erythraeum IMS101; counts= 5; multicellularity status: TRUE**
  - CASPASE+VMAP-C->MoxR->?->vWA(partial)->vWA+HTH+HTH+HTH+HTH+HTH+HTH+HTH+HTH+HTH+FGS-fold_domain*->
  - EAD1+Trypsin->?->EAD1+VMAP-M0+VMAP-C->MoxR->?->||<-?||vWA+FGS-fold_domain*->
  - EAD6+VMAP-M12+VMAP-C->MoxR->vWA+FGS-fold_domain+FGS-fold_domain*->
  - EAD7+VMAP-M1+VMAP-C->MoxR->?->?->vWA+FGS-fold_domain*->FGS-fold_domain->
  - Trypco1->Trypsin+VMAP-M1+VMAP-C->MoxR->vWA+FGS-fold_domain*->four_helix_bundle_protein->PSE->FGS-fold_domain->
- **GCA_001685355.1; Streptomyces lincolnensis; counts= 5; multicellularity status: TRUE**
  - AB_hydrolase->CASPASE+VMAP-M0+VMAP-C->MoxR->vWA+STAND_NTPase+Trypsin+TIR+CASPASE+EAD2*->
  - AB_hydrolase->CASPASE+VMAP-M2+VMAP-C->MoxR->vWA+SFII-helicase+Z1*->
  - EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-CASPASE+EAD2
  - EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-Na_H_Exchanger||AB_hydrolase->CASPASE+EAD2->FXSXX-COOH-like->METALLOPROTEASE+TPRs->
  - Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD*->?->?->?->||<-?||Radical_SAM->Antibiotic_NAT->TIR+FxsC_Cter->
- **GCA_000092385.1; Streptomyces bingchenggensis BCW-1; counts= 4; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like<-?<-?<-Na_H_Exchanger
  - PNP_UDP_1+EAD2->?->vWA->?->?->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs
  - PNP_UDP_1+EAD2->?->vWA*->?->?->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs->||<-METALLOPROTEASE+TPRs
  - Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->Porphobil_deam+Porphobil_deamC->
- **GCA_000761215.1; Streptomyces glaucescens; counts= 4; multicellularity status: TRUE**
  - <-TCAD15||PSE->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TIR+APATPase+Trypsin+HDxxH+VMAP-M0+VMAP-C*->
  - DRHyd+VMAP-M0+VMAP-C->MoxR->vWA+TIR+APATPase+wHTH+TPRs*->
  - EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like
  - Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD*->
- **GCA_001485105.1; Streptomyces acidiscabies; counts= 4; multicellularity status: TRUE**

- Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->
- Trypco2->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+TPRs*->
- vWA+Pkinase+wHTH+cNMP_cyclase+Band7+HAD*->
- vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->

■ **GCA_001298565.1; Actinobacteria bacterium OK006; counts= 4; multicellularity status: NA**

- AB_hydrolase->CASPASE+VMAP-M2+VMAP-C->MoxR->vWA+BetaPropeller*->
- ADP_ribosyl_GH->NUDIX->Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->
- EAD2+TIR->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs
- EAD2+VMAP-M0+VMAP-C->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like<-Trypsin+EAD2<-Trypco2||FXSXX-COOH-like->METALLOPROTEASE+TPRs->

■ **GCA_001514305.1; Streptomyces sp. RV15; counts= 4; multicellularity status: TRUE**

- EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->
- TIR+EAD2->EAD2+VMAP-M10+VMAP-C->MoxR->vWA+APATPase+Trypsin+TIR+FxsC_Cter(partial)*->||<-DUF397
- Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->
- Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD*->

■ **GCA_002019855.1; Streptomyces antibioticus; counts= 4; multicellularity status: TRUE**

- TCAD9+Pkinase+NACHT+HEAT_repeats->EAD2+VMAP-M0+VMAP-C->vWA*->MoxR->vWA+APATPase+TPRs->
- Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD*->
- Trypsin+EAD2+VMAP-C->vWA+APATPase+wHTH+TPRs*->KAP_NTPase->
- vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like<-Trypsin+EAD2||METALLOPROTEASE+TPRs->

■ **GCA_900091315.1; Streptomyces sp. DI166; counts= 4; multicellularity status: TRUE**

- AB_hydrolase->CASPASE+VMAP-M0+VMAP-C->MoxR->vWA_protein*->Trypsin+CASPASE+S1COLD->
- CASPASE+VMAP-M0+VMAP-C->vWA+HTH*->
- EAD2+VMAP-M0+VMAP-C->vWA+APATPase+wHTH+TPRs*->
- Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD*->

■ **GCA_900129855.1; Streptomyces sp. 3124.6; counts= 4; multicellularity status: TRUE**

- <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- AB_hydrolase->CASPASE+VMAP-M2+VMAP-C->MoxR->vWA+SFII-helicase+Z1*->
- Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->
- Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+cNMP_cyclase+Band7+HAD*->

■ **GCA_000346485.2; Scytonema hofmannii; counts= 4; multicellularity status: TRUE**

- EAD1+VMAP-M1+VMAP-C->MoxR->vWA+FGS-fold_domain*->four_helix_bundle_protein->RVT_1->
- low-complexity+VMAP-M26+VMAP-C->MoxR->vWA+CASPASE+APATPase*->
- TCAD3+EAD1+EAD9->EAD9+EAD1+VMAP-C->MoxR->vWA+FGS-fold_domain*->FGS-fold_domain->four_helix_bundle_protein->RVT_1->
- vWA_protein*->

■ **GCF_001189025.1; Streptomyces europaeiscabiei; counts= 4; multicellularity status: TRUE**

- <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->Radical_SAM->TIR+APATPase+TPRs->

- AB_hydrolase->CASPASE+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->
- EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->AB_hydrolase->CASPASE+EAD2->FXSXX-COOH-like->METALLOPROTEASE+TPRs->
- Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->

■ **GCA_001426425.1; Streptomyces sp. Root1310; counts= 4; multicellularity status: TRUE**

- <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- EAD2+VMAP-M0+VMAP-C->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-Trypsin+EAD2||Trypco2->
- Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->
- Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+cNMP_cyclase+Band7+HAD*->

■ **GCF_001650215.1; Streptomyces sp. RTd22; counts= 4; multicellularity status: TRUE**

- AB_hydrolase->CASPASE+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->
- EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-Radical_SAM<-FXSXX-COOH||Voltage_CLC->||<-Trypco1
- PNP_UDP_1+EAD2->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs
- Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->Porphobil_deam+Porphobil_deamC->

■ **GCF_001941325.1; Streptomyces acidiscabies; counts= 4; multicellularity status: TRUE**

- Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->
- Trypco2->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+TPRs*->
- vWA+Pkinase+wHTH+cNMP_cyclase+Band7+HAD*->
- vWA+TIR+FxsC_Cter(partial)*->

■ **GCA_001027285.1; Archangium gephyra; counts= 3; multicellularity status: TRUE**

- EAD1+VMAP-M1+VMAP-C->MoxR->vWA+CASPASE+SLOG+TPRs*->
- EAD1+VMAP-M1+VMAP-C->MoxR->vWA+SLOG+SLOG+TPRs*->EAD1+Trypsin->
- EAD1+VMAP-M1+VMAP-C->vWA+SLOG*->

■ **GCA_001264245.1; Microcystis panniformis FACHB-1757; counts= 3; multicellularity status: TRUE**

- AB_hydrolase->CASPASE+VMAP-M14+VMAP-C->MoxR->vWA+FGS-fold_domain*->
- HTH+VMAP-M9+VMAP-C->MoxR->vWA+FGS-fold_domain*->?->||<-?||FGS-fold_domain->
- Trypco1->Trypsin+VMAP-M1+VMAP-C->MoxR->vWA+FGS-fold_domain*->?->||<-?<-?||FGS-fold_domain->

■ **GCA_001302585.1; Kibdelosporangium phytohabitans; counts= 3; multicellularity status: TRUE**

- AB_hydrolase->CASPASE+VMAP-M2+VMAP-C->MoxR->vWA+SWACOS*->
- EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like||EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like
- EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs||EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like

■ **GCA_001735805.1; Streptomyces puniciscabiei; counts= 3; multicellularity status: TRUE**

- Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->
- Trypsin+EAD2->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like||Trypco1->
- Trypsin+EAD2+VMAP-M0+VMAP-C->vWA+APATPase+wHTH+TPRs*->

■ **GCA_000010605.1; Streptomyces griseus subsp. griseus NBRC 13350; counts= 3; multicellularity status: TRUE**

- AB_hydrolase->CASPASE+VMAP-M2+VMAP-C->MoxR->vWA+TIR+FxsC_Cter*->
- AB_hydrolase->CASPASE+VMAP-M2+VMAP-C->MoxR->vWA+TPRs+TIR+FxsC_Cter(partial)*->
- Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->||<-?<-?<-PSE||?->||<-?<-PSE<-?<-Trypco1

■ **GCA_000328705.1; Saccharothrix espanaensis DSM 44229; counts= 3; multicellularity status: TRUE**

- cNMP_cyclase+EAD2->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs
- EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-?<-?<-TCAD15
- EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like<-cNMP_cyclase+EAD2

■ **GCA_000312185.1; Microcystis aeruginosa PCC 9443; counts= 3; multicellularity status: TRUE**

- CASPASE+VMAP-M14+VMAP-C->MoxR->vWA+FGS-fold_domain*->
- HTH+VMAP-M9+VMAP-C->MoxR->vWA+FGS-fold_domain*->?->?->FGS-fold_domain->
- Trypsin+VMAP-M1+VMAP-C->MoxR->vWA*->

■ **GCA_000826545.1; Kibdelosporangium sp. MJ126-NF4; counts= 3; multicellularity status: TRUE**

- AB_hydrolase->CASPASE+VMAP-M2+VMAP-C->MoxR->vWA+EAD2+VMAP-M0+VMAP-C*->
- EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like||?->||<-?||EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs->
- vWA+APATPase+wHTH+TPRs->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like||?->||<-?||EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs

■ **GCA_000177675.1; Frankia sp. EUN1f; counts= 3; multicellularity status: TRUE**

- EAD2+EAD1->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs
- TIR+VMAP-M2+VMAP-C->MoxR->vWA+DO-GTPase2*->
- vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like

■ **GCA_000158935.1; Streptomyces lividans TK24; counts= 3; multicellularity status: TRUE**

- <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->Trypco1->
- Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA->vWA+Pkinase+HTH+TPRs+cNMP_cyclase*->
- Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA*->vWA+Pkinase+HTH+TPRs+cNMP_cyclase->

■ **GCA_000158955.1; Streptomyces viridochromogenes DSM 40736; counts= 3; multicellularity status: TRUE**

- <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->
- EAD2+VMAP-M0+VMAP-C->MoxR->vWA*->TIR+APATPase+TPRs->?->CASPASE+EAD2->METALLOPROTEASE+TPRs->
- Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA*->

■ **GCA_000316115.1; Leptolyngbya sp. PCC 7375; counts= 3; multicellularity status: TRUE**

- AB_hydrolase->CASPASE+EAD9->EAD9+VMAP-M1+VMAP-C->MoxR->vWA+FGS-fold_domain*->FGS-fold_domain->four_helix_bundle_protein->RVT_1->FGS-fold_domain->
- FGS-fold_domain->||<-?||PNP_UDP_1+VMAP-M1+VMAP-C->MoxR->vWA+Cas_csx3*->
- FGS-fold_domain->EAD1+Trypsin->?->EAD1+VMAP-M1+VMAP-C->MoxR->vWA+BetaPropeller+FGS-fold_domain*->FGS-fold_domain->||<-RVT_1<-four_helix_bundle_protein

■ **GCA_000412595.1; Microcystis aeruginosa SPC777; counts= 3; multicellularity status: TRUE**

- AB_hydrolase->CASPASE+VMAP-M14+VMAP-C->MoxR->vWA(partial)->vWA+FGS-fold_domain*->
- HTH+VMAP-M9+VMAP-C->MoxR->vWA+FGS-fold_domain*->
- MoxR->vWA(partial)->vWA+FGS-fold_domain*->

- **GCA_000414115.1; Streptomyces aurantiacus JA 4570; counts= 3; multicellularity status: TRUE**
  - Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->?->vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->
  - Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->||<-?||vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+HAD*->
  - vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like<-CASPASE+EAD2
- **GCA_000415505.1; Streptomyces afghaniensis 772; counts= 3; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->
  - EAD2+VMAP-M0+VMAP-C->MoxR->vWA+EAD2+CASPASE+EAD2*->
  - Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->?->vWA+cNMP_cyclase+Band7*->
- **GCA_000590515.1; Streptomyces sp. PRh5; counts= 3; multicellularity status: TRUE**
  - AB_hydrolase->CASPASE+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->
  - AB_hydrolase->CASPASE+VMAP-M2+VMAP-C->MoxR->vWA+CASPASE+TCAD13*->
  - PNP_UDP_1+EAD2->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like
- **GCA_000829715.2; Streptomyces sp. NBRC 110027; counts= 3; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->TIR+APATPase+TPRs->
  - Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->
  - Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+wHTH+TPRs+APATPase+wHTH+TPRs*->||<-?||?->||<-AB_hydrolase
- **GCA_001270025.1; Streptomyces azureus; counts= 3; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->AB_hydrolase->CASPASE+EAD2->FXSXX-COOH-like->METALLOPROTEASE+TPRs->
  - MoxR->vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->
  - Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD*->
- **GCA_001949645.1; Streptomyces acidiscabies; counts= 3; multicellularity status: TRUE**
  - vWA+Pkinase+wHTH+cNMP_cyclase+Band7+HAD*->
  - vWA+TIR+FxsC_Cter(partial)*->
  - vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCA_000725125.1; Streptomyces toyocaensis; counts= 3; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-Na_H_Exchanger||FXSXX-COOH-like->METALLOPROTEASE+TPRs->
  - Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->
  - Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD*->
- **GCA_000966965.1; Streptomyces sp. NRRL S-104; counts= 3; multicellularity status: TRUE**
  - <-TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->
  - AB_hydrolase->CASPASE+VMAP-M2+VMAP-C->MoxR->vWA+CASPASE+TCAD12*->
  - VMAP-M0+VMAP-C->MoxR->vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats*->
- **GCA_001279445.1; Streptomyces sp. WM6349; counts= 3; multicellularity status: TRUE**
  - <-TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->
  - AB_hydrolase->CASPASE+VMAP-M0+VMAP-C->MoxR->vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats*->

- AB_hydrolase->CASPASE+VMAP-M2+VMAP-C->MoxR->vWA+CASPASE+TCAD12*->

■ **GCA_001279685.1; Streptomyces sp. WM6373; counts= 3; multicellularity status: TRUE**

- <-TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->
- AB_hydrolase->CASPASE+VMAP-M0+VMAP-C->MoxR->vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats*->
- AB_hydrolase->CASPASE+VMAP-M2+VMAP-C->MoxR->vWA+CASPASE+TCAD12*->

■ **GCA_001279905.1; Streptomyces sp. XY66; counts= 3; multicellularity status: TRUE**

- <-TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->
- AB_hydrolase->CASPASE+VMAP-M0+VMAP-C->MoxR->vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats*->
- AB_hydrolase->CASPASE+VMAP-M2+VMAP-C->MoxR->vWA+CASPASE+TCAD12*->

■ **GCA_001279485.1; Streptomyces sp. XY511; counts= 3; multicellularity status: TRUE**

- <-TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->
- AB_hydrolase->CASPASE+VMAP-M0+VMAP-C->MoxR->vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats*->
- AB_hydrolase->CASPASE+VMAP-M2+VMAP-C->MoxR->vWA+CASPASE+TCAD12*->

■ **GCA_001279765.1; Streptomyces sp. XY413; counts= 3; multicellularity status: TRUE**

- <-TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->
- AB_hydrolase->CASPASE+VMAP-M0+VMAP-C->MoxR->vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats*->
- AB_hydrolase->CASPASE+VMAP-M2+VMAP-C->MoxR->vWA+CASPASE+TCAD12*->

■ **GCA_001279495.1; Streptomyces sp. H021; counts= 3; multicellularity status: TRUE**

- <-TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- AB_hydrolase->CASPASE+VMAP-M0+VMAP-C->MoxR->vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats*->
- AB_hydrolase->CASPASE+VMAP-M2+VMAP-C->MoxR->vWA+CASPASE+TCAD12*->

■ **GCA_001298545.1; Actinobacteria bacterium OV320; counts= 3; multicellularity status: NA**

- <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- DUF397->Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->
- Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+cNMP_cyclase+Band7+HAD*->

■ **GCA_001428885.1; Streptomyces sp. Root264; counts= 3; multicellularity status: TRUE**

- <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- DUF397->MoxR->vWA+APATPase+wHTH+TPRs*->||<-vWA<-EAD2+VMAP-M0+VMAP-C
- EAD2+VMAP-M0+VMAP-C->vWA*->||<-vWA+APATPase+wHTH+TPRs<-MoxR<-DUF397

■ **GCA_001456025.1; Mastigocoleus testarum BC008; counts= 3; multicellularity status: TRUE**

- CASPASE+AB_hydrolase->CASPASE+VMAP-M28+VMAP-C->MoxR->vWA+CASPASE+FGS-fold_domain*->
- EAD1+VMAP-M1+VMAP-C->MoxR->MoxR->vWA_protein*->vWA(partial)->FGS-fold_domain->FGS-fold_domain->
- EAD1+VMAP-M1+VMAP-C->MoxR->vWA+Ntox3+MACRODOMAIN+FGS-fold_domain*->

■ **GCA_001509775.1; Streptomyces violaceusniger; counts= 3; multicellularity status: TRUE**

- AB_hydrolase->CASPASE+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->

- PNP_UDP_1+EAD2->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs
- SIR2->||<-?<-?||Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ZNR+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->Porphobil_deam+Porphobil_deamC->

■ **GCA_001514205.1; Streptomyces griseoruber; counts= 3; multicellularity status: TRUE**

- AB_hydrolase->CASPASE+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+REase+cNMP_cyclase+CASPASE*->
- Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD*->
- Trypsin+EAD2+VMAP-M0+VMAP-C->vWA+APATPase+wHTH+TPRs*->KAP_NTPase->

■ **GCA_001514235.1; Streptomyces caeruleatus; counts= 3; multicellularity status: TRUE**

- AB_hydrolase->CASPASE+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+TIR+FxsC_Cter(partial)*->
- TCAD15->Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->Radical_SAM->TIR+APATPase+TPRs->
- Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->

■ **GCA_001751305.1; Streptomyces nanshensis; counts= 3; multicellularity status: TRUE**

- AB_hydrolase->CASPASE+VMAP-M2+VMAP-C->MoxR->vWA->vWA*->
- AB_hydrolase->CASPASE+VMAP-M2+VMAP-C->MoxR->vWA*->vWA->
- CASPASE+VMAP-M2+VMAP-C->MoxR->PSE->PSE->vWA(partial)+REase+STAND_NTPase+TPRs+cNMP_cyclase*->

■ **GCA_001905005.1; Streptomyces sp. CB02923; counts= 3; multicellularity status: TRUE**

- <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->TIR+APATPase+TPRs->
- Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->?->NUDIX->
- Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+wHTH+TPRs+wHTH+TPRs+APATPase+wHTH+TPRs*->||<-AB_hydrolase

■ **GCA_000935135.2; Streptomyces sp. MNU77; counts= 3; multicellularity status: TRUE**

- <-PNP_UDP_1+EAD2||AB_hydrolase->CASPASE+VMAP-M2+VMAP-C->MoxR->vWA+TIR+FxsC_Cter*->
- AB_hydrolase->CASPASE+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->
- EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->AB_hydrolase->CASPASE+EAD2->FXSXX-COOH-like->METALLOPROTEASE+TPRs->

■ **GCA_001969965.1; Streptomyces sparsogenes DSM 40356; counts= 3; multicellularity status: TRUE**

- AB_hydrolase->CASPASE+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->
- PNP_UDP_1+EAD2->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like
- vWA+Pkinase+Pkinase*->Porphobil_deam+Porphobil_deamC->

■ **GCA_001983105.1; Frankia sp. M16386; counts= 3; multicellularity status: TRUE**

- EAD2+EAD1->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs
- EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->TIR+APATPase+TPRs->||<-METALLOPROTEASE+TPRs
- Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->Voltage_CLC->FXSXX-COOH-like->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->

■ **GCA_900090075.1; Streptomyces sp. MnatMP-M77; counts= 3; multicellularity status: TRUE**

- AB_hydrolase->CASPASE+VMAP-M2+VMAP-C->MoxR->vWA+TIR+FxsC_Cter*->
- AB_hydrolase->CASPASE+VMAP-M2+VMAP-C->MoxR->vWA+TPRs+TIR+FxsC_Cter(partial)*->
- Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->

■ **GCA_900091955.1; Streptomyces sp. Ncost-T10-10d; counts= 3; multicellularity status: TRUE**

- AB_hydrolase->CASPASE+VMAP-M0+VMAP-C->MoxR->vWA+STAND_NTPase+BetaPropeller+REase(Mrr_cat-PDDEXK)*->
- Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+REase+SFI-helicase+DUF4729*->
- vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->

■ **GCA_900090095.1; Streptomyces sp. SceaMP-e96; counts= 3; multicellularity status: TRUE**

- <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->TIR+APATPase+TPRs->
- Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->
- Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+wHTH+TPRs+APATPase+wHTH+TPRs*->?->?->||<-AB_hydrolase

■ **GCA_900105695.1; Streptomyces melanosporofaciens; counts= 3; multicellularity status: TRUE**

- AB_hydrolase->CASPASE+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->
- PNP_UDP_1+EAD2->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like
- SIR2->||<-?<-?||Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ZNR+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->Porphobil_deam+Porphobil_deamC->

■ **GCA_900107925.1; Amycolatopsis pretoriensis; counts= 3; multicellularity status: TRUE**

- cNMP_cyclase+EAD2->EAD2+VMAP-M0+VMAP-C->vWA+APATPase+wHTH+TPRs->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like||EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like
- cNMP_cyclase+EAD2->EAD2+VMAP-M0+VMAP-C->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like||EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like
- EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like

■ **GCA_900107965.1; Streptomyces yanglinensis; counts= 3; multicellularity status: TRUE**

- <-TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->Trypco1->
- PNP_UDP_1+EAD2->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like
- Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->

■ **GCA_900112965.1; Streptomyces mirabilis; counts= 3; multicellularity status: TRUE**

- AB_hydrolase->CASPASE+VMAP-M2+VMAP-C->VMAP-C(partial)->MoxR->vWA+SFII-helicase+Z1*->
- ADP_ribosyl_GH->NUDIX->Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->SIR2->
- EAD2+VMAP-M0+VMAP-C->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-Trypsin+EAD2<-Trypco2||METALLOPROTEASE+TPRs->

■ **GCA_900177255.1; Streptomyces sp. Amel2xC10; counts= 3; multicellularity status: TRUE**

- AB_hydrolase->CASPASE+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+REase+cNMP_cyclase+CASPASE*->
- TCAD9+Pkinase+NACHT+HEAT_repeats->EAD2+VMAP-M0+VMAP-C->vWA*->MoxR->vWA+APATPase+TPRs->
- Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD*->

■ **GCA_000307995.2; Microcystis aeruginosa; counts= 3; multicellularity status: TRUE**

- AB_hydrolase->CASPASE+VMAP-M14+VMAP-C->MoxR->vWA+FGS-fold_domain*->
- HTH+VMAP-M9+VMAP-C->MoxR->vWA+FGS-fold_domain*->?->FGS-fold_domain->
- Trypco1->Trypsin+VMAP-M1+VMAP-C->MoxR->vWA+FGS-fold_domain*->?->PSE->||<-PSE||PSE->FGS-fold_domain->

■ **GCA_000312165.1; Microcystis aeruginosa; counts= 3; multicellularity status: TRUE**

- AB_hydrolase->CASPASE+EAD2->EAD2+VMAP-M11+VMAP-C->MoxR->vWA+FGS-fold_domain*->
- AB_hydrolase->CASPASE+VMAP-M14+VMAP-C->MoxR->vWA+FGS-fold_domain*->

- HTH+VMAP-M9+VMAP-C->MoxR->vWA+FGS-fold_domain*->?->?->?->PSE->FGS-fold_domain->

■ **GCA_000312225.1; Microcystis aeruginosa; counts= 3; multicellularity status: TRUE**

- AB_hydrolase->CASPASE+VMAP-M14+VMAP-C->MoxR->vWA+FGS-fold_domain*->
- HTH+VMAP-M9+VMAP-C->MoxR->vWA+FGS-fold_domain*->
- Trypsin+VMAP-M1+VMAP-C->MoxR->vWA+FGS-fold_domain*->FGS-fold_domain->

■ **GCA_000312265.1; Microcystis aeruginosa; counts= 3; multicellularity status: TRUE**

- CASPASE+EAD2->EAD2+VMAP-M11+VMAP-C->MoxR->vWA+FGS-fold_domain*->
- HTH+VMAP-M9+VMAP-C->MoxR->vWA+FGS-fold_domain*->?->?->FGS-fold_domain->
- Trypco1->Trypsin+VMAP-M1+VMAP-C->MoxR->vWA+FGS-fold_domain*->

■ **GCF_000242715.1; Streptomyces acidiscabies; counts= 3; multicellularity status: TRUE**

- AB_hydrolase->CASPASE+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+TIR+FxsC_Cter(partial)*->
- Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->
- Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+wHTH+cNMP_cyclase+Band7+HAD*->

■ **GCA_000240165.1; Streptomyces cattleya; counts= 3; multicellularity status: TRUE**

- <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->TIR+APATPase+TPRs->
- AB_hydrolase->CASPASE+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->
- Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->

■ **GCA_000312705.1; Anabaena sp. 90; counts= 3; multicellularity status: TRUE**

- <-CASPASE<-?||?->?->EAD10+VMAP-M1+VMAP-C->MoxR->vWA+TPRs*->
- vWA*->
- vWA+FGS-fold_domain*->

■ **GCF_000377965.1; Streptomyces sp. CNB091; counts= 3; multicellularity status: TRUE**

- CASPASE+VMAP-M2+VMAP-C->MoxR->vWA+HTH+HTH+ParA-Soj-PloopNTPase(SIMIBI)*->PSE->PSE->||<-?||?->||<-?||?->DUF397->
- EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->AB_hydrolase->CASPASE+EAD2->FXSXX-COOH-like->METALLOPROTEASE+TPRs->
- Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->

■ **GCF_000331305.1; Calothrix sp. PCC 7103; counts= 3; multicellularity status: TRUE**

- EAD1+VMAP-M23+VMAP-C->MoxR->vWA+Glyco_trans_4_4+Glycos_transf_1*->
- EAD9+VMAP-M1+VMAP-C->MoxR->vWA+FGS-fold_domain*->FGS-fold_domain->EAD1+APATPase+TPRs->
- VMAP-M1+VMAP-C->MoxR->vWA+MNS+CASPASE+MNS*->

■ **GCF_000599945.1; Microcystis aeruginosa; counts= 3; multicellularity status: TRUE**

- AB_hydrolase->CASPASE+VMAP-M14+VMAP-C->MoxR->vWA+FGS-fold_domain*->
- MoxR->vWA+FGS-fold_domain*->
- vWA+FGS-fold_domain*->

■ **GCA_003947255.1; Amycolatopsis balhimycina; counts= 3; multicellularity status: TRUE**

- cNMP_cyclase+EAD2->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs||cNMP_cyclase+EAD2->EAD2+VMAP-M0+VMAP-C->MoxR->TIR+APATPase+TPRs->||<-METALLOPROTEASE+TPRs

- vWA+APATPase+wHTH*->
- vWA+APATPase+wHTH+TPRs->||<-METALLOPROTEASE+TPRs||cNMP_cyclase+EAD2->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs

■ **GCF_000383635.1; Streptomyces sp. 303MFCol5.2; counts= 3; multicellularity status: TRUE**

- <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- DUF397->||<-?||Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->
- Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+cNMP_cyclase+Band7+HAD*->

■ **GCF_000717815.1; Streptomyces rimosus; counts= 3; multicellularity status: TRUE**

- <-FXSXX-COOH-like||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->TIR+APATPase+TPRs->
- Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->?->NUDIX->
- Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+wHTH+TPRs+wHTH+TPRs+APATPase+wHTH+TPRs*->||<-AB_hydrolase

■ **GCF_000718675.1; Streptomyces rimosus; counts= 3; multicellularity status: TRUE**

- <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->TIR+APATPase+TPRs->
- Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->?->NUDIX->
- Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+wHTH+TPRs+wHTH+TPRs+APATPase+wHTH+TPRs*->||<-AB_hydrolase

■ **GCF_000721445.1; Streptomyces sp. NRRL F-5053; counts= 3; multicellularity status: TRUE**

- TCAD15->?->?->PSE->?->MoxR->vWA+Trypsin+HDxxH+VMAP-M0+VMAP-C->PSE->MoxR->vWA+TPRs*->FXSXX-COOH->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- TCAD15->?->?->PSE->?->MoxR->vWA+Trypsin+HDxxH+VMAP-M0+VMAP-C*->PSE->MoxR->vWA+TPRs->FXSXX-COOH->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- Trypco1->PSE->vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->

■ **GCF_000720675.1; Streptomyces sp. NRRL WC-3795; counts= 3; multicellularity status: TRUE**

- EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-Na_H_Exchanger||AB_hydrolase->CASPASE+EAD2->FXSXX-COOH-like->METALLOPROTEASE+TPRs->
- Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->
- Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+wHTH+TPRs+cNMP_cyclase*->

■ **GCF_000716755.1; Saccharothrix syringae; counts= 3; multicellularity status: TRUE**

- EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like||?->||<-?||EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs->
- EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-TCAD15
- vWA+APATPase+wHTH+TPRs->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like||?->||<-?||EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs

■ **GCF_000404005.1; Streptomyces sp. FXJ7.023; counts= 3; multicellularity status: TRUE**

- <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->
- AB_hydrolase->CASPASE+EAD2+VMAP-M0+VMAP-C->MoxR->||<-?||vWA+TPRs*->||<-DUF397
- Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->

■ **GCA_000938975.1; Streptomyces iranensis; counts= 3; multicellularity status: TRUE**

- AB_hydrolase->CASPASE+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->
- PNP_UDP_1+EAD2->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs
- SIR2->||<-?<-?||Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+ZNR+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->Porphobil_deam+Porphobil_deamC->

■ **GCF_001189015.1; Streptomyces acidiscabies; counts= 3; multicellularity status: TRUE**

- <-TCAD15||PSE->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+wHTH+cNMP_cyclase+Band7+HAD*->
- Trypco2->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+TPRs*->

■ **GCF_000717185.1; Kitasatospora phosalacinea; counts= 3; multicellularity status: TRUE**

- AB_hydrolase->CASPASE+VMAP-M2+VMAP-C->MoxR->vWA+CASPASE+TCAD6+cNMP_cyclase+Antibiotic_NAT*->
- Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Coiled-coil+TIR+FxsC_Cter(partial)*->
- Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+CASPASE+TCAD14+PIN+CCCH(ZNR)+FHA*->

■ **GCF_000720325.1; Streptomyces sp. NRRL B-1347; counts= 3; multicellularity status: TRUE**

- DUF397->||<-?||Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->
- Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+HAD*->
- Trypco1->Trypsin+VMAP-M8+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->

■ **GCF_001418335.1; Streptomyces aurantiacus; counts= 3; multicellularity status: TRUE**

- EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->FXSXX-COOH-like->METALLOPROTEASE+TPRs->AB_hydrolase->CASPASE+EAD2->
- Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->
- Trypsin+EAD2->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs||Trypco1->

■ **GCF_001434355.1; Streptomyces anulatus; counts= 3; multicellularity status: TRUE**

- AB_hydrolase->CASPASE+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->
- EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->AB_hydrolase->CASPASE+EAD2->FXSXX-COOH-like->METALLOPROTEASE+TPRs->
- Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->

■ **GCA_001578075.1; Microcystis aeruginosa; counts= 3; multicellularity status: TRUE**

- AB_hydrolase->CASPASE+VMAP-M14+VMAP-C->MoxR->vWA+FGS-fold_domain*->
- HTH+VMAP-M9+VMAP-C->MoxR->vWA+FGS-fold_domain*->?->?->FGS-fold_domain->
- Trypco1->Trypsin+VMAP-M1+VMAP-C->MoxR->vWA+FGS-fold_domain*->

■ **GCF_001552135.1; Actinomadura chibensis; counts= 3; multicellularity status: TRUE**

- AB_hydrolase->BTLCP+VMAP-M0+VMAP-C->MoxR->vWA+Integrin_beta(vWA)*->
- Radical_SAM->METALLOPROTEASE+TPRs->||<-TIR+APATPase+TPRs||FXSXX-COOH->?->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->cNMP_cyclase+EAD2->
- Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH*->?->||<-?<-?<-?||?->?->DUF397->

■ **GCF_001895325.1; Microcystis aeruginosa; counts= 3; multicellularity status: TRUE**

- AB_hydrolase->CASPASE+VMAP-M14+VMAP-C->MoxR->vWA+FGS-fold_domain*->
- HTH+VMAP-M9+VMAP-C->MoxR->vWA+FGS-fold_domain*->
- Trypco1->Trypsin+VMAP-M1+VMAP-C->MoxR->vWA+FGS-fold_domain*->

■ **GCF_001905525.1; Streptomyces sp. TSRI0395; counts= 3; multicellularity status: TRUE**

- AB_hydrolase->CASPASE+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->
- EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->AB_hydrolase->CASPASE+EAD2->FXSXX-COOH-like->METALLOPROTEASE+TPRs->
- Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->

- **GCF_002019855.1; Streptomyces antibioticus; counts= 3; multicellularity status: TRUE**
  - AB_hydrolase->CASPASE+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+REase+cNMP_cyclase+CASPASE*->
  - EAD2+VMAP-M0+VMAP-C->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like<-PSE||METALLOPROTEASE+TPRs->
  - TCAD9+Pkinase+NACHT+HEAT_repeats->EAD2+VMAP-M0+VMAP-C->vWA->MoxR->vWA+APATPase+TPRs*->
- **GCA_002021875.1; Streptomyces hygroscopicus; counts= 3; multicellularity status: TRUE**
  - AB_hydrolase->CASPASE+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->
  - PNP_UDP_1+EAD2->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs
  - SIR2->||<-?<-?||Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ZNR+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->Porphobil_deam+Porphobil_deamC->
- **GCA_000018105.1; Acaryochloris marina MBIC11017; counts= 2; multicellularity status: TRUE**
  - FGS-fold_domain->||<-?||PNP_UDP_1+VMAP-M1+VMAP-C->MoxR->vWA+VMAP-C+FGS-fold_domain*->FGS-fold_domain->||<-PSE||FGS-fold_domain->
  - Trypco1->Trypsin+VMAP-M1+VMAP-C->MoxR->vWA+FGS-fold_domain*->FGS-fold_domain->FGS-fold_domain->
- **GCA_000092985.1; Nocardiopsis dassonvillei subsp. dassonvillei DSM 43111; counts= 2; multicellularity status: TRUE**
  - Trypsin+EAD2->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-DUF397
  - Trypsin+VMAP-M0+VMAP-C->vWA+APATPase+wHTH+TPRs*->||<-DUF397||Trypco1->
- **GCA_000316665.1; Rivularia sp. PCC 7116; counts= 2; multicellularity status: TRUE**
  - EAD1+Trypsin->EAD1+VMAP-M1+VMAP-C->MoxR->vWA+FGS-fold_domain*->FGS-fold_domain->
  - EAD1+VMAP-M1+VMAP-C->MoxR->?->vWA+FGS-fold_domain*->FGS-fold_domain->
- **GCA_000317435.1; Calothrix sp. PCC 6303; counts= 2; multicellularity status: TRUE**
  - <-MoxR<-EAD10+VMAP-M1+VMAP-C<-CASPASE<-?||EAD10+VMAP-M1+VMAP-C->MoxR->vWA+MNS+CASPASE+MNS*->
  - <-vWA+MNS+CASPASE+MNS<-MoxR<-EAD10+VMAP-M1+VMAP-C||?->CASPASE->EAD10+VMAP-M1+VMAP-C->MoxR->vWA+AP-GTPase+COR*->
- **GCA_000400635.2; Amycolatopsis orientalis HCCB10007; counts= 2; multicellularity status: TRUE**
  - AB_hydrolase->CASPASE+VMAP-M0+VMAP-C->MoxR->vWA+GCV_H+HTH+cNMP_cyclase+cNMP_cyclase+TIR+CASPASE*->
  - VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like<-cNMP_binding+HTH_Crp_2
- **GCA_000739105.1; Streptomyces lividans TK24; counts= 2; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->Trypco1->
  - Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+wHTH+TPRs+cNMP_cyclase*->
- **GCA_000772045.1; Streptomyces sp. CCM_MD2014; counts= 2; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->Trypco1->
  - EAD2+VMAP-M0+VMAP-C->vWA*->
- **GCA_001040905.1; Streptomyces sp. PBH53; counts= 2; multicellularity status: TRUE**
  - TCAD15->Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH-like->
  - Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+wHTH+cNMP_cyclase+Band7+HAD*->
- **GCA_001278075.1; Streptomyces pristinaespiralis; counts= 2; multicellularity status: TRUE**
  - Trypco1->Trypsin+VMAP-M7+VMAP-C->MoxR->vWA+Tubulin*->

- VMAP-C->MoxR->vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats*->

■ **GCA_001447075.1; Streptomyces hygroscopicus subsp. limoneus; counts= 2; multicellularity status: TRUE**

- TCAD15->Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH-like->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+cNMP_cyclase+Band7+HAD*->

■ **GCA_001484565.1; Streptomyces sp. CdTB01; counts= 2; multicellularity status: TRUE**

- <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+cNMP_cyclase+Band7+HAD*->

■ **GCA_001611795.1; Streptomyces sp. S10(2016); counts= 2; multicellularity status: TRUE**

- EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->AB_hydrolase->CASPASE+EAD2->FXSXX-COOH-like->METALLOPROTEASE+TPRs->
- Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD*->

■ **GCA_001877055.1; Nocardiopsis dassonvillei; counts= 2; multicellularity status: TRUE**

- Trypsin+EAD2->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-DUF397
- Trypsin+VMAP-M0+VMAP-C->vWA+APATPase+wHTH+TPRs*->||<-DUF397||Trypco1->

■ **GCA_001941845.1; Streptomyces sp. TN58; counts= 2; multicellularity status: TRUE**

- <-TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- AB_hydrolase->CASPASE+VMAP-M0+VMAP-C->MoxR->vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats*->

■ **GCA_001983975.1; Streptomyces autolyticus; counts= 2; multicellularity status: TRUE**

- AB_hydrolase->CASPASE+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->
- PNP_UDP_1+EAD2->?->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like

■ **GCA_002007685.1; Streptomyces sp. fd1-xmd; counts= 2; multicellularity status: TRUE**

- <-TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- AB_hydrolase->CASPASE+VMAP-M0+VMAP-C->MoxR->vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats*->

■ **GCA_002082195.1; Streptomyces gilvosporeus; counts= 2; multicellularity status: TRUE**

- EAD2+VMAP-M0+VMAP-C->vWA*->
- Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->

■ **GCA_002090335.1; Streptomyces sp. MOE7; counts= 2; multicellularity status: TRUE**

- <-TCAD15||Trypco1->PSE->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->TIR+APATPase+TPRs->
- EAD2+VMAP-M0+VMAP-C->vWA(partial)->vWA*->

■ **GCA_002355495.1; Streptomyces laurentii; counts= 2; multicellularity status: TRUE**

- <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- AB_hydrolase->CASPASE+VMAP-M2+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs+cNMP_cyclase+NaeI*->

■ **GCA_000091305.1; Streptomyces scabiei 87.22; counts= 2; multicellularity status: TRUE**

- TCAD9+Pkinase+NACHT+HEAT_repeats->EAD2+VMAP-M0+VMAP-C->vWA->MoxR->vWA+APATPase+TPRs*->

- TCAD9+Pkinase+NACHT+HEAT_repeats->EAD2+VMAP-M0+VMAP-C->vWA*->MoxR->vWA+APATPase+TPRs->

■ **GCA_001013905.1; Streptomyces leeuwenhoekii; counts= 2; multicellularity status: TRUE**

- <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- VMAP-M2+VMAP-C->MoxR->vWA+Pkinase+NUDIX*->

■ **GCA_001406115.1; Streptomyces venezuelae; counts= 2; multicellularity status: TRUE**

- AB_hydrolase->CASPASE+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->
- EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-Na_H_Exchanger||AB_hydrolase->CASPASE+EAD2->FXSXX-COOH-like->METALLOPROTEASE+TPRs->

■ **GCA_001511815.1; Streptomyces reticuli; counts= 2; multicellularity status: TRUE**

- TCAD15->Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH-like->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+wHTH+cNMP_cyclase+Band7+HAD*->

■ **GCA_000169095.1; Lyngbya sp. PCC 8106; counts= 2; multicellularity status: TRUE**

- EAD4+VMAP-M3+VMAP-C->MoxR->vWA+FGS-fold_domain*->FGS-fold_domain->
- vWA+CASPASE*->

■ **GCA_000158915.1; Streptomyces himastatinicus ATCC 53653; counts= 2; multicellularity status: TRUE**

- EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like
- SIR2->||<-?<-?<-?<-PSE||Trypco1->PSE->MoxR->vWA+Pkinase+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->Porphobil_deam+Porphobil_deamC->

■ **GCA_000177175.2; Streptomyces sp. ACT-1; counts= 2; multicellularity status: TRUE**

- AB_hydrolase->CASPASE+VMAP-M2+VMAP-C->MoxR->vWA+TIR+FxsC_Cter*->
- AB_hydrolase->CASPASE+VMAP-M2+VMAP-C->MoxR->vWA+TPRs+TIR+FxsC_Cter(partial)*->

■ **GCA_000239075.2; Streptomyces sp. W007; counts= 2; multicellularity status: TRUE**

- <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->Radical_SAM->TIR+APATPase+TPRs->
- EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->AB_hydrolase->CASPASE+EAD2->METALLOPROTEASE+TPRs->

■ **GCA_000297155.2; Streptomyces tsukubensis NRRL18488; counts= 2; multicellularity status: TRUE**

- vWA+Pkinase*->
- vWA+TPRs*->

■ **GCA_000331185.1; Streptomyces rimosus subsp. rimosus ATCC 10970; counts= 2; multicellularity status: TRUE**

- <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA*->
- vWA+wHTH+TPRs+wHTH+TPRs+APATPase+wHTH+TPRs*->

■ **GCA_000403665.1; Streptomyces lividans 1326; counts= 2; multicellularity status: TRUE**

- <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA*->?->?->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->Trypco1->
- Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase*->

■ **GCA_000411315.1; Streptomyces sp. HGB0020; counts= 2; multicellularity status: TRUE**

- <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->

- Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+cNMP_cyclase+Band7+HAD*->

■ **GCA_000497425.1; Streptomyces niveus NCIMB 11891; counts= 2; multicellularity status: TRUE**

- <-TCAD15||PSE->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- Trypco2->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+TPRs*->

■ **GCA_000497445.1; Streptomyces roseochromogenus subsp. oscitans DS 12.976; counts= 2; multicellularity status: TRUE**

- EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like
- TCAD15->Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->PSE->PSE->TIR+APATPase+TPRs->

■ **GCA_000612545.1; Streptomyces sp. PCS3-D2; counts= 2; multicellularity status: TRUE**

- AB_hydrolase->CASPASE+VMAP-M0+VMAP-C->MoxR->vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats*->
- AB_hydrolase->CASPASE+VMAP-M2+VMAP-C->MoxR->vWA+TIR+FxsC_Cter*->

■ **GCA_000955965.1; Streptomyces variegatus; counts= 2; multicellularity status: TRUE**

- EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->AB_hydrolase->CASPASE+EAD2->FXSXX-COOH-like->METALLOPROTEASE+TPRs->
- Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD*->

■ **GCA_001047335.1; Streptomyces regensis; counts= 2; multicellularity status: TRUE**

- Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH-like->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+cNMP_cyclase+Band7+HAD*->

■ **GCA_000972705.2; Limnoraphis robusta CS-951; counts= 2; multicellularity status: TRUE**

- FGS-fold_domain->||<-?<-?||EAD4+VMAP-M3+VMAP-C->MoxR->vWA_protein*->
- FGS-fold_domain->||<-?<-?||EAD4+VMAP-M3+VMAP-C->MoxR->vWA+FGS-fold_domain*->?->FGS-fold_domain->

■ **GCA_001189015.1; Streptomyces acidiscabies; counts= 2; multicellularity status: TRUE**

- <-TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->?->vWA+Pkinase+wHTH+cNMP_cyclase+Band7+HAD*->

■ **GCA_001270515.1; Streptomyces viridochromogenes; counts= 2; multicellularity status: TRUE**

- EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->AB_hydrolase->CASPASE+EAD2->FXSXX-COOH-like->METALLOPROTEASE+TPRs->
- Trypco2->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA_protein*->

■ **GCA_001270565.1; Streptomyces virginiae; counts= 2; multicellularity status: TRUE**

- <-TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats*->

■ **GCA_001270635.1; Streptomyces antibioticus; counts= 2; multicellularity status: TRUE**

- TCAD15->Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH-like->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+cNMP_cyclase+Band7+HAD*->

■ **GCA_001279065.1; Streptomyces rimosus subsp. rimosus; counts= 2; multicellularity status: TRUE**

- <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->Radical_SAM->TIR+APATPase+TPRs->

- Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+wHTH+TPRs+wHTH+TPRs+APATPase+wHTH+TPRs*->||<-AB_hydrolase

■ **GCA_001279365.1; Streptomyces sp. NRRL F-5755; counts= 2; multicellularity status: TRUE**

- <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->Radical_SAM->TIR+APATPase+TPRs->TIR+APATPase+TPRs->
- Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+wHTH+TPRs+wHTH+TPRs+APATPase+wHTH+TPRs*->||<-AB_hydrolase

■ **GCA_001279345.1; Streptomyces rimosus subsp. pseudoverticillatus; counts= 2; multicellularity status: TRUE**

- <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->Radical_SAM->TIR+APATPase+TPRs->
- Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+wHTH+TPRs+wHTH+TPRs+APATPase+wHTH+TPRs*->||<-AB_hydrolase

■ **GCA_001279625.1; Streptomyces sp. WM6368; counts= 2; multicellularity status: TRUE**

- <-TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->
- AB_hydrolase->CASPASE+VMAP-M0+VMAP-C->MoxR->vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats*->

■ **GCA_001279775.1; Streptomyces sp. MMG1533; counts= 2; multicellularity status: TRUE**

- EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-Na_H_Exchanger||AB_hydrolase->CASPASE+EAD2->FXSXX-COOH-like->METALLOPROTEASE+TPRs->
- vWA+APATPase+Trypsin+TIR+FxsC_Cter(partial)*->||<-DUF397

■ **GCA_001279935.1; Streptomyces sp. IGB124; counts= 2; multicellularity status: TRUE**

- <-TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->
- AB_hydrolase->CASPASE+VMAP-M0+VMAP-C->MoxR->vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats*->

■ **GCA_001279855.1; Streptomyces sp. XY58; counts= 2; multicellularity status: TRUE**

- <-TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->
- AB_hydrolase->CASPASE+VMAP-M2+VMAP-C->MoxR->vWA+CASPASE+TCAD12*->

■ **GCA_001280045.1; Streptomyces sp. NRRL WC-3723; counts= 2; multicellularity status: TRUE**

- TCAD15->Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH-like->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+cNMP_cyclase+Band7+HAD*->

■ **GCA_001279555.1; Micromonospora sp. NRRL B-16802; counts= 2; multicellularity status: TRUE**

- CASPASE+TPRs->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-Radical_SAM<-FXSXX-COOH-like
- EAD2+VMAP-M0+VMAP-C->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs

■ **GCA_001298555.1; Actinobacteria bacterium OV450; counts= 2; multicellularity status: NA**

- <-TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-Na_H_Exchanger||AB_hydrolase->CASPASE+EAD2->METALLOPROTEASE+TPRs->

■ **GCA_001314865.1; Phormidesmis priestleyi Ana; counts= 2; multicellularity status: TRUE**

- EAD1+Trypsin->?->EAD1+VMAP-M1+VMAP-C->MoxR->vWA+FGS-fold_domain*->FGS-fold_domain->FGS-fold_domain->
- Trypco1->Trypsin+VMAP-M1+VMAP-C->MoxR->vWA+FGS-fold_domain*->FGS-fold_domain->||<-RVT_1<-four_helix_bundle_protein

■ **GCA_001514035.1; Streptomyces yokosukanensis; counts= 2; multicellularity status: TRUE**

- TCAD15->Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->

- Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->

■ **GCA_001514065.1; Streptomyces antibioticus; counts= 2; multicellularity status: TRUE**

- DRHyd+VMAP-M0+VMAP-C->MoxR->vWA+TIR+APATPase+wHTH+TPRs*->
- Trypco1->PSE->MoxR->vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD*->

■ **GCA_001514125.1; Streptomyces longwoodensis; counts= 2; multicellularity status: TRUE**

- <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD*->

■ **GCA_001595515.1; Streptomyces sp. CC71; counts= 2; multicellularity status: TRUE**

- Trypco1->MoxR->vWA+Pkinase+wHTH+TPRs+cNMP_cyclase*->
- vWA+APATPase+wHTH+TPRs*->||<-Na_H_Exchanger

■ **GCA_001854645.1; Frankia sp. EUN1h; counts= 2; multicellularity status: TRUE**

- EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs->||<-?||EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs
- EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-?||EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs->||<-METALLOPROTEASE+TPRs

■ **GCA_000980885.2; Streptomyces malaysiense; counts= 2; multicellularity status: TRUE**

- Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+cNMP_cyclase+Band7+HAD*->
- Trypco2->EAD2+VMAP-M0+VMAP-C->vWA+APATPase+wHTH+TPRs*->||<-PSE<-FXSXX-COOH-like<-Trypsin+EAD2

■ **GCA_001905065.1; Saccharothrix sp. CB00851; counts= 2; multicellularity status: TRUE**

- EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like
- EAD2+VMAP-M0+VMAP-C->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-cNMP_cyclase+EAD2

■ **GCA_001905025.1; Streptomyces sp. CB03578; counts= 2; multicellularity status: TRUE**

- <-cNMP_binding+HTH_Crp_2<-?||EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-Na_H_Exchanger||AB_hydrolase->CASPASE+EAD2->FXSXX-COOH-like->METALLOPROTEASE+TPRs->
- <-TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->

■ **GCA_001905855.1; Streptomyces sp. CB01883; counts= 2; multicellularity status: TRUE**

- EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->AB_hydrolase->CASPASE+EAD2->FXSXX-COOH-like->METALLOPROTEASE+TPRs->
- Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+wHTH+cNMP_cyclase+Band7+HAD*->

■ **GCA_001905725.1; Streptomyces sp. CB02400; counts= 2; multicellularity status: TRUE**

- EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->FXSXX-COOH-like->METALLOPROTEASE+TPRs->
- Trypsin+EAD2->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-Radical_SAM<-FXSXX-COOH||Voltage_CLC->

■ **GCA_001953885.1; Streptomyces sp. IMTB 2501; counts= 2; multicellularity status: TRUE**

- EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like
- TCAD15->Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->Radical_SAM->TIR+APATPase+TPRs->

■ **GCA_001953875.1; Streptomyces amritsarensis; counts= 2; multicellularity status: TRUE**

- <-TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->

- AB_hydrolase->CASPASE+VMAP-M0+VMAP-C->MoxR->vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats*->

■ **GCA_002128465.1; Streptomyces pharetrae CZA14; counts= 2; multicellularity status: TRUE**

- <-TCAD15||PSE->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TIR+APATPase+Trypsin+HDxxH+VMAP-M0+VMAP-C*->
- Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->

■ **GCA_900091975.1; Streptomyces sp. LamerLS-31b; counts= 2; multicellularity status: TRUE**

- Trypco2->EAD2+VMAP-M0+VMAP-C->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like<-Trypsin+EAD2<-HTH_31
- VMAP-C(partial)->MoxR->vWA+Pkinase+cNMP_cyclase+Band7+HAD*->

■ **GCA_900090105.1; Micromonospora humi; counts= 2; multicellularity status: TRUE**

- EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs
- Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+Trypsin+HDxxH+VMAP-M0+VMAP-C*->?->||<-?<-?||?->DUF397->

■ **GCA_900103455.1; Streptomyces wuyuanensis; counts= 2; multicellularity status: TRUE**

- <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- ADP_ribosyl_GH->Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+FtsK+TPRs*->NUDIX->SIR2->

■ **GCA_900103585.1; Streptomyces sp. cf386; counts= 2; multicellularity status: TRUE**

- EAD2+VMAP-M0+VMAP-C->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like<-Trypsin+EAD2<-Trypco2||FXSXX-COOH-like->METALLOPROTEASE+TPRs->
- Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD*->

■ **GCA_900104935.1; Streptomyces sp. 2114.2; counts= 2; multicellularity status: TRUE**

- <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->Trypco1->
- Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+wHTH+TPRs+cNMP_cyclase*->

■ **GCA_900107045.1; Amycolatopsis xylanica; counts= 2; multicellularity status: TRUE**

- <-cNMP_binding+HTH_Crp_2||cNMP_cyclase+EAD2->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs
- CASPASE+VMAP-M2+VMAP-C->MoxR->vWA+APATPase+wHTH+Pkinase*->

■ **GCA_900105465.1; Streptomyces sp. PAN_FS17; counts= 2; multicellularity status: TRUE**

- AB_hydrolase->CASPASE+EAD2+VMAP-M0+VMAP-C->MoxR->vWA_protein*->vWA+TIR+FxsC_Cter->
- Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD*->

■ **GCA_900105515.1; Streptomyces sp. 2131.1; counts= 2; multicellularity status: TRUE**

- <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+CASPASE+NACHT+PIN*->

■ **GCA_900105945.1; Amycolatopsis tolypomycina; counts= 2; multicellularity status: TRUE**

- cNMP_cyclase+EAD2->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like
- HTH+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH*->

■ **GCA_900105245.1; Streptomyces sp. 1222.5; counts= 2; multicellularity status: TRUE**

- EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-Na_H_Exchanger||AB_hydrolase->CASPASE+EAD2->FXSXX-COOH-like->METALLOPROTEASE+TPRs->

- Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+wHTH+cNMP_cyclase+Band7+HAD*->

■ **GCA_900105605.1; Streptomyces sp. 2231.1; counts= 2; multicellularity status: TRUE**

- EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-Na_H_Exchanger||AB_hydrolase->CASPASE+EAD2->FXSXX-COOH-like->METALLOPROTEASE+TPRs->
- Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+wHTH+cNMP_cyclase+Band7+HAD*->

■ **GCA_900105275.1; Streptomyces sp. KS_5; counts= 2; multicellularity status: TRUE**

- Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD*->
- vWA+APATPase+wHTH+TPRs*->?->||<-?<-?<-S1COLD

■ **GCA_900104815.1; Streptomyces misionensis; counts= 2; multicellularity status: TRUE**

- Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+cNMP_cyclase+Band7+HAD*->
- Trypco2->EAD2+VMAP-M0+VMAP-C->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like<-Trypsin+EAD2

■ **GCA_900105525.1; Streptomyces sp. 2314.4; counts= 2; multicellularity status: TRUE**

- <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->TIR+APATPase+TPRs->
- Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->

■ **GCA_900108175.1; Actinomadura echinospora; counts= 2; multicellularity status: TRUE**

- Radical_SAM->METALLOPROTEASE+TPRs->||<-TIR+APATPase+TPRs||FXSXX-COOH-like->?->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-Radical_SAM<-FXSXX-COOH
- Trypco1->Trypsin+VMAP-M8+VMAP-C->MoxR->vWA+BetaPropeller+SWACOS+STAND_NTPase*->

■ **GCA_900110755.1; Streptomyces sp. yr375; counts= 2; multicellularity status: TRUE**

- <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->
- Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+wHTH+cNMP_cyclase+Band7+HAD*->

■ **GCA_900115095.1; Actinomadura madurae; counts= 2; multicellularity status: TRUE**

- Radical_SAM->||<-TIR+APATPase+TPRs||?->SWACOS->?->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-Radical_SAM<-?||cNMP_cyclase+EAD2->
- Trypco1->Trypsin+VMAP-M8+VMAP-C->MoxR->vWA+FtsK+FtsK+FtsK*->

■ **GCA_900114955.1; Streptomyces sp. cf124; counts= 2; multicellularity status: TRUE**

- Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+GGDEF+EAD2+VMAP-M0->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->
- Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+GGDEF+EAD2+VMAP-M0*->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs->

■ **GCA_900115955.1; Lentzea waywayandensis; counts= 2; multicellularity status: TRUE**

- <-cNMP_binding+HTH_Crp_2||cNMP_cyclase+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like
- AB_hydrolase->BTLCP+VMAP-M2+VMAP-C->MoxR->vWA+CASPASE+NACHT+TPRs*->

■ **GCA_900079405.3; Streptomyces sp. F-1; counts= 2; multicellularity status: TRUE**

- Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+cNMP_cyclase+Band7+HAD*->
- Trypco2->tRNA->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like<-Trypsin+EAD2

■ **GCA_000330925.1; Microcystis aeruginosa; counts= 2; multicellularity status: TRUE**

- HTH+VMAP-M9+VMAP-C->MoxR->vWA+FGS-fold_domain*->||<-?||?->?->PSE->FGS-fold_domain->

- Trypco1->Trypsin+VMAP-M1+VMAP-C->MoxR->vWA+FGS-fold_domain*->

■ **GCA_000312725.1; Microcystis aeruginosa; counts= 2; multicellularity status: TRUE**

- AB_hydrolase->CASPASE+VMAP-M14+VMAP-C->MoxR->vWA+FGS-fold_domain*->
- vWA+FGS-fold_domain*->

■ **GCA_000312245.1; Microcystis aeruginosa; counts= 2; multicellularity status: TRUE**

- AB_hydrolase->PSE->MoxR->vWA+FGS-fold_domain*->
- Trypsin+VMAP-M1+VMAP-C->MoxR->vWA+FGS-fold_domain*->

■ **GCA_000163875.1; Streptomyces clavuligerus; counts= 2; multicellularity status: TRUE**

- <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->?->vWA+TPRs*->
- Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+wHTH+TPRs+wHTH+TPRs+APATPase+wHTH+TPRs*->

■ **GCA_000332625.1; Streptomyces viridochromogenes; counts= 2; multicellularity status: TRUE**

- Trypsin+EAD2->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like
- vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD*->

■ **GCA_000312285.1; Microcystis aeruginosa; counts= 2; multicellularity status: TRUE**

- AB_hydrolase->CASPASE+VMAP-M14+VMAP-C->MoxR->vWA+FGS-fold_domain*->
- HTH+VMAP-M9+VMAP-C->MoxR->vWA+FGS-fold_domain*->PSE->FGS-fold_domain->

■ **GCA_000280865.1; Streptomyces auratus; counts= 2; multicellularity status: TRUE**

- <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->TIR+APATPase+TPRs->
- Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->?->PSE->vWA+TPRs*->||<-AB_hydrolase

■ **GCA_000211815.1; Moorea producens; counts= 2; multicellularity status: TRUE**

- AB_hydrolase->CASPASE+VMAP-M14+VMAP-C->MoxR->vWA+FGS-fold_domain*->FGS-fold_domain->four_helix_bundle_protein->FGS-fold_domain->four_helix_bundle_protein->
- EAD1+Trypsin->EAD1+VMAP-M1+Calcineurin-like->EAD1+VMAP-M1+VMAP-C->MoxR->vWA+TPRs+CASPASE*->

■ **GCF_000332095.2; Leptolyngbya sp. PCC 6406; counts= 2; multicellularity status: TRUE**

- EAD1+Trypsin->?->EAD1+VMAP-C->MoxR->vWA+FGS-fold_domain*->four_helix_bundle_protein->PSE->?->RVT_1->FGS-fold_domain->
- FGS-fold_domain->||<-?||?->?->PNP_UDP_1+VMAP-M1+VMAP-C->MoxR->vWA+FGS-fold_domain*->||<-PSE||?->||<-?||?->FGS-fold_domain->FGS-fold_domain->

■ **GCA_900236475.1; Streptomyces chartreusis; counts= 2; multicellularity status: TRUE**

- EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-Na_H_Exchanger||AB_hydrolase->CASPASE+EAD2->FXSXX-COOH-like->METALLOPROTEASE+TPRs->
- Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+cNMP_cyclase+Band7+HAD*->

■ **GCF_000203835.1; Streptomyces coelicolor; counts= 2; multicellularity status: TRUE**

- <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->Trypco1->
- Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+wHTH+TPRs+cNMP_cyclase*->

■ **GCA_000010625.1; Microcystis aeruginosa; counts= 2; multicellularity status: TRUE**

- HTH+VMAP-M9+VMAP-C->VMAP-C(partial)->MoxR->vWA+FGS-fold_domain*->?->?->?->FGS-fold_domain->

- Trypco1->||<-?||Trypsin+VMAP-M1+VMAP-C->PSE->?->vWA+FGS-fold_domain*->

■ **GCA_000024025.1; Catenulispora acidiphila; counts= 2; multicellularity status: TRUE**

- AB_hydrolase->CASPASE+VMAP-M0+VMAP-C->MoxR->vWA+TPRs+CASPASE*->
- Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->?->Radical_SAM->

■ **GCA_000177195.2; Streptomyces; counts= 2; multicellularity status: TRUE**

- AB_hydrolase->CASPASE+VMAP-M2+VMAP-C->MoxR->vWA+SFII-helicase+Z1*->
- EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->AB_hydrolase->CASPASE+EAD2->FXSXX-COOH-like->METALLOPROTEASE+TPRs->

■ **GCA_000147815.3; Streptomyces violaceusniger; counts= 2; multicellularity status: TRUE**

- ADP_ribosyl_GH->SIR2->||<-?<-?||Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ZNR+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->Porphobil_deam+Porphobil_deamC->
- PNP_UDP_1+EAD2->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs

■ **GCA_000245355.1; Streptomyces hygroscopicus; counts= 2; multicellularity status: TRUE**

- TCAD15->Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH-like->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+cNMP_cyclase+Band7+HAD*->

■ **GCA_001886595.1; Streptomyces venezuelae; counts= 2; multicellularity status: TRUE**

- <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+wHTH+TPRs+wHTH+TPRs+APATPase+wHTH+TPRs*->

■ **GCF_000340945.1; Nocardiopsis synnemataformans; counts= 2; multicellularity status: TRUE**

- Trypsin+EAD2->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-DUF397
- Trypsin+VMAP-M0+VMAP-C->vWA+APATPase+wHTH+TPRs*->||<-DUF397||Trypco1->

■ **GCF_000341065.1; Nocardiopsis halotolerans; counts= 2; multicellularity status: TRUE**

- Trypsin+EAD2->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-DUF397
- Trypsin+VMAP-M0+VMAP-C->vWA+APATPase+wHTH+TPRs*->||<-DUF397||Trypco1->

■ **GCF_000341105.1; Nocardiopsis potens; counts= 2; multicellularity status: TRUE**

- Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-DUF397
- Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-DUF397||Trypco1->

■ **GCF_000341145.1; Nocardiopsis xinjiangensis; counts= 2; multicellularity status: TRUE**

- Trypsin+EAD2->EAD2+VMAP-M0+VMAP-C->MoxR->vWA*->Trypco1->
- Trypsin+VMAP-M0+VMAP-C->vWA+APATPase+wHTH+TPRs*->||<-DUF397||Trypco1->

■ **GCF_000341025.1; Nocardiopsis salina; counts= 2; multicellularity status: TRUE**

- EAD2+VMAP-M0+VMAP-C->MoxR->vWA*->Trypco1->
- Trypsin+VMAP-M0+VMAP-C->vWA+APATPase+wHTH+TPRs*->||<-DUF397||Trypco1->

■ **GCA_001445835.1; Streptomyces vitaminophilus; counts= 2; multicellularity status: TRUE**

- AB_hydrolase->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-CASPASE+EAD2

- Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->

■ **GCF_000373565.1; Streptomyces sp. HmicA12; counts= 2; multicellularity status: TRUE**

- EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->AB_hydrolase->CASPASE+EAD2->FXSXX-COOH-like->METALLOPROTEASE+TPRs->
- Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+EAD2+Band7+HAD*->

■ **GCF_000373625.1; Streptomyces sp. LaPpAH-108; counts= 2; multicellularity status: TRUE**

- Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->
- Trypsin+EAD2->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like||Trypco1->

■ **GCF_000377165.1; Streptomyces sp. CNY243; counts= 2; multicellularity status: TRUE**

- <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->TIR+APATPase+TPRs->
- Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->

■ **GCF_000381685.1; Nocardiopsis sp. CNS-639; counts= 2; multicellularity status: TRUE**

- Trypsin+EAD2->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-DUF397
- Trypsin+VMAP-M0+VMAP-C->vWA+APATPase+wHTH+TPRs*->||<-DUF397||Trypco1->

■ **GCF_000468475.2; Actinomadura madurae; counts= 2; multicellularity status: TRUE**

- Radical_SAM->||<-TIR+APATPase+TPRs||SWACOS->?->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-Radical_SAM<-?||cNMP_cyclase+EAD2->||<-?<-?||cNMP_binding+HTH_Crp_2->
- Trypco1->Trypsin+VMAP-M8+VMAP-C->MoxR->vWA+FtsK+FtsK+FtsK*->

■ **GCF_000376565.1; Streptomyces hokutonensis; counts= 2; multicellularity status: TRUE**

- TIR+EAD2->EAD2+VMAP-M10+VMAP-C->MoxR->vWA+APATPase+Trypsin+TIR+FxsC_Cter(partial)*->
- Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->

■ **GCF_000377125.1; Streptomyces sp. CNS335; counts= 2; multicellularity status: TRUE**

- <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->TIR+APATPase+TPRs->
- Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->

■ **GCF_000425065.1; Actinomadura rifamycini; counts= 2; multicellularity status: TRUE**

- Radical_SAM->METALLOPROTEASE+TPRs->||<-TIR+APATPase+TPRs||?->?->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-FXSXX-COOH-like||cNMP_cyclase+EAD2->
- Trypco1->Trypsin+VMAP-M8+VMAP-C->MoxR->vWA+FtsK+FtsK+cNMP_cyclase+FtsK*->

■ **GCF_000424805.1; Streptomyces sp. CNQ865; counts= 2; multicellularity status: TRUE**

- <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->TIR+APATPase+TPRs->
- Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->

■ **GCA_000707945.1; Streptomyces; counts= 2; multicellularity status: TRUE**

- <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->TIR+APATPase+TPRs->
- Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+wHTH+TPRs+wHTH+TPRs+APATPase+wHTH+TPRs*->||<-AB_hydrolase

■ **GCF_000717995.1; Streptomyces violaceorubidus; counts= 2; multicellularity status: TRUE**

- TCAD15->Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH-like->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->

- Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->

■ **GCF_000718785.1; Streptomyces sp. NRRL WC-3626; counts= 2; multicellularity status: TRUE**

- EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->FXSXX-COOH-like->METALLOPROTEASE+TPRs->
- Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD*->

■ **GCF_000717925.1; Streptomyces sp. NRRL S-241; counts= 2; multicellularity status: TRUE**

- <-TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->?->Radical_SAM->
- AB_hydrolase->CASPASE+VMAP-M0+VMAP-C->MoxR->vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats*->

■ **GCF_000718025.1; Streptomyces purpeofuscus; counts= 2; multicellularity status: TRUE**

- AB_hydrolase->?->||<-?||MoxR->vWA+CASPASE+TCAD6+cNMP_cyclase+Antibiotic_NAT*->
- Trypsin+EAD2->EAD2+VMAP-M10+VMAP-C->MoxR->vWA+APATPase+SWACOS+wHTH+TPRs+Beta-rich-tail*->

■ **GCA_001270585.1; Streptomyces; counts= 2; multicellularity status: TRUE**

- <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->TIR+APATPase+TPRs->
- Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+wHTH+TPRs+wHTH+TPRs+APATPase+wHTH+TPRs*->||<-AB_hydrolase

■ **GCF_000716455.1; Streptomyces; counts= 2; multicellularity status: TRUE**

- <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->TIR+APATPase+TPRs->
- Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->?->NUDIX->

■ **GCF_000720595.1; Streptomyces rimosus; counts= 2; multicellularity status: TRUE**

- Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->?->NUDIX->
- Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+wHTH+TPRs+wHTH+TPRs+APATPase+wHTH+TPRs*->||<-AB_hydrolase

■ **GCF_000720725.1; Streptomyces rimosus; counts= 2; multicellularity status: TRUE**

- <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->TIR+APATPase+TPRs->
- Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->?->NUDIX->

■ **GCF_000718935.1; Streptomyces sp. NRRL S-237; counts= 2; multicellularity status: TRUE**

- <-TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- AB_hydrolase->CASPASE+VMAP-M0+VMAP-C->MoxR->vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats*->

■ **GCF_000720115.1; Streptomyces sp. NRRL F-2580; counts= 2; multicellularity status: TRUE**

- <-TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- AB_hydrolase->CASPASE+VMAP-M0+VMAP-C->MoxR->vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats*->

■ **GCF_000719345.1; Streptomyces sp. NRRL F-2664; counts= 2; multicellularity status: TRUE**

- <-TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->
- AB_hydrolase->CASPASE+VMAP-M0+VMAP-C->MoxR->vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats*->

■ **GCF_000720795.1; Streptomyces; counts= 2; multicellularity status: TRUE**

- <-TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->

- AB_hydrolase->CASPASE+VMAP-M0+VMAP-C->MoxR->vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats*->

■ **GCF_000721535.1; Streptomyces hygroscopicus; counts= 2; multicellularity status: TRUE**

- AB_hydrolase->CASPASE+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->
- PNP_UDP_1+EAD2->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs

■ **GCF_000720215.1; Streptomyces sp. NRRL S-475; counts= 2; multicellularity status: TRUE**

- <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->Radical_SAM->TIR+APATPase+TPRs->
- Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+cNMP_cyclase+Band7+HAD*->

■ **GCF_000719855.1; Streptomyces sp. NRRL F-4474; counts= 2; multicellularity status: TRUE**

- <-TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->
- AB_hydrolase->CASPASE+VMAP-M0+VMAP-C->MoxR->vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats*->

■ **GCF_000717845.1; Streptomyces violaceoruber; counts= 2; multicellularity status: TRUE**

- <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->Trypco1->
- Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+wHTH+TPRs+cNMP_cyclase*->

■ **GCF_000720455.1; Streptomyces virginiae; counts= 2; multicellularity status: TRUE**

- <-TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- AB_hydrolase->CASPASE+VMAP-M0+VMAP-C->MoxR->vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats*->

■ **GCF_000720805.1; Streptomyces violaceoruber; counts= 2; multicellularity status: TRUE**

- AB_hydrolase->CASPASE+VMAP-M0+VMAP-C->MoxR->vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats+HAD*->
- EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->

■ **GCF_000720765.1; Streptomyces sp. NRRL S-646; counts= 2; multicellularity status: TRUE**

- <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TIR+APATPase+Trypsin+HDxxH+VMAP-M0+VMAP-C*->
- vWA+APATPase+wHTH+TPRs*->KAP_NTPase->

■ **GCF_000719605.1; Streptomyces sp. NRRL S-1813; counts= 2; multicellularity status: TRUE**

- <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->TIR+APATPase+TPRs->
- AB_hydrolase->CASPASE+VMAP-M2+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs+SFI-helicase*->

■ **GCF_000721365.1; Streptomyces sp. NRRL F-5650; counts= 2; multicellularity status: TRUE**

- <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->Trypco1->
- Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->

■ **GCF_000725555.1; Streptomyces erythrochromogenes; counts= 2; multicellularity status: TRUE**

- <-TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->?->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- AB_hydrolase->CASPASE+VMAP-M0+VMAP-C->MoxR->vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats*->

■ **GCF_000725725.1; Streptomyces xanthophaeus; counts= 2; multicellularity status: TRUE**

- <-TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->

- AB_hydrolase->CASPASE+VMAP-M0+VMAP-C->MoxR->vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats*->

■ **GCF_000716515.1; Streptomyces rimosus; counts= 2; multicellularity status: TRUE**

- <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->TIR+APATPase+TPRs->
- Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+wHTH+TPRs+wHTH+TPRs+APATPase+wHTH+TPRs*->||<-AB_hydrolase

■ **GCF_001984445.1; Streptomyces lydicus; counts= 2; multicellularity status: TRUE**

- <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->TIR+APATPase+TPRs->
- EAD2+VMAP-M0+VMAP-C->vWA*->

■ **GCF_000725495.1; Streptomyces aureus; counts= 2; multicellularity status: TRUE**

- <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- AB_hydrolase->CASPASE+VMAP-M18+VMAP-C->MoxR->vWA+DO-GTPase2*->

■ **GCF_000718315.1; Streptomyces griseofuscus; counts= 2; multicellularity status: TRUE**

- Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+cNMP_cyclase+Band7+HAD*->
- Trypco2->EAD2+VMAP-M0+VMAP-C->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-Trypsin+EAD2<-HTH_31

■ **GCF_000720255.1; Streptomyces griseus; counts= 2; multicellularity status: TRUE**

- Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+cNMP_cyclase+Band7+HAD*->
- Trypco2->?->EAD2+VMAP-M0+VMAP-C->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-Trypsin+EAD2

■ **GCF_000745675.1; Streptomyces atratus; counts= 2; multicellularity status: TRUE**

- <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->AB_hydrolase->CASPASE+EAD2->FXSXX-COOH-like->METALLOPROTEASE+TPRs->

■ **GCF_000725805.1; Streptomyces xanthophaeus; counts= 2; multicellularity status: TRUE**

- <-TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- AB_hydrolase->CASPASE+VMAP-M0+VMAP-C->MoxR->vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats*->

■ **GCF_000158915.1; Streptomyces himastatinicus; counts= 2; multicellularity status: TRUE**

- EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like
- vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-Radical_SAM<-FXSXX-COOH||?->?->||<-Trypco1

■ **GCA_000707965.1; Streptomyces rimosus; counts= 2; multicellularity status: TRUE**

- <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->TIR+APATPase+TPRs->
- Trypco1->PSE->MoxR->vWA+wHTH+TPRs+wHTH+TPRs+APATPase+wHTH+TPRs*->||<-AB_hydrolase

■ **GCF_000710405.2; Kitasatospora sp. MBT66; counts= 2; multicellularity status: TRUE**

- AB_hydrolase->CASPASE+VMAP-M2+VMAP-C->MoxR->vWA+CASPASE+TCAD6+cNMP_cyclase+Antibiotic_NAT*->
- Trypsin+EAD2->EAD2+VMAP-M10+VMAP-C->MoxR->||<-?||vWA+APATPase+SWACOS+wHTH+TPRs+Beta-rich-tail*->

■ **GCF_000981225.1; Allosalinactinospora lopnorensis; counts= 2; multicellularity status: TRUE**

- <-Trypco1||Trypsin+EAD2->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-DUF397

- Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-DUF397||Trypco1->

■ **GCA_000974985.2; Streptomyces mangrovisoli; counts= 2; multicellularity status: TRUE**

- <-vWA+CASPASE+NACHT+PIN<-MoxR<-Trypsin+HDxxH+VMAP-M0+VMAP-C<-Trypco1||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->TIR+APATPase+TPRs->
- <-vWA+TPRs<-MoxR<-Trypsin+HDxxH+VMAP-M0+VMAP-C<-Trypco1||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+CASPASE+NACHT+PIN*->

■ **GCF_001005295.1; Streptomyces yangpuensis; counts= 2; multicellularity status: TRUE**

- <-TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->PSE->PSE->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- AB_hydrolase->CASPASE+VMAP-M0+VMAP-C->MoxR->vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats*->

■ **GCF_001047325.1; Streptomyces viridochromogenes; counts= 2; multicellularity status: TRUE**

- TCAD15->Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->Radical_SAM->TIR+APATPase+TPRs->
- Trypco2->EAD2+VMAP-M0+VMAP-C->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like<-Trypsin+EAD2

■ **GCF_000302615.1; Streptomyces sp. SS; counts= 2; multicellularity status: TRUE**

- EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-Na_H_Exchanger||AB_hydrolase->CASPASE+EAD2->FXSXX-COOH-like->METALLOPROTEASE+TPRs->
- Trypco2->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->AB_hydrolase->

■ **GCF_000424945.1; Streptomyces sp. 142MFCol3.1; counts= 2; multicellularity status: TRUE**

- <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD*->?->?->?->Radical_SAM->Antibiotic_NAT->TIR+FxsC_Cter->

■ **GCF_000717915.1; Streptomyces sp. NRRL S-244; counts= 2; multicellularity status: TRUE**

- <-TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->PSE->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->

■ **GCF_000716595.1; Saccharothrix sp. NRRL B-16314; counts= 2; multicellularity status: TRUE**

- EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->?->||<-METALLOPROTEASE+TPRs
- EAD2+VMAP-M0+VMAP-C->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-cNMP_cyclase+EAD2

■ **GCF_001417675.1; Streptomyces; counts= 2; multicellularity status: TRUE**

- <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->Trypco1->
- Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->

■ **GCF_000720135.1; Streptomyces sp. NRRL S-1022; counts= 2; multicellularity status: TRUE**

- AB_hydrolase->CASPASE+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+PNP_UDP_1+APATPase+wHTH+TPRs*->
- Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+wHTH+TPRs*->

■ **GCF_000716675.1; Streptomyces; counts= 2; multicellularity status: TRUE**

- ADP_ribosyl_GH->Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->PSE->PSE->vWA+Pkinase+FtsK+TPRs*->NUDIX->
- MoxR->vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+HAD*->

■ **GCF_000717595.1; Streptomyces flavochromogenes; counts= 2; multicellularity status: TRUE**

- <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->

- Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->

■ **GCF_000717745.1; Streptomyces violens; counts= 2; multicellularity status: TRUE**

- <-TCAD15<-?||Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->TIR+APATPase+TPRs->
- Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+SWACOS+wHTH*->

■ **GCF_000725475.1; Streptomyces durhamensis; counts= 2; multicellularity status: TRUE**

- Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+TIR+APATPase+wHTH+TPRs*->
- Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD*->

■ **GCF_000785985.1; Actinoplanes utahensis; counts= 2; multicellularity status: TRUE**

- AB_hydrolase->CASPASE+EAD2->VMAP-M0+VMAP-C->MoxR->vWA+CASPASE(partial)*->
- EAD2+VMAP-M0+VMAP-C->MoxR->vWA+cNMP_cyclase+HTH+HTH+TPRs*->

■ **GCF_000716335.1; Streptomyces sp. NRRL S-118; counts= 2; multicellularity status: TRUE**

- Trypco1->MoxR->vWA+NACHT+CASPASE+BetaPropeller*->
- Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->

■ **GCF_000830005.1; Streptomyces vietnamensis; counts= 2; multicellularity status: TRUE**

- <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- AB_hydrolase->CASPASE+VMAP-M2+VMAP-C->MoxR->vWA+REase+SWACOS+TPRs+cNMP_cyclase*->

■ **GCF_000956015.1; Streptomyces sp. NRRL F-4428; counts= 2; multicellularity status: TRUE**

- AB_hydrolase->CASPASE+VMAP-M0+VMAP-C->MoxR->vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats*->
- Trypco2->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+TPRs*->

■ **GCA_000952035.2; Streptomyces lydicus; counts= 2; multicellularity status: TRUE**

- <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->TIR+APATPase+TPRs->
- Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-AB_hydrolase

■ **GCF_000962825.1; Actinoplanes rectilineatus; counts= 2; multicellularity status: TRUE**

- TIR+EAD2->METALLOPROTEASE+TPRs->EAD2+VMAP-M0+VMAP-C->vWA+APATPase+wHTH+TPRs*->
- Trypco1->Trypsin+VMAP-M8+VMAP-C->MoxR->vWA+SWACOS+TPRs*->

■ **GCF_000718305.1; Streptomyces niger; counts= 2; multicellularity status: TRUE**

- <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->Trypco1->
- Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+SWACOS+wHTH*->

■ **GCA_001267885.1; Streptomyces ambofaciens; counts= 2; multicellularity status: TRUE**

- EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-Na_H_Exchanger||AB_hydrolase->CASPASE+EAD2->FXSXX-COOH-like->PSE->METALLOPROTEASE+TPRs->
- Trypco1->Trypsin+VMAP-M0+VMAP-C->?->MoxR->vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+HAD*->

■ **GCF_001279805.1; Streptomyces sp. XY431; counts= 2; multicellularity status: TRUE**

- AB_hydrolase->CASPASE+EAD2+VMAP-C->MoxR->vWA+TPRs*->

- vWA+APATPase+SWACOS+wHTH+TPRs+Beta-rich-tail*->

■ **GCF_001279615.1; Streptomyces sp. NRRL F-7442; counts= 2; multicellularity status: TRUE**

- <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->Trypco1->PSE->?->CASPASE->
- Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->

■ **GCF_001280095.1; Streptomyces sp. NRRL F-6491; counts= 2; multicellularity status: TRUE**

- <-TCAD15||PSE->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- AB_hydrolase->CASPASE+VMAP-M2+VMAP-C->MoxR->vWA+SFII-helicase+Trypsin+cNMP_cyclase+Coiled-coil+CASPASE*->

■ **GCA_001279885.1; Streptomyces sp. XY593; counts= 2; multicellularity status: TRUE**

- AB_hydrolase->CASPASE+VMAP-M0+VMAP-C->MoxR->vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats*->
- AB_hydrolase->CASPASE+VMAP-M2+VMAP-C->MoxR->vWA+CASPASE+TCAD12*->

■ **GCA_001279525.1; Nocardia sp. NRRL S-836; counts= 2; multicellularity status: TRUE**

- <-cNMP_binding+HTH_Crp_2||cNMP_cyclase+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like
- AB_hydrolase->BTLCP+VMAP-M2+VMAP-C->MoxR->vWA+CASPASE+APATPase+TPRs*->

■ **GCA_002005225.1; Streptomyces pactum; counts= 2; multicellularity status: TRUE**

- EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->
- EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-Na_H_Exchanger||AB_hydrolase->CASPASE+EAD2->FXSXX-COOH-like->METALLOPROTEASE+TPRs->

■ **GCF_001417775.1; Streptomyces sp. TP-A0356; counts= 2; multicellularity status: TRUE**

- Trypsin+EAD2->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-Radical_SAM<-FXSXX-COOH||Voltage_CLC->
- Trypsin+VMAP-M6+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-Radical_SAM<-FXSXX-COOH-like<-Trypco1

■ **GCF_001417735.1; Streptomyces sp. NBRC 110028; counts= 2; multicellularity status: TRUE**

- AB_hydrolase->CASPASE+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->
- PNP_UDP_1+EAD2->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs

■ **GCF_001418135.1; Streptomyces aureus; counts= 2; multicellularity status: TRUE**

- vWA+Pkinase+TPRs*->
- vWA+TPRs*->FXSXX-COOH->METALLOPROTEASE+TPRs->

■ **GCF_001418655.1; Streptomyces phaeochromogenes; counts= 2; multicellularity status: TRUE**

- Trypsin+EAD2->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like||Trypco1->
- vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD*->

■ **GCA_001443625.1; Streptomyces venezuelae; counts= 2; multicellularity status: TRUE**

- AB_hydrolase->CASPASE+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->
- EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-Na_H_Exchanger||AB_hydrolase->CASPASE+EAD2->FXSXX-COOH-like->METALLOPROTEASE+TPRs->

■ **GCF_001419685.1; Streptomyces puniciscabiei; counts= 2; multicellularity status: TRUE**

- Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+DNA-primase-like_ZnR+S1+KH+KH*->

- Trypco2->EAD2+VMAP-M0+VMAP-C->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-Trypsin+EAD2

■ **GCA_001426325.1; Streptomyces; counts= 2; multicellularity status: TRUE**

- AB_hydrolase->CASPASE+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->
- Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->

■ **GCA_001424875.1; Kitasatospora sp. Root107; counts= 2; multicellularity status: TRUE**

- Trypco1->Trypsin+EAD2->EAD2+VMAP-M10+VMAP-C->MoxR->vWA+APATPase+BetaPropeller+Pkinase+wHTH+TPRs+wHTH+TPRs+FtsK*->
- Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+CASPASE+TIR+FxsC_Cter(partial)*->

■ **GCA_001484705.1; Streptomyces sp. 4F; counts= 2; multicellularity status: TRUE**

- EAD2+VMAP-M0+VMAP-C->vWA*->
- EAD2+VMAP-M0+VMAP-C->vWA*->

■ **GCA_001514055.1; Streptomyces corchorusii; counts= 2; multicellularity status: TRUE**

- TCAD15->Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH-like->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+cNMP_cyclase+Band7+HAD*->

■ **GCA_001541145.1; Streptomyces albus; counts= 2; multicellularity status: TRUE**

- <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->TIR+APATPase+TPRs->
- Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+wHTH+TPRs+wHTH+TPRs+APATPase+wHTH+TPRs*->||<-AB_hydrolase

■ **GCF_001553455.1; Streptomyces hygroscopicus; counts= 2; multicellularity status: TRUE**

- vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs
- vWA+TPRs*->

■ **GCF_001553435.1; Streptomyces hygroscopicus; counts= 2; multicellularity status: TRUE**

- AB_hydrolase->CASPASE+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->
- PNP_UDP_1+EAD2->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs

■ **GCF_000772045.1; Streptomyces sp. CCM_MD2014; counts= 2; multicellularity status: TRUE**

- <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->Trypco1->
- Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->

■ **GCF_001184025.1; Streptomyces sp. NBRC 110468; counts= 2; multicellularity status: TRUE**

- <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->Trypco1->
- DUF397->Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->

■ **GCA_001632865.1; Streptomyces ambofaciens; counts= 2; multicellularity status: TRUE**

- EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-Na_H_Exchanger||AB_hydrolase->CASPASE+EAD2->FXSXX-COOH-like->METALLOPROTEASE+TPRs->
- Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+HAD*->

■ **GCF_001640565.1; Streptomyces sp. RTd22; counts= 2; multicellularity status: TRUE**

- EAD1+Trypsin->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+BetaPropeller+CASPASE+APATPase+wHTH+TPRs+AB_hydrolase*->

- vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-Radical_SAM<-FXSXX-COOH||Voltage_CLC->PSE->||<-Trypco1

■ **GCF_001652895.1; Streptomyces sp. NBRC 109436; counts= 2; multicellularity status: TRUE**

- CASPASE+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->
- PNP_UDP_1+EAD2->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs

■ **GCA_001701025.1; Lentzea guizhouensis; counts= 2; multicellularity status: TRUE**

- <-cNMP_binding+HTH_Crp_2||cNMP_cyclase+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like
- AB_hydrolase->BTLCP+VMAP-M2+VMAP-C->MoxR->vWA+CASPASE+NACHT+TPRs*->

■ **GCF_001704635.1; Streptomyces sparsogenes; counts= 2; multicellularity status: TRUE**

- PNP_UDP_1+EAD2->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs
- Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+Pkinase*->Porphobil_deam+Porphobil_deamC->

■ **GCF_001705785.1; Streptomyces sporocinereus; counts= 2; multicellularity status: TRUE**

- AB_hydrolase->CASPASE+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->
- PNP_UDP_1+EAD2->||<-?||EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs

■ **GCF_001590865.1; Streptomyces sp. NBRC 110611; counts= 2; multicellularity status: TRUE**

- <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->TIR+APATPase+TPRs->
- Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->?->vWA+wHTH+TPRs+APATPase+wHTH+TPRs*->

■ **GCA_001513965.1; Streptomyces cellostaticus; counts= 2; multicellularity status: TRUE**

- DUF397->?->?->?->Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD*->
- Trypco2->EAD2+VMAP-M0+VMAP-C->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-Trypsin+EAD2

■ **GCA_001636945.1; Streptomyces sp. FXJ1.172; counts= 2; multicellularity status: TRUE**

- TCAD15->Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->

■ **GCF_001553475.1; Streptomyces endus; counts= 2; multicellularity status: TRUE**

- AB_hydrolase->CASPASE+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->
- PNP_UDP_1+EAD2->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs

■ **GCA_001653515.1; Streptomyces sp. ERV7; counts= 2; multicellularity status: TRUE**

- NUDIX->Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->
- vWA+TPRs*->Radical_SAM->TIR+APATPase+TPRs->

■ **GCA_002335465.1; Streptomyces olivochromogenes; counts= 2; multicellularity status: TRUE**

- ADP_ribosyl_GH->NUDIX->Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->
- Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+CASPASE+TIR+NUDIX*->

■ **GCF_001552215.1; Actinomadura macra; counts= 2; multicellularity status: TRUE**

- Trypsin+VMAP-M8+VMAP-C->MoxR->vWA+FtsK+FtsK+FtsK*->

- Trypsin+VMAP-M8+VMAP-C->MoxR->vWA+Pkinase+DO-GTPase2*->

■ **GCF_001552195.1; Actinomadura latina; counts= 2; multicellularity status: TRUE**

- Radical_SAM->||<-TIR+APATPase+TPRs||SWACOS->PSE->?->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-Radical_SAM<-?||cNMP_cyclase+EAD2->
- Trypco1->Trypsin+VMAP-M8+VMAP-C->MoxR->vWA+FtsK+FtsK+CASPASE+FtsK*->

■ **GCF_001723065.1; Streptomyces rubidus; counts= 2; multicellularity status: TRUE**

- EAD2+VMAP-M0+VMAP-C->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-Trypsin+EAD2<-Trypco2
- vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-Trypsin+EAD2<-Trypco2

■ **GCA_001729485.1; Streptomyces lydicus; counts= 2; multicellularity status: TRUE**

- <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->
- EAD2+VMAP-M0+VMAP-C->vWA*->

■ **GCF_001723075.1; Streptomyces niveus; counts= 2; multicellularity status: TRUE**

- Trypco2->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase*->
- vWA+TPRs*->FXSXX-COOH->METALLOPROTEASE+TPRs->

■ **GCF_001723055.1; Streptomyces niveus; counts= 2; multicellularity status: TRUE**

- AB_hydrolase->CASPASE+VMAP-M0+VMAP-C->MoxR->vWA+STAND_NTPase+BetaPropeller+REase(Mrr_cat-PDDEXK)*->
- Trypco2->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+TPRs*->

■ **GCF_001748165.1; Streptomyces sp. SPMA113; counts= 2; multicellularity status: TRUE**

- AB_hydrolase->CASPASE+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->
- PNP_UDP_1+EAD2->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like

■ **GCA_001767375.1; Streptomyces pactum; counts= 2; multicellularity status: TRUE**

- <-TCAD15||PSE->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->PSE->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->

■ **GCA_001854205.1; Moorea producens; counts= 2; multicellularity status: TRUE**

- AB_hydrolase->CASPASE+VMAP-M14+VMAP-C->MoxR->vWA+FGS-fold_domain*->FGS-fold_domain->four_helix_bundle_protein->
- EAD1+Trypsin->EAD1+VMAP-M1+Calcineurin-like->EAD1+VMAP-M1+VMAP-C->MoxR->vWA+FGS-fold_domain*->

■ **GCA_001866675.1; Streptomyces sp. MUSC 14; counts= 2; multicellularity status: TRUE**

- <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+cNMP_cyclase+Band7+HAD*->

■ **GCA_001866665.1; Streptomyces sp. MUSC 1; counts= 2; multicellularity status: TRUE**

- <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+cNMP_cyclase+Band7+HAD*->

■ **GCA_002368235.1; Scytonema sp. HK-05; counts= 2; multicellularity status: TRUE**

- Trypco1->Trypsin+EAD9->EAD9+EAD1+VMAP-C->MoxR->vWA+FGS-fold_domain*->||<-?||FGS-fold_domain->

- Trypco2->TCAD3+TCAD4+CASPASE+EAD1->EAD1+VMAP-M1+VMAP-C->MoxR->vWA+FGS-fold_domain*->FGS-fold_domain->

■ **GCA_001905125.1; Streptomyces sp. TSRI0281; counts= 2; multicellularity status: TRUE**

- <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->Radical_SAM->TIR+APATPase+TPRs->
- EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->AB_hydrolase->CASPASE+EAD2->FXSXX-COOH-like->METALLOPROTEASE+TPRs->

■ **GCF_001905125.1; Streptomyces sp. TSRI0281; counts= 2; multicellularity status: TRUE**

- Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+wHTH+TPRs+wHTH+TPRs+APATPase+wHTH+TPRs*->
- Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+NaeI*->

■ **GCA_001905385.1; Streptomyces sp. CB02414; counts= 2; multicellularity status: TRUE**

- EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-Na_H_Exchanger||AB_hydrolase->CASPASE+EAD2->FXSXX-COOH-like->PSE->METALLOPROTEASE+TPRs->
- Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+wHTH+TPRs+cNMP_cyclase*->

■ **GCF_001905885.1; Streptomyces sp. CB03234; counts= 2; multicellularity status: TRUE**

- AB_hydrolase->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like<-CASPASE+EAD2
- Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+wHTH+TPRs+wHTH+TPRs+APATPase+wHTH+TPRs*->

■ **GCF_001905575.1; Streptomyces sp. CB00072; counts= 2; multicellularity status: TRUE**

- <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->Radical_SAM->TIR+APATPase+TPRs->
- EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->AB_hydrolase->CASPASE+EAD2->FXSXX-COOH-like->METALLOPROTEASE+TPRs->

■ **GCF_001905845.1; Streptomyces sp. TSRI0107; counts= 2; multicellularity status: TRUE**

- EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-Na_H_Exchanger||CASPASE+EAD2->FXSXX-COOH-like->METALLOPROTEASE+TPRs->
- Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD*->

■ **GCF_001941265.1; Streptomyces acidiscabies; counts= 2; multicellularity status: TRUE**

- vWA+Pkinase+wHTH+cNMP_cyclase+Band7+HAD*->
- vWA+TIR+FxsC_Cter(partial)*->

■ **GCF_001941285.1; Streptomyces acidiscabies; counts= 2; multicellularity status: TRUE**

- vWA+Pkinase+wHTH+cNMP_cyclase+Band7+HAD*->
- vWA+TIR+FxsC_Cter(partial)*->

■ **GCA_001942465.1; Actinomadura sp. CNU-125; counts= 2; multicellularity status: TRUE**

- AB_hydrolase->BTLCP+VMAP-M2+VMAP-C->MoxR->vWA_protein*->
- Radical_SAM->PSE->||<-PSE||FXSXX-COOH-like->?->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-FXSXX-COOH-like||cNMP_cyclase+EAD2->

■ **GCA_001942495.1; Moorea bouillonii; counts= 2; multicellularity status: TRUE**

- AB_hydrolase->CASPASE+VMAP-M14+VMAP-C->MoxR->vWA+FGS-fold_domain*->FGS-fold_domain->four_helix_bundle_protein->
- EAD1+Trypsin->EAD1+VMAP-M1+Calcineurin-like->EAD1+VMAP-M1+VMAP-C->MoxR->vWA+FGS-fold_domain*->

■ **GCA_001942255.1; Nocardiopsis sp. CNR-923; counts= 2; multicellularity status: TRUE**

- Trypsin+EAD2->VMAP-C->MoxR->?->vWA_protein*->TIR+APATPase+TPRs->||<-DUF397||Trypco1->||<-PSE<-?<-PSE<-PSE<-DUF397

- Trypsin+VMAP-M8->VMAP-C->MoxR->vWA+APATPase+wHTH*->

■ **GCA_001953865.1; Amycolatopsis coloradensis; counts= 2; multicellularity status: TRUE**

- AB_hydrolase->CASPASE+VMAP-M2+VMAP-C->MoxR->vWA+TPRs*->
- cNMP_cyclase+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like<-cNMP_binding+HTH_Crp_2

■ **GCA_001970135.1; Streptomyces sp. M1013; counts= 2; multicellularity status: TRUE**

- TCAD15->Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH-like->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- Trypsin+VMAP-M6+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-Radical_SAM<-Trypco1

■ **GCA_001984155.1; Actinosynnema sp. ALI-1.44; counts= 2; multicellularity status: TRUE**

- EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like||EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like
- EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like||EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like

■ **GCA_002025445.1; Microcystis aeruginosa; counts= 2; multicellularity status: TRUE**

- AB_hydrolase->PSE->||<-PSE||EAD2+VMAP-M11+VMAP-C->MoxR->vWA+FGS-fold_domain*->
- Trypco1->||<-?||Trypsin+VMAP-M1+VMAP-C->MoxR->vWA+FGS-fold_domain*->

■ **GCF_002028385.1; Streptomyces sp. 3211; counts= 2; multicellularity status: TRUE**

- <-TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- AB_hydrolase->CASPASE+VMAP-M0+VMAP-C->MoxR->vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats*->

■ **GCF_900129855.1; Streptomyces sp. 3124.6; counts= 2; multicellularity status: TRUE**

- <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->

■ **GCA_002080455.1; Streptomyces sp. Sge12; counts= 2; multicellularity status: TRUE**

- <-TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- AB_hydrolase->CASPASE+VMAP-M0+VMAP-C->MoxR->vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats*->

■ **GCA_000012405.1; Thermobifida fusca YX; counts= 1; multicellularity status: TRUE**

- Trypsin+EAD2->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->Trypco1->

■ **GCA_000018005.1; Frankia sp. EAN1pec; counts= 1; multicellularity status: TRUE**

- EAD2+EAD1->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs

■ **GCA_000020025.1; Nostoc punctiforme PCC 73102; counts= 1; multicellularity status: TRUE**

- VMAP-M1+VMAP-C->MoxR->vWA+Calcineurin-like+SAVED*->

■ **GCA_000022045.1; Cyanothece sp. PCC 7425; counts= 1; multicellularity status: TRUE**

- <-FGS-fold_domain<-?<-?<-?||VMAP-M1+VMAP-C->MoxR->vWA*->||<-zf-IS66+DDE_Tnp_IS66<-TIR+EAD9<-?<-Trypsin<-Trypco1

■ **GCA_000024385.1; Thermomonospora curvata DSM 43183; counts= 1; multicellularity status: TRUE**

- Radical_SAM->METALLOPROTEASE+TPRs->||<-TIR+APATPase+TPRs||EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->

- **GCA_000237145.1; Actinoplanes sp. SE50/110; counts= 1; multicellularity status: TRUE**
  - EAD1+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->
- **GCA_000359525.1; Streptomyces albus J1074; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCA_000418455.1; Streptomyces rapamycinicus NRRL 5491; counts= 1; multicellularity status: TRUE**
  - PNP_UDP_1+EAD2->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like
- **GCA_000444875.1; Streptomyces collinus Tu 365; counts= 1; multicellularity status: TRUE**
  - TCAD15->Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH-like->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCA_000525635.1; Kutzneria albida DSM 43870; counts= 1; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->MoxR->?->vWA+TIR+BetaPropeller*->?->?->||<-cNMP_cyclase+EAD2||cNMP_binding+HTH_Crp_2->?->SIR2->
- **GCA_000340565.3; Nodularia spumigena CCY9414; counts= 1; multicellularity status: TRUE**
  - TIR+EAD6->EAD6+VMAP-M5->VMAP-C->MoxR->vWA+beta-rich-region+HTH+FGS-fold_domain*->four_helix_bundle_protein->RVT_1->
- **GCA_000732925.1; Amycolatopsis japonica; counts= 1; multicellularity status: TRUE**
  - cNMP_cyclase+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like<-cNMP_binding+HTH_Crp_2
- **GCA_000749465.2; Amycolatopsis lurida NRRL 2430; counts= 1; multicellularity status: TRUE**
  - cNMP_cyclase+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-?||?->||<-FXSXX-COOH-like<-cNMP_binding+HTH_Crp_2
- **GCA_000931445.1; Streptomyces cyaneogriseus subsp. noncyanogenus; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCA_001027185.1; Streptomyces incarnatus; counts= 1; multicellularity status: TRUE**
  - Trypco2->EAD2+VMAP-M0+VMAP-C->vWA+APATPase+wHTH+TPRs*->||<-FXSXX-COOH-like<-Trypsin+EAD2||?->?->?->?->DUF397->
- **GCA_001277295.1; Anabaena sp. WA102; counts= 1; multicellularity status: TRUE**
  - EAD6+VMAP-C->MoxR->vWA+FGS-fold_domain*->FGS-fold_domain->
- **GCA_001278095.1; Streptomyces sp. CFMR 7; counts= 1; multicellularity status: TRUE**
  - CASPASE+VMAP-M2+VMAP-C->MoxR->vWA+REase+SWACOS+TPRs+cNMP_cyclase*->
- **GCA_001431765.1; Streptomyces sp. FR-008; counts= 1; multicellularity status: TRUE**
  - low-complexity+HDxxH+VMAP-M0->VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->?->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCA_001577385.1; Streptomyces albus; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCA_001610855.1; Gemmata sp. SH-PL17; counts= 1; multicellularity status: FALSE**
  - <-EAD1+HD<-EAD1+Trypsin||VMAP-M21+VMAP-C->MoxR->EAD1+HD+vWA+NEFF1*->

- **GCA_001660045.1; Streptomyces parvulus; counts= 1; multicellularity status: TRUE**
  - Trypco2->EAD2+VMAP-M0+VMAP-C->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like<-Trypsin+EAD2
- **GCA_001664405.1; Rhizobium phaseoli; counts= 1; multicellularity status: TRUE**
  - EAD5+Trypsin->EAD5+VMAP-M4+VMAP-C->MoxR->vWA+REC+SLOG+CASPASE*->
- **GCA_000943515.2; Amycolatopsis orientalis; counts= 1; multicellularity status: TRUE**
  - cNMP_cyclase+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like<-cNMP_binding+HTH_Crp_2
- **GCA_001542625.2; Streptomyces griseochromogenes; counts= 1; multicellularity status: TRUE**
  - Trypco2->EAD2+VMAP-M0+VMAP-C->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-Trypsin+EAD2||?->Trypco2->
- **GCA_001750785.1; Streptomyces rubrolavendulae; counts= 1; multicellularity status: TRUE**
  - Trypco1->?->?->AB_hydrolase->CASPASE+VMAP-M2+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs+cNMP_cyclase+NaeI*->
- **GCA_002128305.1; Streptomyces sp. SCSIO 03032; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||PSE->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCA_002142475.1; Leptolyngbya boryana IAM M-101; counts= 1; multicellularity status: TRUE**
  - TIR+EAD9->EAD9+VMAP-M1+VMAP-C->MoxR->vWA+FGS-fold_domain*->
- **GCA_002368175.1; Calothrix sp. NIES-2098; counts= 1; multicellularity status: TRUE**
  - EAD8+VMAP-M1+VMAP-C->MoxR->?->vWA+MNS*->
- **GCA_002368455.1; Calothrix sp. NIES-4071; counts= 1; multicellularity status: TRUE**
  - EAD1+Trypsin->EAD1+VMAP-M1+VMAP-C->MoxR->vWA+GUN4+FGS-fold_domain*->
- **GCA_003994795.1; Cylindrospermum sp. NIES-4074; counts= 1; multicellularity status: TRUE**
  - cNMP_cyclase+VMAP-M1+VMAP-C->MoxR->vWA+Glyco_trans_4_4+Glycos_transf_1*->FGS-fold_domain->
- **GCA_001160225.1; Mycobacterium tuberculosis; counts= 1; multicellularity status: FALSE**
  - Trypco1->Trypsin+VMAP-M8+VMAP-C->MoxR->vWA+FtsK+FtsK+CASPASE+FtsK*->
- **GCA_001536285.1; Frankia sp. G2; counts= 1; multicellularity status: TRUE**
  - EAD2+EAD1->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like
- **GCA_000154885.1; Streptomyces sp. Mg1; counts= 1; multicellularity status: TRUE**
  - <-cNMP_binding+HTH_Crp_2<-?<-?||EAD2+VMAP-M0+VMAP-C->MoxR->vWA*->
- **GCA_000156455.1; Streptomyces roseosporus NRRL 15998; counts= 1; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->AB_hydrolase->CASPASE+EAD2->FXSXX-COOH-like->METALLOPROTEASE+TPRs->
- **GCA_000154945.1; Streptomyces pristinaespiralis ATCC 25486; counts= 1; multicellularity status: TRUE**
  - AB_hydrolase->CASPASE+VMAP-M2+VMAP-C->MoxR->vWA+TIR+FxsC_Cter*->||<-DUF397

- **GCA_000158895.1; Streptomyces sp. C; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCA_000152145.1; Oscillochloris trichoides DG-6; counts= 1; multicellularity status: TRUE**
  - <-CASPASE+TCAD1+TCAD2||CASPASE+TCAD1+DUF4404->VMAP-M13+VMAP-C->MoxR->vWA+TPRs*->
- **GCA_000244995.1; Burkholderiales bacterium JOSHI_001; counts= 1; multicellularity status: FALSE**
  - AB_hydrolase->CASPASE+VMAP-M15+VMAP-C->MoxR->vWA+HTH*->
- **GCA_000243495.3; Opitutaceae bacterium TAV1; counts= 1; multicellularity status: FALSE**
  - TCAD5+AB_hydrolase+TCAD7+macroglobulin-like+CASPASE->CASPASE+VMAP-C->MoxR->vWA+REC+HTH+SLOG*->
- **GCA_000262465.1; Frankia sp. QA3; counts= 1; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-?<-EAD5+TIR
- **GCA_000342005.1; Amycolatopsis decaplanina DSM 44594; counts= 1; multicellularity status: TRUE**
  - cNMP_cyclase+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like<-cNMP_binding+HTH_Crp_2
- **GCA_000342125.1; Streptomyces mobaraensis NBRC 13819 = DSM 40847; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH-like->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCA_000495635.1; Streptomyces sp. GBA 94-10; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCA_000495755.1; Streptomyces sp. PVA 94-07; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCA_000495615.1; uncultured Thiohalocapsa sp. PB-PSB1; counts= 1; multicellularity status: NA**
  - Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA_protein*->
- **GCA_000568255.1; Kutzneria sp. 744; counts= 1; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->vWA+TIR+BetaPropeller*->?->?->cNMP_binding+HTH_Crp_2->
- **GCA_001485125.1; Streptomyces scabiei; counts= 1; multicellularity status: TRUE**
  - AB_hydrolase->CASPASE+VMAP-M2+VMAP-C->MoxR->vWA+SFII-helicase+Trypsin+cNMP_cyclase+Coiled-coil+CASPASE*->||<-?<-?<-TIR+APATPase+TPRs
- **GCA_001653115.1; Streptomyces sp. F-3; counts= 1; multicellularity status: TRUE**
  - Trypsin+EAD2->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs||?->Trypco1->
- **GCA_000175415.3; Arthrospira platensis str. Paraca; counts= 1; multicellularity status: TRUE**
  - VMAP-C_protein->MoxR->vWA*->
- **GCA_000817745.1; Aphanocapsa montana BDHKU210001; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+VMAP-M1+VMAP-C->MoxR->vWA+FGS-fold_domain*->FGS-fold_domain->

- **GCA_000818195.1; Streptomyces sp. 150FB; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCA_000826685.1; Streptomonospora alba; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-Radical_SAM<-FXSXX-COOH-like
- **GCA_000876225.1; Micromonospora carbonacea; counts= 1; multicellularity status: TRUE**
  - Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->?->TIR+APATPase+TPRs->
- **GCA_000955955.1; Lechevalieria aerocolonigenes; counts= 1; multicellularity status: TRUE**
  - <-cNMP_binding+HTH_Crp_2||MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like
- **GCA_000966975.1; Streptomyces katrae; counts= 1; multicellularity status: TRUE**
  - vWA*->
- **GCA_000966985.1; Streptomyces sp. NRRL S-444; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA*->
- **GCA_001044425.1; Streptomyces roseus; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCA_001047325.1; Streptomyces viridochromogenes; counts= 1; multicellularity status: TRUE**
  - Trypco2->EAD2+VMAP-M0+VMAP-C->vWA+APATPase+wHTH+TPRs*->||<-FXSXX-COOH-like<-Trypsin+EAD2
- **GCA_001047315.1; Streptomyces leeuwenhoekii; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCA_001189025.1; Streptomyces europaeiscabiei; counts= 1; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->AB_hydrolase->CASPASE+EAD2->FXSXX-COOH-like->METALLOPROTEASE+TPRs->
- **GCA_001279025.1; Streptomyces sp. NRRL WC-3701; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+wHTH+TPRs+wHTH+TPRs+APATPase+wHTH+TPRs*->||<-AB_hydrolase
- **GCA_001279015.1; Streptomyces rimosus subsp. rimosus; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->Radical_SAM->TIR+APATPase+TPRs->
- **GCA_001279355.1; Streptomyces sp. NRRL F-4711; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->Trypco1->
- **GCA_001279725.1; Streptomyces sp. WM4235; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C->vWA+TPRs*->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCA_001279805.1; Streptomyces sp. XY431; counts= 1; multicellularity status: TRUE**
  - AB_hydrolase->CASPASE+EAD2+VMAP-C->MoxR->vWA+TPRs*->

- **GCA_001279985.1; Streptomyces sp. AS58; counts= 1; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like<-Trypsin+EAD2<-Trypco2||METALLOPROTEASE+TPRs->
- **GCA_001280005.1; Streptomyces sp. NRRL WC-3618; counts= 1; multicellularity status: TRUE**
  - MoxR->vWA+TPRs*->Radical_SAM->TIR+APATPase+TPRs->Radical_SAM->?->STAND_NTPase->TIR+APATPase+TPRs->||<-DUF397
- **GCA_001279605.1; Streptomyces sp. NRRL F-4707; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->?->?->CASPASE->
- **GCA_001279615.1; Streptomyces sp. NRRL F-7442; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->?->CASPASE->TIR+APATPase+TPRs->
- **GCA_001294335.1; Streptomyces chattanoogensis; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->TIR+APATPase+TPRs->
- **GCA_001294395.1; Streptomyces sp. NRRL WC-3753; counts= 1; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-Na_H_Exchanger||AB_hydrolase->CASPASE+EAD2->FXSXX-COOH-like->METALLOPROTEASE+TPRs->
- **GCA_001294325.1; Streptomyces sp. NRRL F-6602; counts= 1; multicellularity status: TRUE**
  - TCAD15->?->?->Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCA_001298575.1; Actinobacteria bacterium OK074; counts= 1; multicellularity status: NA**
  - NUDIX->Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->SIR2->
- **GCA_001414035.1; Frankia sp. ACN1ag; counts= 1; multicellularity status: TRUE**
  - EAD2+EAD1->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-FXSXX-COOH-like
- **GCA_001421075.1; Frankia sp. CpI1-P; counts= 1; multicellularity status: TRUE**
  - EAD2+EAD1->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like
- **GCA_001482415.1; Streptomyces silvensis; counts= 1; multicellularity status: TRUE**
  - Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->
- **GCA_001484625.1; Streptomyces kanasensis; counts= 1; multicellularity status: TRUE**
  - AB_hydrolase->CASPASE+VMAP-M2+VMAP-C->MoxR->vWA_protein*->vWA(partial)+APATPase+wHTH+cNMP_cyclase+NaeI->
- **GCA_001507455.1; Streptomyces albus subsp. albus; counts= 1; multicellularity status: TRUE**
  - PNP_UDP_1+EAD2->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-PSE<-FXSXX-COOH-like
- **GCA_001509495.1; Actinoplanes awajinensis subsp. mycoplanecinus; counts= 1; multicellularity status: TRUE**
  - FXSXX-COOH-like->METALLOPROTEASE+TPRs->PNP_UDP_1+VMAP-M0+VMAP-C->vWA+APATPase+wHTH+TPRs*->
- **GCA_001514115.1; Streptomyces olivochromogenes; counts= 1; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-Trypsin+EAD2<-Trypco2||METALLOPROTEASE+TPRs->

- **GCA_001514135.1; Streptomyces avermitilis; counts= 1; multicellularity status: TRUE**
  - AB_hydrolase->CASPASE+VMAP-M2+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs+cNMP_cyclase+NaeI*->
- **GCA_001672255.1; Anabaena sp. AL09; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+VMAP-M1+VMAP-C->MoxR->vWA+FGS-fold_domain*->
- **GCA_001672225.1; Anabaena sp. LE011-02; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+VMAP-M1+VMAP-C->MoxR->vWA+FGS-fold_domain*->
- **GCA_001672085.1; Anabaena sp. AL93; counts= 1; multicellularity status: TRUE**
  - vWA+FGS-fold_domain*->
- **GCA_001672075.1; Anabaena sp. CRKS33; counts= 1; multicellularity status: TRUE**
  - Trypco1->VMAP-M1+EAD6+VMAP-C->MoxR->vWA+FGS-fold_domain*->
- **GCA_001672195.1; Anabaena sp. MDT14b; counts= 1; multicellularity status: TRUE**
  - Trypco1->MoxR->vWA+FGS-fold_domain*->
- **GCA_001672105.1; Aphanizomenon flos-aquae WA102; counts= 1; multicellularity status: TRUE**
  - cNMP_cyclase+EAD1->EAD1+VMAP-M24+VMAP-C->MoxR->vWA+beta-rich-region+HTH+FGS-fold_domain*->?->||<-RVT_1<-four_helix_bundle_protein<-FGS-fold_domain
- **GCA_001751255.1; Streptomyces nanshensis; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA*->
- **GCA_001751265.1; Streptomyces nanshensis; counts= 1; multicellularity status: TRUE**
  - Trypsin+HDxxH+VMAP-M0+VMAP-C->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA*->?->TIR+APATPase+TPRs->
- **GCA_001866645.1; Streptomyces sp. MUSC 93; counts= 1; multicellularity status: TRUE**
  - AB_hydrolase->CASPASE+VMAP-M2+VMAP-C->MoxR->vWA+SFII-helicase+DUF3427*->
- **GCA_001904725.1; Phormidium ambiguum IAM M-71; counts= 1; multicellularity status: TRUE**
  - cNMP_cyclase+VMAP-M1+VMAP-C->MoxR->vWA+FGS-fold_domain*->FGS-fold_domain->
- **GCA_001905575.1; Streptomyces sp. CB00072; counts= 1; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->AB_hydrolase->CASPASE+EAD2->METALLOPROTEASE+TPRs->
- **GCA_001905425.1; Streptomyces sp. MJM1172; counts= 1; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-Na_H_Exchanger||AB_hydrolase->CASPASE+EAD2->METALLOPROTEASE+TPRs->
- **GCA_001905405.1; Streptomyces sp. TSRI0445; counts= 1; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->AB_hydrolase->CASPASE+EAD2->FXSXX-COOH-like->METALLOPROTEASE+TPRs->
- **GCA_001905525.1; Streptomyces sp. TSRI0395; counts= 1; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->AB_hydrolase->CASPASE+EAD2->FXSXX-COOH-like->METALLOPROTEASE+TPRs->

- **GCA_001905795.1; Streptomyces sp. CB01580; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCA_001905645.1; Streptomyces sp. CB02115; counts= 1; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->AB_hydrolase->CASPASE+EAD2->FXSXX-COOH-like->METALLOPROTEASE+TPRs->
- **GCA_001905845.1; Streptomyces sp. TSRI0107; counts= 1; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-Na_H_Exchanger||AB_hydrolase->CASPASE+EAD2->FXSXX-COOH-like->METALLOPROTEASE+TPRs->
- **GCA_001905885.1; Streptomyces sp. CB03234; counts= 1; multicellularity status: TRUE**
  - AB_hydrolase->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like
- **GCA_001905445.1; Streptomyces sp. CB00455; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCA_001918255.1; Ktedonobacter sp. 13_1_40CM_4_52_4; counts= 1; multicellularity status: TRUE**
  - MoxR->vWA+Glyco_transf_20*->
- **GCA_001995215.1; Amycolatopsis azurea DSM 43854; counts= 1; multicellularity status: TRUE**
  - cNMP_cyclase+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like<-cNMP_binding+HTH_Crp_2
- **GCA_002085445.1; Beggiatoa sp. 4572_84; counts= 1; multicellularity status: TRUE**
  - VMAP-C(partial)->VMAP-C(partial)->?->?->?->MoxR->vWA_protein*->
- **GCA_002104855.1; Streptomyces sp. 4F; counts= 1; multicellularity status: TRUE**
  - AB_hydrolase->CASPASE+EAD2->VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->
- **GCA_002104865.1; Streptomyces sp. BF-3; counts= 1; multicellularity status: TRUE**
  - vWA(partial)+REase+STAND_NTPase+TPRs+cNMP_cyclase*->
- **GCA_002148405.1; Alkalinema sp. CACIAM 70d; counts= 1; multicellularity status: TRUE**
  - Trypsin+VMAP-M1+VMAP-C->MoxR->vWA_protein*->FGS-fold_domain->FGS-fold_domain->
- **GCA_002300485.1; Streptomyces sp. Ag82_O1-15; counts= 1; multicellularity status: TRUE**
  - AB_hydrolase->CASPASE+VMAP-M0+VMAP-C->MoxR->vWA+cNMP_binding+HTH_Crp_2+TerD*->
- **GCA_002532535.1; Chloroflexi bacterium Kir15-3F; counts= 1; multicellularity status: TRUE**
  - vWA+Pkinase+REC+TCAD9+APHkinase*->
- **GCA_002803145.1; Kitasatospora sp. CB02891; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+BetaPropeller+Pkinase+TIR*->
- **GCA_900090065.1; Streptomyces sp. OspMP-M45; counts= 1; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->AB_hydrolase->CASPASE+EAD2->FXSXX-COOH-like->METALLOPROTEASE+TPRs->

- **GCA_900090085.1; Streptomyces sp. Ncost-T6T-1; counts= 1; multicellularity status: TRUE**
  - DUF397->Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+REase+STAND_NTPase+SFI-helicase*->
- **GCA_900091765.1; Streptomyces sp. PalvLS-984; counts= 1; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->AB_hydrolase->CASPASE+EAD2->FXSXX-COOH-like->METALLOPROTEASE+TPRs->
- **GCA_900091835.1; Streptomyces sp. PpalLS-921; counts= 1; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->AB_hydrolase->CASPASE+EAD2->FXSXX-COOH-like->METALLOPROTEASE+TPRs->
- **GCA_900091875.1; Streptomyces sp. BpilaLS-43; counts= 1; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->MoxR->?->vWA+APATPase+wHTH+TPRs*->AB_hydrolase->
- **GCA_900091865.1; Streptomyces sp. DvalAA-19; counts= 1; multicellularity status: TRUE**
  - AB_hydrolase->CASPASE+VMAP-M2+VMAP-C->MoxR->vWA+REase+SWACOS+TPRs+cNMP_cyclase*->
- **GCA_900091755.1; Streptomyces sp. TverLS-915; counts= 1; multicellularity status: TRUE**
  - VMAP-C->MoxR->vWA_protein*->
- **GCA_900091785.1; Streptomyces sp. BvitLS-983; counts= 1; multicellularity status: TRUE**
  - vWA+TPRs*->FXSXX-COOH->Radical_SAM->
- **GCA_900091885.1; Streptomyces sp. ScaeMP-6W; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->
- **GCA_900091845.1; Streptomyces sp. SolWspMP-5a-2; counts= 1; multicellularity status: TRUE**
  - vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like||Trypco1->
- **GCA_900091855.1; Streptomyces sp. DvalAA-14; counts= 1; multicellularity status: TRUE**
  - vWA+TPRs*->
- **GCA_900091905.1; Streptomyces sp. OspMP-M43; counts= 1; multicellularity status: TRUE**
  - AB_hydrolase->CASPASE+VMAP-M2+VMAP-C->MoxR->vWA+TPRs*->
- **GCA_900091725.1; Streptomyces sp. DvalAA-43; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->Trypco1->
- **GCA_900091595.1; Micromonospora haikouensis; counts= 1; multicellularity status: TRUE**
  - Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->?->Radical_SAM->TIR+APATPase+TPRs->||<-Voltage_CLC
- **GCA_900091525.1; Micromonospora matsumotoense; counts= 1; multicellularity status: TRUE**
  - CASPASE(partial)+VMAP-M2+VMAP-C->MoxR->vWA_protein*->
- **GCA_900091485.1; Streptomyces sp. LcepLS; counts= 1; multicellularity status: TRUE**
  - VMAP-C->MoxR->?->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->Trypco1->

- **GCA_900091995.1; Streptomyces sp. MnatMP-M17; counts= 1; multicellularity status: TRUE**
  - AB_hydrolase->CASPASE+VMAP-M2+VMAP-C->MoxR->vWA+TIR+FxsC_Cter*->
- **GCA_900092005.1; Streptomyces sp. Cmuel-A718b; counts= 1; multicellularity status: TRUE**
  - AB_hydrolase->CASPASE+VMAP-M2+VMAP-C->MoxR->vWA+REase+SWACOS+TPRs+cNMP_cyclase*->
- **GCA_900091985.1; Streptomyces sp. DconLS; counts= 1; multicellularity status: TRUE**
  - vWA+Pkinase+cNMP_cyclase+Band7*->
- **GCA_900091445.1; Micromonospora echinofusca; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+VMAP-M8+VMAP-C->MoxR->vWA+SWACOS+TPRs*->
- **GCA_900090145.1; Streptomyces sp. WMMB 322; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCA_900090165.1; Streptomyces; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+wHTH+TPRs+cNMP_cyclase*->
- **GCA_900091415.1; Micromonospora inyonensis; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+Calcineurin-like+NACHT*->
- **GCA_900091585.1; Micromonospora nigra; counts= 1; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like
- **GCA_900095575.1; Streptomyces sp. DpondAA-F4; counts= 1; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->AB_hydrolase->
- **GCA_900101975.1; Streptomyces sp. 136MFCol5.1; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCA_900103675.1; Janthinobacterium sp. 551a; counts= 1; multicellularity status: FALSE**
  - AB_hydrolase->CASPASE+VMAP-M4+VMAP-C->MoxR->vWA+Calcineurin-like+APATPase+SFII-helicase*->
- **GCA_900101585.1; Streptomyces emeiensis; counts= 1; multicellularity status: TRUE**
  - AB_hydrolase->CASPASE+VMAP-M2+VMAP-C->MoxR->vWA+SFII-helicase+Trypsin+cNMP_cyclase*->
- **GCA_900100955.1; Lechevalieria fradiae; counts= 1; multicellularity status: TRUE**
  - cNMP_cyclase+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like
- **GCA_900102095.1; Streptomyces jietaisiensis; counts= 1; multicellularity status: TRUE**
  - AB_hydrolase->CASPASE+VMAP-M0+VMAP-C->MoxR->vWA+STAND_NTPase+Trypsin+CASPASE+S1COLD*->
- **GCA_900100315.1; Streptomyces indicus; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD*->

- **GCA_900100275.1; Lentzea violacea; counts= 1; multicellularity status: TRUE**
  - <-cNMP_binding+HTH_Crp_2||cNMP_cyclase+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like||?->?->TIR+TPRs->
- **GCA_900103985.1; Streptomyces guanduensis; counts= 1; multicellularity status: TRUE**
  - PNP_UDP_1+EAD2->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like
- **GCA_900102245.1; Streptomyces sp. KS_16; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->TIR+APATPase+TPRs->
- **GCA_900105395.1; Streptomyces sp. TLI_053; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+EAD2->EAD2+VMAP-M10+VMAP-C->MoxR->vWA+APATPase+SWACOS+wHTH+TPRs+Beta-rich-tail*->
- **GCA_900105855.1; Amycolatopsis keratiniphila; counts= 1; multicellularity status: TRUE**
  - cNMP_cyclase+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like<-cNMP_binding+HTH_Crp_2
- **GCA_900106925.1; Thiocapsa roseopersicina; counts= 1; multicellularity status: TRUE**
  - AB_hydrolase->CASPASE+VMAP-M4+VMAP-C->MoxR->vWA+FGS-fold_domain+FGS-fold_domain+FGS-fold_domain*->
- **GCA_900105915.1; Streptomyces sp. 2224.1; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->TIR+APATPase+TPRs->
- **GCA_900105415.1; Streptomyces sp. TLI_105; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCA_900105705.1; Streptomyces griseus; counts= 1; multicellularity status: TRUE**
  - AB_hydrolase->CASPASE+VMAP-M2+VMAP-C->MoxR->vWA+TIR+FxsC_Cter*->
- **GCA_900105775.1; Streptomyces sp. 2112.3; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->TIR+APATPase+TPRs->
- **GCA_900108335.1; Nonomuraea solani; counts= 1; multicellularity status: TRUE**
  - Trypsin+EAD2->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like
- **GCA_900110255.1; Streptomyces rubidus; counts= 1; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like<-Trypsin+EAD2<-Trypco2
- **GCA_900110955.1; Lechevalieria xinjiangensis; counts= 1; multicellularity status: TRUE**
  - <-cNMP_binding+HTH_Crp_2||cNMP_cyclase+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like
- **GCA_900111005.1; Lentzea albida; counts= 1; multicellularity status: TRUE**
  - <-cNMP_binding+HTH_Crp_2||cNMP_cyclase+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like
- **GCA_900111175.1; Actinokineospora terrae; counts= 1; multicellularity status: TRUE**
  - CASPASE+VMAP-M2+VMAP-C->MoxR->vWA+Trypsin+TCAD11+TPRs*->

- **GCA_900110985.1; Lentzea flaviverrucosa; counts= 1; multicellularity status: TRUE**
  - <-cNMP_binding+HTH_Crp_2||cNMP_cyclase+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like
- **GCA_900113015.1; Actinoplanes philippinensis; counts= 1; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like
- **GCA_900112845.1; Streptomyces alni; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCA_900114705.1; Rugamonas rubra; counts= 1; multicellularity status: FALSE**
  - AB_hydrolase->CASPASE+VMAP-M4+VMAP-C->MoxR->vWA+METALLOPROTEASE+TCAD8*->
- **GCA_900116325.1; Streptomyces sp. ok210; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCA_900116135.1; Saccharopolyspora flava; counts= 1; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->MoxR->vWA_protein*->TIR+APATPase+TPRs->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like<-TIR+EAD2
- **GCA_900116145.1; Streptomyces harbinensis; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCA_900116675.1; Bradyrhizobium arachidis; counts= 1; multicellularity status: TRUE**
  - AB_hydrolase->CASPASE+VMAP-M4+VMAP-C->MoxR->vWA+CASPASE+TPRs*->
- **GCA_900119165.1; Amycolatopsis australiensis; counts= 1; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like
- **GCA_900119365.1; Streptomyces atratus; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->Trypco1->
- **GCA_900142575.1; Streptomyces paucisporeus; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCA_900176515.1; Kibdelosporangium aridum; counts= 1; multicellularity status: TRUE**
  - cNMP_cyclase+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs
- **GCA_900230275.1; Streptomyces sp. OV198; counts= 1; multicellularity status: TRUE**
  - AB_hydrolase->CASPASE+VMAP-M0+VMAP-C->MoxR->vWA+cNMP_binding+HTH_Crp_2+TerD*->
- **GCA_000332585.1; Microcystis aeruginosa; counts= 1; multicellularity status: TRUE**
  - HTH+VMAP-M9+VMAP-C->MoxR->vWA+FGS-fold_domain*->
- **GCA_000312205.1; Microcystis aeruginosa; counts= 1; multicellularity status: TRUE**
  - AB_hydrolase->CASPASE+VMAP-M14+VMAP-C->MoxR->vWA+FGS-fold_domain*->

- **GCA_000388135.1; Amycolatopsis vancoresmycina; counts= 1; multicellularity status: TRUE**
  - cNMP_cyclase+EAD2->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs
- **GCA_000340415.1; Amycolatopsis azurea; counts= 1; multicellularity status: TRUE**
  - cNMP_cyclase+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like<-cNMP_binding+HTH_Crp_2
- **GCA_000155555.1; Coleofasciculus chthonoplastes; counts= 1; multicellularity status: TRUE**
  - EAD9+EAD1+VMAP-C->?->MoxR->||<-?||?->?->vWA+FGS-fold_domain*->FGS-fold_domain->||<-?<-?||FGS-fold_domain->FGS-fold_domain->?->FGS-fold_domain->
- **GCA_000307915.1; Arthrospira platensis; counts= 1; multicellularity status: TRUE**
  - VMAP-C_protein->MoxR->vWA+TPRs*->
- **GCA_000173555.1; Arthrospira maxima; counts= 1; multicellularity status: TRUE**
  - VMAP-C_protein->MoxR->vWA+TPRs+CASPASE*->
- **GCA_000241835.2; Streptomyces coelicoflavus; counts= 1; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-Na_H_Exchanger
- **GCF_000235425.2; Frankia sp. CN3; counts= 1; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs->||<-METALLOPROTEASE+TPRs||EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs
- **GCA_000213055.1; Streptomyces sp. Tu6071; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->Trypco1->
- **GCA_000176895.2; Arthrospira sp. PCC 8005; counts= 1; multicellularity status: TRUE**
  - VMAP-C_protein->MoxR->vWA+TPRs+CASPASE*->
- **GCA_000297435.1; Microcystis sp. T1-4; counts= 1; multicellularity status: TRUE**
  - AB_hydrolase->CASPASE+VMAP-M14+VMAP-C->MoxR->vWA+FGS-fold_domain*->
- **GCA_900091815.1; Streptomyces sp. SA3_actG; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->Trypco1->
- **GCA_002846475.1; Saccharopolyspora spinosa; counts= 1; multicellularity status: TRUE**
  - S1COLD->PSE->?->PSE->||<-?||?->Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->Voltage_CLC->FXSXX-COOH-like->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCF_000258595.1; Streptomyces somaliensis; counts= 1; multicellularity status: TRUE**
  - Trypco1->AB_hydrolase->CASPASE+VMAP-M2+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs+cNMP_cyclase+NaeI*->
- **GCA_000009765.2; Streptomyces avermitilis; counts= 1; multicellularity status: TRUE**
  - AB_hydrolase->CASPASE+VMAP-M2+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs+cNMP_cyclase+NaeI*->
- **GCA_000058485.1; Frankia alni; counts= 1; multicellularity status: TRUE**
  - EAD2->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs

- **GCA_000196835.1; Amycolatopsis mediterranei; counts= 1; multicellularity status: TRUE**
  - cNMP_cyclase+EAD2->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like
- **GCA_000166135.1; Frankia inefficax; counts= 1; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->EAD2+EAD1->
- **GCA_000269985.1; Kitasatospora setae; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+CASPASE+TCAD14+PIN+CCCH(ZNR)+FHA*->
- **GCA_000210375.1; Arthrospira platensis; counts= 1; multicellularity status: TRUE**
  - VMAP-C_protein->MoxR->vWA+TPRs+CASPASE*->
- **GCA_000316605.1; Leptolyngbya sp. PCC 7376; counts= 1; multicellularity status: TRUE**
  - FGS-fold_domain->||<-RVT_1<-four_helix_bundle_protein||FGS-fold_domain->PSE->Trypsin+VMAP-M1+VMAP-C->MoxR->vWA+GAF+FGS-fold_domain*->
- **GCA_000389965.1; Actinoplanes sp. N902-109; counts= 1; multicellularity status: TRUE**
  - AB_hydrolase->CASPASE+VMAP-M2+VMAP-C->MoxR->vWA+TCAD13+NaeI+TPRs*->
- **GCA_000401915.1; Thermobifida fusca; counts= 1; multicellularity status: TRUE**
  - vWA+APATPase+wHTH+TPRs*->||<-DUF397||Trypco1->
- **GCA_000411495.1; Streptomyces; counts= 1; multicellularity status: TRUE**
  - TCAD15->?->?->Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH-like->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCF_000262345.1; Streptomyces xiaopingdaonensis; counts= 1; multicellularity status: TRUE**
  - <-Trypco1||Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCF_000308175.1; Pseudomonas fluorescens; counts= 1; multicellularity status: FALSE**
  - AB_hydrolase->CASPASE+VMAP-M16+VMAP-C->MoxR->vWA+BetaPropeller+TCAD10+REC*->
- **GCF_000340965.1; Nocardiopsis kunsanensis; counts= 1; multicellularity status: TRUE**
  - Trypsin+VMAP-M0+VMAP-C->vWA+APATPase+wHTH+TPRs*->||<-DUF397||Trypco1->
- **GCF_000341085.1; Nocardiopsis ganjiahuensis; counts= 1; multicellularity status: TRUE**
  - Trypsin+EAD2->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-DUF397
- **GCF_000341125.1; Nocardiopsis lucentensis; counts= 1; multicellularity status: TRUE**
  - vWA+APATPase+wHTH+TPRs*->||<-DUF397||Trypco1->
- **GCF_000341185.1; Nocardiopsis chromatogenes; counts= 1; multicellularity status: TRUE**
  - Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-DUF397||Trypco1->
- **GCF_000375625.1; Streptomyces sp. FxanaC1; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+wHTH+TPRs+APATPase+wHTH+TPRs*->?->?->||<-AB_hydrolase

- **GCF_000375725.1; Streptomyces; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->Trypco1->
- **GCA_003688775.1; Streptomyces sp. LaPpAH-202; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCF_000373665.1; Streptomyces sp. BoleA5; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+EAD2->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like
- **GCF_000377105.1; Streptomyces sp. CNQ766; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->TIR+APATPase+TPRs->
- **GCF_000377545.1; Streptomyces sp. CNY228; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCA_003984925.1; Streptomyces sp. TOR3209; counts= 1; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-Na_H_Exchanger
- **GCF_000280905.1; Streptomyces sp. AA1529; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH-like->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCF_000297635.1; Streptomyces sp. AA0539; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->
- **GCF_000381025.1; Streptomyces sulphureus; counts= 1; multicellularity status: TRUE**
  - <-TCAD15<-?||?->||<-Trypco1||Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCF_000384175.1; Streptomyces purpureus; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->Radical_SAM->TIR+APATPase+TPRs->
- **GCF_000379525.1; Lamprocystis purpurea; counts= 1; multicellularity status: TRUE**
  - CASPASE+VMAP-M27+VMAP-C->MoxR->vWA+FGS-fold_domain+FGS-fold_domain+PilP+FGS-fold_domain*->
- **GCA_002234385.1; Amycolatopsis alba; counts= 1; multicellularity status: TRUE**
  - cNMP_cyclase+VMAP-M0+VMAP-C->PSE->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like<-cNMP_binding+HTH_Crp_2
- **GCF_000384295.1; Amycolatopsis balhimycina; counts= 1; multicellularity status: TRUE**
  - <-Trypco1<-?||EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs
- **GCA_000478195.2; Lyngbya aestuarii; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+VMAP-M1+VMAP-C->MoxR->vWA+FGS-fold_domain*->||<-?||FGS-fold_domain->
- **GCA_000482245.1; Leptolyngbya sp. Heron Island J; counts= 1; multicellularity status: TRUE**
  - FGS-fold_domain->||<-?||PNP_UDP_1+VMAP-M1+VMAP-C->MoxR->vWA+FGS-fold_domain*->FGS-fold_domain->

- **GCA_000478605.2; Streptomyces thermolilacinus; counts= 1; multicellularity status: TRUE**
  - Trypco1->?->?->AB_hydrolase->CASPASE+VMAP-M2+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs+cNMP_cyclase+NaeI*->
- **GCA_000508205.1; Pseudomonas; counts= 1; multicellularity status: FALSE**
  - AB_hydrolase->CASPASE+VMAP-M16+VMAP-C->MoxR->vWA+BetaPropeller+TCAD10+REC*->
- **GCF_000470535.1; Streptomyces sp. AW19M42; counts= 1; multicellularity status: TRUE**
  - AB_hydrolase->CASPASE+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->
- **GCF_000518045.1; Streptomyces exfoliatus; counts= 1; multicellularity status: TRUE**
  - Trypsin+EAD2->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs
- **GCF_000239155.1; Actinoalloteichus spitiensis; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH-like->
- **GCF_000341205.1; Nocardiopsis baichengensis; counts= 1; multicellularity status: TRUE**
  - Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-DUF397||Trypco1->
- **GCF_000379645.1; Actinoplanes globisporus; counts= 1; multicellularity status: TRUE**
  - AB_hydrolase->CASPASE+VMAP-M2+VMAP-C->MoxR->vWA+CASPASE*->
- **GCF_000379825.1; Longispora albida; counts= 1; multicellularity status: TRUE**
  - Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs+CASPASE*->
- **GCF_000372745.1; Streptomyces scabrisporus; counts= 1; multicellularity status: TRUE**
  - CASPASE+VMAP-M19->VMAP-C->MoxR->vWA+BetaPropeller*->
- **GCF_000373645.1; Streptomyces sp. ATexAB-D23; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->Trypco1->
- **GCA_002895405.1; Actinoalloteichus cyanogriseus; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH-like->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCF_000482865.1; Actinokineospora inagensis; counts= 1; multicellularity status: TRUE**
  - CASPASE+VMAP-M2+VMAP-C->MoxR->vWA+Trypsin+TCAD11*->
- **GCF_000428945.1; Hamadaea tsunoensis; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+VMAP-M8+VMAP-C->MoxR->vWA+Trypsin+APATPase+wHTH+TPRs*->
- **GCF_000472685.1; Bradyrhizobium; counts= 1; multicellularity status: TRUE**
  - AB_hydrolase->CASPASE+VMAP-M4+VMAP-C->MoxR->vWA+CASPASE+TPRs*->
- **GCF_000514995.1; Streptomyces sp. CNT371; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->TIR+APATPase+TPRs->

- **GCF_000514715.1; Streptomyces sp. CNH099; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->TIR+APATPase+TPRs->
- **GCF_000424765.1; Streptomyces sp. CNT318; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH-like->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCF_000426325.1; Streptomyces sp. CNS606; counts= 1; multicellularity status: TRUE**
  - AB_hydrolase->CASPASE+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->
- **GCF_000482585.1; Streptomyces sp. CNQ329; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->TIR+APATPase+TPRs->
- **GCA_900091745.1; Streptomyces sp. DpondAA-B6; counts= 1; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->AB_hydrolase->CASPASE+EAD2->FXSXX-COOH-like->METALLOPROTEASE+TPRs->
- **GCF_000383615.1; Streptomyces canus; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->
- **GCF_000429085.1; Streptomyces flavidovirens; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCF_000715845.1; Streptomyces monomycini; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->TIR+APATPase+TPRs->
- **GCF_000716025.1; Streptomyces baarnensis; counts= 1; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->AB_hydrolase->CASPASE+EAD2->PSE->METALLOPROTEASE+TPRs->
- **GCF_000718945.1; Streptomyces sp. NRRL S-813; counts= 1; multicellularity status: TRUE**
  - Trypsin+EAD2->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like
- **GCA_001270665.1; Streptomyces; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->TIR+APATPase+TPRs->
- **GCF_000719335.1; Streptomyces sp. NRRL S-87; counts= 1; multicellularity status: TRUE**
  - AB_hydrolase->CASPASE+VMAP-M0+VMAP-C->MoxR->vWA+Trypsin+cNMP_cyclase+TPRs*->
- **GCF_000717875.1; Streptomyces sp. NRRL S-455; counts= 1; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-Na_H_Exchanger||AB_hydrolase->CASPASE+EAD2->FXSXX-COOH-like->METALLOPROTEASE+TPRs->
- **GCA_001509565.1; Streptomyces; counts= 1; multicellularity status: TRUE**
  - MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCF_000718515.1; Micromonospora parva; counts= 1; multicellularity status: TRUE**
  - CASPASE+TPRs->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-Radical_SAM<-FXSXX-COOH-like

- **GCA_003073355.1; Streptomyces scopuliridis; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCF_000721345.1; Kitasatospora sp. NRRL B-11411; counts= 1; multicellularity status: TRUE**
  - MoxR->vWA+CASPASE+TCAD14+PIN+CCCH(ZNR)+FHA*->
- **GCF_000719205.1; Lechevalieria aerocolonigenes; counts= 1; multicellularity status: TRUE**
  - cNMP_cyclase+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like||TIR+APATPase+TPRs->||<-DUF397
- **GCF_000725545.1; Streptomyces exfoliatus; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCF_000720915.1; Streptomyces albus; counts= 1; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->AB_hydrolase->CASPASE+EAD2->PSE->METALLOPROTEASE+TPRs->
- **GCF_000720535.1; Streptomyces; counts= 1; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->AB_hydrolase->CASPASE+EAD2->FXSXX-COOH-like->METALLOPROTEASE+TPRs->
- **GCF_000716535.1; Streptomyces; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+cNMP_cyclase+Band7+HAD*->
- **GCF_000718705.1; Streptomyces; counts= 1; multicellularity status: TRUE**
  - AB_hydrolase->CASPASE+VMAP-M0+VMAP-C->MoxR->vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats*->
- **GCF_000721105.1; Streptomyces cellulosae; counts= 1; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->?->||<-Na_H_Exchanger||AB_hydrolase->CASPASE+EAD2->FXSXX-COOH-like->
- **GCF_000719495.1; Streptomyces griseus; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->||<-?||Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCF_000717795.1; Streptomyces griseus; counts= 1; multicellularity status: TRUE**
  - AB_hydrolase->CASPASE+VMAP-M2+VMAP-C->MoxR->vWA_protein*->TIR+FxsC_Cter->
- **GCF_000719355.1; Streptomyces griseus; counts= 1; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->AB_hydrolase->CASPASE+EAD2->FXSXX-COOH-like->METALLOPROTEASE+TPRs->
- **GCF_000719775.1; Streptomyces sp. NRRL F-5135; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->?->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCF_000719435.1; Streptomyces griseus; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCF_000719895.1; Streptomyces sp. NRRL F-2799; counts= 1; multicellularity status: TRUE**
  - Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->

- **GCA_001279005.1; Streptomyces; counts= 1; multicellularity status: TRUE**
  - Trypsin+EAD2->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-Radical_SAM<-FXSXX-COOH||Voltage_CLC->
- **GCF_000721605.1; Streptomyces sp. NRRL S-37; counts= 1; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-Na_H_Exchanger<-?||METALLOPROTEASE+TPRs->
- **GCF_000722015.1; Streptomyces sp. NRRL S-474; counts= 1; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-Na_H_Exchanger||AB_hydrolase->CASPASE+EAD2->FXSXX-COOH-like->METALLOPROTEASE+TPRs->
- **GCF_000721265.1; Streptomyces sp. NRRL F-5126; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCF_000717895.1; Streptomyces sp. NRRL WC-3744; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+cNMP_cyclase+Band7+HAD*->
- **GCF_000719475.1; Streptomyces sp. NRRL F-5630; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->Trypco1->
- **GCF_000720295.1; Streptomyces sp. NRRL WC-3725; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+cNMP_cyclase+Band7+HAD*->
- **GCF_000721935.1; Streptomyces sp. NRRL WC-3549; counts= 1; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->PSE->PSE->CASPASE+EAD2->FXSXX-COOH-like->METALLOPROTEASE+TPRs->
- **GCF_000722185.1; Streptomyces; counts= 1; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->AB_hydrolase->CASPASE+EAD2->FXSXX-COOH-like->METALLOPROTEASE+TPRs->
- **GCF_000725635.1; Streptomyces sp. NRRL B-3253; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCA_004328625.1; Streptomyces seoulensis; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||PSE->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCF_000725645.1; Streptomyces sp. NRRL F-5635; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->Trypco1->
- **GCF_000156695.2; Streptomyces filamentosus; counts= 1; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->PSE->CASPASE+EAD2->FXSXX-COOH-like->METALLOPROTEASE+TPRs->
- **GCF_000373305.1; Streptomyces sp. CcalMP-8W; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->
- **GCF_000156455.1; Streptomyces filamentosus; counts= 1; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->PSE->PSE->CASPASE+EAD2->FXSXX-COOH-like->

- **GCF_000717375.1; Streptomyces griseus; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCF_000717345.1; Streptomyces lydicus; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->TIR+APATPase+TPRs->
- **GCF_000717025.1; Streptomyces atroolivaceus; counts= 1; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->AB_hydrolase->CASPASE+EAD2->FXSXX-COOH-like->METALLOPROTEASE+TPRs->
- **GCF_000717055.1; Streptomyces iakyrus; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD*->
- **GCF_000797385.1; Streptomyces sp. CNQ431; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCF_000504285.1; Actinospica robiniae; counts= 1; multicellularity status: TRUE**
  - PNP_UDP_1+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs||METALLOPROTEASE+TPRs->||<-PNP_UDP_1+EAD2<-EAD2+VMAP-M0+APATPase+TPRs
- **GCF_000744785.1; Kitasatospora azatica; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+EAD2->EAD2+VMAP-M10+VMAP-C->MoxR->vWA+APATPase+BetaPropeller+cNMP_cyclase+NaeI*->
- **GCA_000696185.1; Kitasatospora cheerisanensis; counts= 1; multicellularity status: TRUE**
  - AB_hydrolase->CASPASE+VMAP-M2+VMAP-C->MoxR->vWA_protein*->
- **GCA_900176525.1; Lentzea albidocapillata; counts= 1; multicellularity status: TRUE**
  - <-cNMP_binding+HTH_Crp_2||cNMP_cyclase+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like||TIR+TPRs->
- **GCA_004768505.1; Streptomyces albus; counts= 1; multicellularity status: TRUE**
  - TCAD15->?->?->Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH-like->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCF_000415505.1; Streptomyces afghaniensis; counts= 1; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->PSE->vWA+APATPase+wHTH+TPRs*->
- **GCA_000738695.1; Streptomyces scabiei; counts= 1; multicellularity status: TRUE**
  - vWA_protein*->
- **GCA_000738715.1; Streptomyces scabiei; counts= 1; multicellularity status: TRUE**
  - TCAD9+Pkinase+NACHT+HEAT_repeats->EAD2+VMAP-M0+VMAP-C->vWA*->MoxR->vWA+APATPase+TPRs->
- **GCF_000746395.1; Streptomyces mirabilis; counts= 1; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-Na_H_Exchanger||AB_hydrolase->CASPASE+EAD2->FXSXX-COOH-like->METALLOPROTEASE+TPRs->
- **GCF_000701285.1; Streptomyces sp. CNQ-525; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->TIR+APATPase+TPRs->

- **GCA_000696115.1; Streptomyces olindensis; counts= 1; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->AB_hydrolase->CASPASE+EAD2->FXSXX-COOH-like->METALLOPROTEASE+TPRs->
- **GCF_000495635.1; Streptomyces sp. GBA 94-10; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCA_000412265.2; Streptomyces sp. Mg1; counts= 1; multicellularity status: TRUE**
  - <-cNMP_binding+HTH_Crp_2<-?||EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-Na_H_Exchanger||AB_hydrolase->CASPASE+EAD2->FXSXX-COOH-like->METALLOPROTEASE+TPRs->
- **GCF_000719665.1; Streptomyces; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->Trypco1->
- **GCF_000721335.1; Streptomyces sp. NRRL S-1831; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->Trypco1->
- **GCF_000720175.1; Streptomyces sp. NRRL S-337; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||PSE->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->TIR+APATPase+TPRs->
- **GCF_000721455.1; Streptomyces sp. NRRL F-6628; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCA_000698495.1; Streptomyces sp. NTK 937; counts= 1; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->AB_hydrolase->CASPASE+EAD2->FXSXX-COOH-like->METALLOPROTEASE+TPRs->
- **GCF_000495755.1; Streptomyces sp. PVA 94-07; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCA_000802245.2; Streptomyces; counts= 1; multicellularity status: TRUE**
  - TCAD15->?->Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH-like->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCA_004212215.1; Lyngbya confervoides; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+VMAP-M1+VMAP-C->MoxR->vWA+FGS-fold_domain*->?->FGS-fold_domain->
- **GCF_000308675.1; Nocardia paucivorans; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->Voltage_CLC->METALLOPROTEASE->TIR+APATPase+wHTH+TPRs->
- **GCF_000308495.1; Nocardia brevicatena; counts= 1; multicellularity status: TRUE**
  - Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->Voltage_CLC->METALLOPROTEASE->TIR+APATPase+wHTH+TPRs->
- **GCA_003182435.1; Streptomyces albus; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCA_000818175.1; Streptomyces sp. AcH 505; counts= 1; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-Na_H_Exchanger||AB_hydrolase->CASPASE+EAD2->FXSXX-COOH-like->

- **GCA_900109465.1; Streptacidiphilus jiangxiensis; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCF_000719915.1; Streptomyces sp. NRRL F-2890; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCF_000805335.1; Streptomyces sp. CT34; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->
- **GCF_000819545.1; Streptomyces nodosus; counts= 1; multicellularity status: TRUE**
  - Trypsin+EAD2->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-Radical_SAM<-FXSXX-COOH||Voltage_CLC->||<-Trypco1
- **GCF_000716435.1; Streptomyces xylophagus; counts= 1; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->AB_hydrolase->CASPASE+EAD2->FXSXX-COOH-like->METALLOPROTEASE+TPRs->
- **GCA_000695625.1; Amycolatopsis rifamycinica; counts= 1; multicellularity status: TRUE**
  - cNMP_cyclase+EAD2->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like
- **GCF_000312185.1; Microcystis aeruginosa; counts= 1; multicellularity status: TRUE**
  - HTH+VMAP-M9+VMAP-C->MoxR->?->vWA+FGS-fold_domain*->?->PSE->FGS-fold_domain->
- **GCA_000935125.1; Streptomyces natalensis; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->
- **GCA_003147545.1; Streptomyces griseus; counts= 1; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->AB_hydrolase->CASPASE+EAD2->FXSXX-COOH-like->METALLOPROTEASE+TPRs->
- **GCA_000952105.1; Chromobacterium violaceum; counts= 1; multicellularity status: FALSE**
  - AB_hydrolase->CASPASE+VMAP-M4+VMAP-C->MoxR->vWA+REC+TCAD8*->
- **GCA_000955975.1; Saccharothrix sp. ST-888; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->
- **GCF_000969605.1; Aquincola tertiaricarbonis; counts= 1; multicellularity status: TRUE**
  - AB_hydrolase->CASPASE+VMAP-M0+VMAP-C->MoxR->vWA+BetaPropeller+REC*->
- **GCF_003060805.1; Arthrospira sp. TJSD091; counts= 1; multicellularity status: TRUE**
  - VMAP-C_protein->MoxR->vWA+TPRs+CASPASE*->
- **GCF_000981895.1; Streptomyces sp. NRRL B-24891; counts= 1; multicellularity status: TRUE**
  - vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCA_000993785.2; Streptomyces xiamenensis; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->

- **GCF_001005085.2; Streptomyces humi; counts= 1; multicellularity status: TRUE**
  - Trypsin+EAD2+VMAP-M0+VMAP-C->vWA+APATPase+wHTH+TPRs*->KAP_NTPase->
- **GCA_001011035.1; Streptomyces sp. CNQ-509; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->TIR+APATPase+TPRs->
- **GCA_001014595.1; Streptomyces sp. KE1; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->
- **GCF_000800535.1; Streptomyces sp. M10; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCF_001027285.1; Archangium gephyra; counts= 1; multicellularity status: TRUE**
  - EAD1+VMAP-M1+VMAP-C->vWA+SLOG*->
- **GCA_001039005.1; Burkholderia cepacia; counts= 1; multicellularity status: FALSE**
  - AB_hydrolase->CASPASE+VMAP-M4+VMAP-C->MoxR->vWA+APATPase+wHTH*->
- **GCF_000718635.1; Streptomyces varsoviensis; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCF_001083795.1; Streptomyces sp. SBT349; counts= 1; multicellularity status: TRUE**
  - vWA+TPRs*->FXSXX-COOH->
- **GCA_001187435.1; Streptomyces caatingaensis; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCF_000022045.1; Cyanothece sp. PCC 7425; counts= 1; multicellularity status: TRUE**
  - <-FGS-fold_domain<-?<-?<-?||?->VMAP-M1+VMAP-C->MoxR->vWA*->||<-zf-IS66+DDE_Tnp_IS66<-TIR+EAD9<-PSE<-Trypsin<-Trypco1
- **GCA_000698945.1; Streptomyces wadayamensis; counts= 1; multicellularity status: TRUE**
  - <-TCAD15<-?||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCF_000739635.1; Verrucomicrobium sp. BvORR034; counts= 1; multicellularity status: FALSE**
  - VMAP-M22+VMAP-C->MoxR->vWA+AP-GTPase+COR+EAD1+Trypsin*->
- **GCF_000716945.1; Streptomyces albus; counts= 1; multicellularity status: TRUE**
  - Trypco2->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+TPRs*->
- **GCF_000259895.1; Streptomyces sp. TOR3209; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+wHTH+TPRs+cNMP_cyclase*->
- **GCF_000373465.1; Streptomyces sp. FxanaD5; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7*->

- **GCF_000381885.1; Actinomadura atramentaria; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+VMAP-M8+VMAP-C->MoxR->vWA+cNMP_cyclase+cNMP_cyclase+FtsK+TPRs*->?->?->||<-DUF397<-DUF397
- **GCF_000349325.1; Streptomyces davawensis; counts= 1; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like<-Trypsin+EAD2||METALLOPROTEASE+TPRs->
- **GCF_000424825.1; Streptomyces sp. CNH287; counts= 1; multicellularity status: TRUE**
  - TCAD15->?->||<-?||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCF_000497425.1; Streptomyces niveus; counts= 1; multicellularity status: TRUE**
  - Trypco2->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+TPRs*->
- **GCA_001756925.1; Streptomyces fradiae; counts= 1; multicellularity status: TRUE**
  - NUDIX->Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->SIR2->
- **GCF_000696185.1; Kitasatospora cheerisanensis; counts= 1; multicellularity status: TRUE**
  - Trypsin+EAD2+VMAP-M0+VMAP-C->PSE->vWA_protein*->BetaPropeller->
- **GCF_000701325.1; Streptomyces sp. URHA0041; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCF_000719555.1; Streptomyces sp. NRRL F-5727; counts= 1; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-Na_H_Exchanger||AB_hydrolase->CASPASE+EAD2->FXSXX-COOH-like->METALLOPROTEASE+TPRs->
- **GCF_000718985.1; Streptomyces megasporus; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCA_000707925.1; Streptomyces rimosus; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->TIR+APATPase+TPRs->
- **GCF_000716805.1; Streptomyces yerevanensis; counts= 1; multicellularity status: TRUE**
  - Trypco1->PSE->MoxR->vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD*->
- **GCF_000718475.1; Microbispora rosea; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+VMAP-M8+VMAP-C->MoxR->vWA+TIR+FxsC_Cter*->
- **GCF_000716685.1; Streptomyces virginiae; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCF_000719695.1; Streptomyces sp. NRRL F-6131; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+EAD2->EAD2+VMAP-M10+VMAP-C->MoxR->vWA+APATPase+SWACOS+wHTH+TPRs+Beta-rich-tail*->
- **GCF_000716445.1; Streptomyces; counts= 1; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-Na_H_Exchanger||AB_hydrolase->CASPASE+EAD2->FXSXX-COOH-like->METALLOPROTEASE+TPRs->

- **GCF_000717135.1; Catenuloplanes japonicus; counts= 1; multicellularity status: TRUE**
  - METALLOPROTEASE+TPRs->EAD2+VMAP-M0+VMAP-C->vWA+APATPase+wHTH+TPRs*->
- **GCF_000718525.1; Streptomyces griseus; counts= 1; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-Na_H_Exchanger||AB_hydrolase->CASPASE+EAD2->FXSXX-COOH-like->METALLOPROTEASE+TPRs->
- **GCF_000720145.1; Streptomyces sp. NRRL F-2747; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCF_000721705.1; Actinoplanes subtropicus; counts= 1; multicellularity status: TRUE**
  - PNP_UDP_1+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs
- **GCF_000725465.1; Streptomyces bicolor; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->
- **GCF_000717655.1; Streptomyces katrae; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCF_000720635.1; Streptomyces sp. NRRL WC-3742; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+VMAP-M0+VMAP-C->vWA+TIR+FxsC_Cter*->
- **GCA_002803845.1; Streptomyces lavendulae; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCF_000721515.1; Streptomyces sp. NRRL F-5193; counts= 1; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-Na_H_Exchanger||AB_hydrolase->CASPASE+EAD2->FXSXX-COOH-like->METALLOPROTEASE+TPRs->
- **GCF_000721305.1; Streptomyces sp. NRRL S-1868; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->
- **GCF_000725125.1; Streptomyces toyocaensis; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->
- **GCF_000720485.1; Streptomyces ochraceiscleroticus; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+SWACOS+wHTH*->
- **GCF_000725785.1; Streptomyces; counts= 1; multicellularity status: TRUE**
  - SIR2->?->||<-?||AB_hydrolase->CASPASE+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+REase+cNMP_cyclase+CASPASE*->
- **GCF_000745715.1; Streptomyces mirabilis; counts= 1; multicellularity status: TRUE**
  - AB_hydrolase->CASPASE+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+PNP_UDP_1+APATPase+wHTH+TPRs*->
- **GCF_000612545.1; Streptomyces sp. PCS3-D2; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->

- **GCF_000772895.1; Streptomyces galbus; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+wHTH+TPRs+cNMP_cyclase*->?->?->||<-?||Radical_SAM->Antibiotic_NAT->TIR+FxsC_Cter->
- **GCF_000686765.1; Streptomyces sp. UNC401CLCol; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7*->
- **GCF_000814065.1; Pseudomonas sp. C5pp; counts= 1; multicellularity status: FALSE**
  - AB_hydrolase->CASPASE+VMAP-M16+VMAP-C->MoxR->vWA+BetaPropeller+TCAD10+REC*->
- **GCF_000158955.1; Streptomyces viridochromogenes; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->
- **GCF_000525635.1; Kutzneria albida; counts= 1; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->MoxR->?->vWA+TIR+BetaPropeller*->?->?->||<-cNMP_cyclase+EAD2||cNMP_binding+HTH_Crp_2->?->SIR2->
- **GCF_000717715.1; Streptomyces sp. NRRL B-24484; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->
- **GCF_000721495.1; Streptomyces sp. NRRL F-5123; counts= 1; multicellularity status: TRUE**
  - Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+BetaPropeller*->
- **GCF_000721235.1; Streptomyces olivaceus; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->
- **GCF_000718165.1; Streptomyces fulvoviolaceus; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+STAND_NTPase+STAND_NTPase*->
- **GCF_000829695.1; Streptomyces sp. NBRC 110035; counts= 1; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-Trypsin+EAD2<-Trypco2||METALLOPROTEASE+TPRs->
- **GCA_000733295.1; Archangium violaceum; counts= 1; multicellularity status: TRUE**
  - EAD1+Trypsin->EAD1+VMAP-M1+VMAP-C->MoxR->vWA+SLOG+EAD1+TIR*->
- **GCF_000955975.1; Saccharothrix sp. ST-888; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+CASPASE+TIR+FxsC_Cter(partial)*->
- **GCF_000966955.1; Streptomyces sp. NRRL S-495; counts= 1; multicellularity status: TRUE**
  - Trypsin+EAD2->EAD2+VMAP-M10+VMAP-C->MoxR->vWA+APATPase+SWACOS+wHTH+TPRs+Beta-rich-tail*->
- **GCF_001305595.1; Azospirillum thiophilum; counts= 1; multicellularity status: FALSE**
  - AB_hydrolase->CASPASE+VMAP-M4+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->
- **GCF_000720235.1; Streptomyces; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->

- **GCF_000829715.2; Streptomyces sp. NBRC 110027; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->TIR+APATPase+TPRs->
- **GCF_000972435.1; Streptomyces sp. MBT28; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TIR+APATPase+Trypsin+HDxxH+VMAP-M0+VMAP-C*->
- **GCF_000982955.1; Micromonospora sp. HK10; counts= 1; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like<-CASPASE+EAD2
- **GCF_001005405.1; Streptomyces scabiei; counts= 1; multicellularity status: TRUE**
  - MoxR->vWA+APATPase+wHTH+TPRs*->
- **GCF_000718775.1; Streptomyces sp. NRRL S-31; counts= 1; multicellularity status: TRUE**
  - vWA+TPRs*->FXSXX-COOH->Radical_SAM->TIR+APATPase+TPRs->FXSXX-COOH->Radical_SAM->
- **GCF_000720995.1; Streptomyces celluloflavus; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->TIR+APATPase+TPRs->
- **GCF_000980885.2; Streptomyces malaysiense; counts= 1; multicellularity status: TRUE**
  - Trypco2->EAD2+VMAP-M0+VMAP-C->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like<-Trypsin+EAD2
- **GCF_000412265.2; Streptomyces sp. Mg1; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCF_001044425.1; Streptomyces roseus; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->PSE->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCF_001270565.1; Streptomyces virginiae; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCF_001270485.1; Streptomyces viridochromogenes; counts= 1; multicellularity status: TRUE**
  - Trypco2->EAD2+VMAP-M0+VMAP-C->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like<-Trypsin+EAD2
- **GCA_001279845.1; Streptomyces sp. XY533; counts= 1; multicellularity status: TRUE**
  - AB_hydrolase->CASPASE+VMAP-M0+VMAP-C->MoxR->vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats*->
- **GCF_001279445.1; Streptomyces; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->
- **GCF_001279485.1; Streptomyces sp. XY511; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->
- **GCF_001279495.1; Streptomyces sp. H021; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->

- **GCF_001279855.1; Streptomyces; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->
- **GCF_001279455.1; Streptomyces sp. XY152; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD*->
- **GCF_001279605.1; Streptomyces sp. NRRL F-4707; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->Trypco1->
- **GCF_001280125.1; Streptomyces sp. NRRL F-6492; counts= 1; multicellularity status: TRUE**
  - vWA+TPRs*->FXSXX-COOH->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCF_001279555.1; Micromonospora sp. NRRL B-16802; counts= 1; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs
- **GCF_001280015.1; Streptomyces sp. MMG1121; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->
- **GCA_001280015.1; Streptomyces sp. MMG1121; counts= 1; multicellularity status: TRUE**
  - TCAD15->Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH-like->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCF_001279905.1; Streptomyces sp. XY66; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->
- **GCF_001279935.1; Streptomyces sp. IGB124; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->
- **GCF_001279365.1; Streptomyces sp. NRRL F-5755; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->TIR+APATPase+TPRs->TIR+APATPase+TPRs->
- **GCF_001279625.1; Streptomyces sp. WM6368; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->
- **GCF_001279685.1; Streptomyces sp. WM6373; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->
- **GCF_001279765.1; Streptomyces sp. XY413; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->
- **GCF_001280005.1; Streptomyces sp. NRRL WC-3618; counts= 1; multicellularity status: TRUE**
  - MoxR->vWA+TPRs*->Radical_SAM->TIR+APATPase+TPRs->Radical_SAM->?->STAND_NTPase->vWA->TIR+APATPase+TPRs->
- **GCF_001279985.1; Streptomyces sp. AS58; counts= 1; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like<-Trypsin+EAD2<-Trypco2||METALLOPROTEASE+TPRs->

- **GCF_001280885.1; Streptomyces sp. XY332; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCF_001279345.1; Streptomyces rimosus; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->TIR+APATPase+TPRs->
- **GCF_001294335.1; Streptomyces chattanoogensis; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->TIR+APATPase+TPRs->
- **GCA_001294345.1; Streptomyces sp. NRRL S-4; counts= 1; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->AB_hydrolase->CASPASE+EAD2->FXSXX-COOH-like->METALLOPROTEASE+TPRs->
- **GCF_001298575.1; Actinobacteria bacterium OK074; counts= 1; multicellularity status: NA**
  - NUDIX->Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->SIR2->
- **GCF_001298565.1; Actinobacteria bacterium OK006; counts= 1; multicellularity status: NA**
  - AB_hydrolase->CASPASE+VMAP-M2+VMAP-C->MoxR->vWA+BetaPropeller*->
- **GCF_001298545.1; Actinobacteria bacterium OV320; counts= 1; multicellularity status: NA**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCA_001306465.1; Frankia sp. R43; counts= 1; multicellularity status: TRUE**
  - EAD2+EAD1->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs
- **GCF_001418505.1; Streptomyces flocculus; counts= 1; multicellularity status: TRUE**
  - vWA+TPRs*->FXSXX-COOH-like->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCF_001418465.1; Streptomyces kanamyceticus; counts= 1; multicellularity status: TRUE**
  - vWA+Pkinase+FtsK+TPRs*->
- **GCF_001418325.1; Streptomyces atriruber; counts= 1; multicellularity status: TRUE**
  - vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+HAD*->
- **GCF_001419765.1; Streptomyces torulosus; counts= 1; multicellularity status: TRUE**
  - Trypsin+EAD2+VMAP-M0+VMAP-C->vWA+APATPase+wHTH+TPRs*->
- **GCF_001420875.1; Frankia sp. AvcI1; counts= 1; multicellularity status: TRUE**
  - EAD2->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like
- **GCA_001426405.1; Streptomyces; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||PSE->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCA_001426585.1; Streptomyces sp. Root431; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->

- **GCA_001426615.1; Streptomyces; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->
- **GCA_001429805.1; Kitasatospora sp. Root187; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+EAD2->EAD2+VMAP-M10+VMAP-C->MoxR->vWA+APATPase+BetaPropeller+Pkinase+wHTH+TPRs+wHTH+TPRs+FtsK*->
- **GCF_001428885.1; Streptomyces sp. Root264; counts= 1; multicellularity status: TRUE**
  - DUF397->MoxR->vWA+APATPase+wHTH+TPRs*->||<-vWA<-EAD2+VMAP-M0+VMAP-C
- **GCA_001484605.1; Pseudarthrobacter sulfonivorans; counts= 1; multicellularity status: FALSE**
  - AB_hydrolase->CASPASE+VMAP-M17+VMAP-C->MoxR->vWA+BetaPropeller+CASPASE+STAND_NTPase*->
- **GCF_001493375.1; Streptomyces specialis; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->PSE->?->?->TIR+APATPase+TPRs->
- **GCF_001485105.1; Streptomyces acidiscabies; counts= 1; multicellularity status: TRUE**
  - vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCA_001507435.1; Streptomyces sp. NRRL F-5122; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCF_001511815.1; Streptomyces reticuli; counts= 1; multicellularity status: TRUE**
  - TCAD15->Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH-like->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCF_000974445.1; Lechevalieria aerocolonigenes; counts= 1; multicellularity status: TRUE**
  - cNMP_cyclase+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like||TIR+APATPase+TPRs->||<-DUF397
- **GCF_001531145.1; Streptomyces sp. IMTB 1903; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCF_001550225.1; Streptomyces scabiei; counts= 1; multicellularity status: TRUE**
  - MoxR->vWA+APATPase+wHTH+TPRs*->
- **GCF_001550315.1; Streptomyces; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+wHTH+TPRs+cNMP_cyclase*->
- **GCF_001550215.1; Streptomyces scabiei; counts= 1; multicellularity status: TRUE**
  - vWA*->
- **GCF_001572115.1; Streptomyces scabiei; counts= 1; multicellularity status: TRUE**
  - MoxR->vWA+APATPase+wHTH+TPRs*->
- **GCF_001592045.1; Thermobifida fusca; counts= 1; multicellularity status: TRUE**
  - Trypsin+EAD2->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-DUF397||Trypco1->

- **GCA_003719195.1; Herbaspirillum rubrisubalbicans; counts= 1; multicellularity status: FALSE**
  - AB_hydrolase->CASPASE+VMAP-M20+VMAP-C->MoxR->vWA+DRHyd+TCAD8*->
- **GCA_001514215.1; Streptomyces bungoensis; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||PSE->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->Trypco1->
- **GCA_001613935.1; Amycolatopsis regifaucium; counts= 1; multicellularity status: TRUE**
  - cNMP_cyclase+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like<-cNMP_binding+HTH_Crp_2
- **GCF_001570645.1; Streptomyces sporocinereus; counts= 1; multicellularity status: TRUE**
  - AB_hydrolase->CASPASE+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->
- **GCA_001513975.1; Streptomyces curacoi; counts= 1; multicellularity status: TRUE**
  - Trypsin+EAD2->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like
- **GCA_001469455.2; Streptomyces sp. AVP053U2; counts= 1; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-Trypsin+EAD2
- **GCF_000974485.1; Streptomyces sp. NBRC 109706; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->?->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCA_001509475.1; Streptomyces regalis; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->Radical_SAM->TIR+APATPase+TPRs->||<-TCAD15
- **GCF_001514235.1; Streptomyces caeruleatus; counts= 1; multicellularity status: TRUE**
  - Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->
- **GCF_000158935.1; Streptomyces lividans; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->PSE->vWA+Pkinase+wHTH+TPRs+cNMP_cyclase*->
- **GCA_001270575.1; Streptomyces decoyicus; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->TIR+APATPase+TPRs->
- **GCF_001270495.1; Streptomyces viridochromogenes; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD*->
- **GCF_000373365.1; Frankia discariae; counts= 1; multicellularity status: TRUE**
  - EAD2+EAD1->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs
- **GCA_001687325.1; Streptomyces sp. PTY087I2; counts= 1; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->AB_hydrolase->CASPASE+EAD2->FXSXX-COOH-like->METALLOPROTEASE+TPRs->
- **GCA_001693675.1; Streptomyces clavuligerus; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->

- **GCF_001514035.1; Streptomyces yokosukanensis; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->
- **GCA_001514285.1; Streptomyces sp. DSM 15324; counts= 1; multicellularity status: TRUE**
  - AB_hydrolase->CASPASE+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+REase+cNMP_cyclase+CASPASE*->
- **GCF_001653115.1; Streptomyces sp. F-3; counts= 1; multicellularity status: TRUE**
  - Trypsin+EAD2->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like||Trypco1->
- **GCF_001704195.1; Streptomyces sampsonii; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCF_001552155.1; Actinomadura formosensis; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+VMAP-M8+VMAP-C->MoxR->vWA+FtsK+FtsK+FtsK*->
- **GCF_001552175.1; Actinomadura kijaniata; counts= 1; multicellularity status: TRUE**
  - Trypsin+VMAP-M8+VMAP-C->MoxR->vWA+FtsK+FtsK+FtsK+FtsK+FtsK+FtsK*->
- **GCF_001552555.1; Nocardiopsis trehalosi; counts= 1; multicellularity status: TRUE**
  - Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-DUF397
- **GCA_003350525.1; Nocardia mexicana; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->Voltage_CLC->METALLOPROTEASE->TIR+APATPase+wHTH+TPRs->Radical_SAM->
- **GCA_001517975.1; Thermobifida cellulosilytica; counts= 1; multicellularity status: TRUE**
  - Trypsin+EAD2->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-DUF397||Trypco1->
- **GCA_001637315.1; Phormidium willei; counts= 1; multicellularity status: TRUE**
  - VMAP-C->MoxR->vWA+FGS-fold_domain*->FGS-fold_domain->
- **GCF_001715295.1; Streptomyces griseus; counts= 1; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->AB_hydrolase->CASPASE+EAD2->FXSXX-COOH-like->METALLOPROTEASE+TPRs->
- **GCF_001746315.1; Streptomyces sp. EN27; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->
- **GCF_001746305.1; Streptomyces sp. EN23; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->
- **GCF_001746295.1; Streptomyces sp. LUP47B; counts= 1; multicellularity status: TRUE**
  - Trypsin+EAD2->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like||Trypco1->
- **GCF_001748305.1; Streptomyces luteocolor; counts= 1; multicellularity status: TRUE**
  - ADP_ribosyl_GH->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+FtsK+TPRs*->NUDIX->

- **GCA_001746425.1; Streptomyces subrutilus; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCA_001746465.1; Streptomyces agglomeratus; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||PSE->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCA_001746415.1; Streptomyces agglomeratus; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||PSE->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCA_001751375.1; Streptomyces; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH-like->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCA_001746485.1; Streptomyces agglomeratus; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||PSE->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCA_001767235.1; Moorea producens; counts= 1; multicellularity status: TRUE**
  - EAD1+Trypsin->||<-?||PSE->EAD1+VMAP-M1+VMAP-C->MoxR->vWA+FGS-fold_domain*->
- **GCF_001865315.1; Streptomyces sampsonii; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCF_001865795.1; Streptomyces albidoflavus; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCA_001953855.1; Amycolatopsis keratiniphila; counts= 1; multicellularity status: TRUE**
  - cNMP_cyclase+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like<-cNMP_binding+HTH_Crp_2
- **GCF_001578075.1; Microcystis aeruginosa; counts= 1; multicellularity status: TRUE**
  - AB_hydrolase->CASPASE+EAD2->EAD2+VMAP-M11+VMAP-C->MoxR->vWA+FGS-fold_domain*->
- **GCF_001895105.1; Streptomyces sp. NBRC 110465; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->
- **GCA_900141985.1; Nocardiopsis flavescens; counts= 1; multicellularity status: TRUE**
  - Trypsin+EAD2->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-DUF397||Trypco1->
- **GCA_001905145.1; Nocardiopsis sp. TSRI0078; counts= 1; multicellularity status: TRUE**
  - Trypsin+VMAP-M0+VMAP-C->vWA+APATPase+wHTH+TPRs*->||<-DUF397||Trypco1->
- **GCA_001905365.1; Streptomyces sp. CB02488; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->Trypco1->
- **GCF_001905645.1; Streptomyces sp. CB02115; counts= 1; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->AB_hydrolase->CASPASE+EAD2->FXSXX-COOH-like->METALLOPROTEASE+TPRs->

- **GCF_001905905.1; Streptomyces sp. CB02366; counts= 1; multicellularity status: TRUE**
  - AB_hydrolase->CASPASE+VMAP-M0+VMAP-C->MoxR->vWA+STAND_NTPase+Trypsin+CASPASE+S1COLD*->
- **GCF_001905405.1; Streptomyces sp. TSRI0445; counts= 1; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->AB_hydrolase->CASPASE+EAD2->FXSXX-COOH-like->METALLOPROTEASE+TPRs->
- **GCF_001905795.1; Streptomyces sp. CB01580; counts= 1; multicellularity status: TRUE**
  - AB_hydrolase->CASPASE+VMAP-M2+VMAP-C->MoxR->vWA+cNMP_cyclase+TCAD13*->
- **GCF_001905345.1; Streptomyces uncialis; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+wHTH+TPRs+cNMP_cyclase*->
- **GCF_001905485.1; Streptomyces sp. TSRI0261; counts= 1; multicellularity status: TRUE**
  - AB_hydrolase->CASPASE+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->
- **GCA_001905485.1; Streptomyces sp. TSRI0261; counts= 1; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->AB_hydrolase->CASPASE+EAD2->FXSXX-COOH-like->METALLOPROTEASE+TPRs->
- **GCA_001905755.1; Amycolatopsis sp. CB00013; counts= 1; multicellularity status: TRUE**
  - cNMP_cyclase+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like<-cNMP_binding+HTH_Crp_2
- **GCA_001905735.1; Streptomyces sp. CB01249; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->Trypco1->
- **GCF_001905735.1; Streptomyces sp. CB01249; counts= 1; multicellularity status: TRUE**
  - AB_hydrolase->CASPASE+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->
- **GCF_001905825.1; Streptomyces sp. CB02009; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCA_001905705.1; Streptomyces sp. CB02460; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCA_900111245.1; Streptomyces qinglanensis; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH-like->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCA_001921205.1; Actinophytocola xanthii; counts= 1; multicellularity status: TRUE**
  - cNMP_cyclase+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like<-cNMP_binding+HTH_Crp_2
- **GCA_001921215.1; Actinophytocola xinjiangensis; counts= 1; multicellularity status: TRUE**
  - cNMP_cyclase+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like<-cNMP_binding+HTH_Crp_2
- **GCA_001939115.1; Oscillatoriales cyanobacterium 'hensonii'; counts= 1; multicellularity status: TRUE**
  - EAD1+Trypsin->?->EAD1+VMAP-M1+VMAP-C->MoxR->vWA+FGS-fold_domain*->four_helix_bundle_protein->RVT_1->FGS-fold_domain->

- **GCF_001941275.1; Streptomyces acidiscabies; counts= 1; multicellularity status: TRUE**
  - vWA+Pkinase+wHTH+cNMP_cyclase+Band7+HAD*->
- **GCA_001983215.1; Frankia sp. CcI49; counts= 1; multicellularity status: TRUE**
  - EAD2+EAD1->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs
- **GCA_001977425.1; Burkholderia pseudomallei; counts= 1; multicellularity status: FALSE**
  - AB_hydrolase->CASPASE+VMAP-M4+VMAP-C->MoxR->vWA+REC*->
- **GCA_001984175.1; Saccharothrix sp. ALI-22-I; counts= 1; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-cNMP_cyclase+EAD2
- **GCF_001984575.1; Streptomyces sp. MP131-18; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCA_001984575.1; Streptomyces sp. MP131-18; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->
- **GCA_001989395.1; Nocardia donostiensis; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->Voltage_CLC->METALLOPROTEASE->TIR+APATPase+wHTH+TPRs->
- **GCA_001998325.1; Nocardiopsis sinuspersici; counts= 1; multicellularity status: TRUE**
  - Trypsin+VMAP-M0+VMAP-C->vWA+APATPase+wHTH+TPRs*->||<-DUF397||Trypco1->
- **GCF_002005565.1; Streptomyces sp. JHA26; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->
- **GCA_001642995.1; Streptomyces jeddahensis; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||PSE->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCF_002007685.1; Streptomyces sp. fd1-xmd; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCF_000239075.1; Streptomyces sp. W007; counts= 1; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->AB_hydrolase->CASPASE+EAD2->FXSXX-COOH-like->METALLOPROTEASE+TPRs->
- **GCF_000497445.1; Streptomyces roseochromogenus; counts= 1; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like
- **GCA_900167435.1; Marinactinospora thermotolerans; counts= 1; multicellularity status: TRUE**
  - Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-DUF397||Trypco1->
- **GCF_000721685.1; Streptomyces mediolani; counts= 1; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->AB_hydrolase->CASPASE+EAD2->FXSXX-COOH-like->METALLOPROTEASE+TPRs->

- **GCF_001279545.1; Streptomyces sp. NRRL B-3648; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+wHTH+TPRs*->
- **GCF_001270575.1; Streptomyces decoyicus; counts= 1; multicellularity status: TRUE**
  - AB_hydrolase->CASPASE+VMAP-M2+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs+SFI-helicase*->
- **GCF_000931445.1; Streptomyces cyaneogriseus; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCA_002024165.1; Streptomyces scabrisporus; counts= 1; multicellularity status: TRUE**
  - CASPASE+VMAP-M19+VMAP-C->MoxR->vWA+BetaPropeller*->
- **GCF_001047315.1; Streptomyces leeuwenhoekii; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCF_001418645.1; Streptomyces neyagawaensis; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*->
- **GCF_001509775.1; Streptomyces violaceusniger; counts= 1; multicellularity status: TRUE**
  - AB_hydrolase->CASPASE+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+TIR+cNMP_cyclase+S1COLD+EAD2*->
- **GCF_001514065.1; Streptomyces antibioticus; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD*->
- **GCF_001514305.1; Streptomyces sp. RV15; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD*->
- **GCF_001700515.1; Streptomyces lushanensis; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCF_001595515.1; Streptomyces sp. CC71; counts= 1; multicellularity status: TRUE**
  - Trypco1->PSE->MoxR->vWA+Pkinase+wHTH+TPRs+cNMP_cyclase*->
- **GCF_001746285.1; Streptomyces sp. EN16; counts= 1; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->
- **GCF_001542625.1; Streptomyces griseochromogenes; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7*->
- **GCF_001660045.1; Streptomyces parvulus; counts= 1; multicellularity status: TRUE**
  - Trypco2->EAD2+VMAP-M0+VMAP-C->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like<-Trypsin+EAD2
- **GCF_001013905.1; Streptomyces leeuwenhoekii; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->

- **GCF_001866675.1; Streptomyces sp. MUSC 14; counts= 1; multicellularity status: TRUE**
  - Trypco2->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+Pkinase+NaeI*->
- **GCF_001905855.1; Streptomyces sp. CB01883; counts= 1; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-Na_H_Exchanger||AB_hydrolase->CASPASE+EAD2->FXSXX-COOH-like->METALLOPROTEASE+TPRs->
- **GCF_001905725.1; Streptomyces sp. CB02400; counts= 1; multicellularity status: TRUE**
  - CASPASE+VMAP-M2+VMAP-C->MoxR->||<-?||vWA+SWACOS+Trypsin+TIR+HTH*->
- **GCF_001953885.1; Streptomyces sp. IMTB 2501; counts= 1; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like
- **GCF_001953875.1; Streptomyces amritsarensis; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCF_001941845.1; Streptomyces sp. TN58; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCA_002027195.1; Streptomyces sp. GKU 895; counts= 1; multicellularity status: TRUE**
  - MoxR->vWA_protein*->
- **GCF_002028425.1; Streptomyces katrae; counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->?->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCA_003814735.1; Streptomyces katrae; counts= 1; multicellularity status: TRUE**
  - AB_hydrolase->||<-?||MoxR->vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats*->
- **GCF_001570465.1; Mycobacterium fortuitum; counts= 1; multicellularity status: FALSE**
  - AB_hydrolase->CASPASE+VMAP-M2+VMAP-C->MoxR->vWA+HD+RelA+TGS*->
- **GCA_002078175.1; Streptomyces sp. M41(2017); counts= 1; multicellularity status: TRUE**
  - <-TCAD15||Trypco1->Trypsin+HDxxH+VMAP-M0+VMAP-C->MoxR->vWA+TPRs*->FXSXX-COOH->Radical_SAM->METALLOPROTEASE+TPRs->TIR+APATPase+TPRs->
- **GCF_001983105.1; Frankia sp. M16386; counts= 1; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->TIR+APATPase+TPRs->||<-METALLOPROTEASE+TPRs
- **GCF_000447295.1; Fischerella sp. PCC 9431; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+EAD9->EAD9+EAD1+VMAP-C->MoxR->vWA+FGS-fold_domain*->FGS-fold_domain->four_helix_bundle_protein->RVT_1->
- **GCF_000464825.1; Planktothrix agardhii; counts= 1; multicellularity status: TRUE**
  - CASPASE+VMAP-M1+VMAP-C->MoxR->vWA+MNS+MNS*->
- **GCF_000478275.1; Amycolatopsis orientalis; counts= 1; multicellularity status: TRUE**
  - cNMP_cyclase+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like<-cNMP_binding+HTH_Crp_2

- **GCA__000754115.1; Amycolatopsis sp. MJM2582; counts= 1; multicellularity status: TRUE**
  - cNMP_cyclase+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like<-cNMP_binding+HTH_Crp_2
- **GCF__000955955.1; Lechevalieria aerocolonigenes; counts= 1; multicellularity status: TRUE**
  - <-cNMP_binding+HTH_Crp_2||cNMP_cyclase+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like
- **GCA__000948395.1; Frankia sp. CpI1-S; counts= 1; multicellularity status: TRUE**
  - EAD2+EAD1->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like
- **GCF__000972705.2; Limnoraphis robusta; counts= 1; multicellularity status: TRUE**
  - FGS-fold_domain->||<-?<-?||EAD4+VMAP-M3+VMAP-C->MoxR->vWA+FGS-fold_domain*->?->FGS-fold_domain->
- **GCA__900113515.1; Amycolatopsis regifaucium; counts= 1; multicellularity status: TRUE**
  - cNMP_cyclase+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like<-cNMP_binding+HTH_Crp_2
- **GCF__000943515.2; Amycolatopsis orientalis; counts= 1; multicellularity status: TRUE**
  - cNMP_cyclase+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like<-cNMP_binding+HTH_Crp_2
- **GCF__001854645.1; Frankia sp. EUN1h; counts= 1; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs->||<-METALLOPROTEASE+TPRs||EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs
- **GCF__000826545.1; Kibdelosporangium sp. MJ126-NF4; counts= 1; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like<-?||EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs->||<-METALLOPROTEASE+TPRs
- **GCF__001414035.1; Frankia sp. ACN1ag; counts= 1; multicellularity status: TRUE**
  - EAD2+EAD1->EAD2+VMAP-M0+VMAP-C->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like
- **GCA__900010725.1; Planktothrix serta; counts= 1; multicellularity status: TRUE**
  - vWA+MACRODOMAIN+GUN4+DO-GTPase2*->
- **GCF__001905755.1; Amycolatopsis sp. CB00013; counts= 1; multicellularity status: TRUE**
  - cNMP_cyclase+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like<-cNMP_binding+HTH_Crp_2
- **GCF__000620785.1; Pseudonocardia acaciae; counts= 1; multicellularity status: TRUE**
  - cNMP_binding+HTH_Crp_2->?->cNMP_cyclase+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs
- **GCF__001904725.1; Phormidium ambiguum; counts= 1; multicellularity status: TRUE**
  - cNMP_cyclase+VMAP-M1+VMAP-C->MoxR->vWA+FGS-fold_domain*->FGS-fold_domain->
- **GCF__001953865.1; Amycolatopsis coloradensis; counts= 1; multicellularity status: TRUE**
  - cNMP_cyclase+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-FXSXX-COOH-like<-cNMP_binding+HTH_Crp_2
- **GCF__000582685.1; [Scytonema hofmanni] UTEX B 1581; counts= 1; multicellularity status: TRUE**
  - EAD10+VMAP-M1+VMAP-C->MoxR->vWA+MNS+GUN4+EAD10+BetaPropeller*->

- **GCA_002099185.1; Streptomyces sp. CB03238; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+wHTH+TPRs+wHTH+TPRs+APATPase+wHTH+TPRs*->
- **GCA_002095975.1; Microcystis aeruginosa; counts= 1; multicellularity status: TRUE**
  - HTH+VMAP-M9+VMAP-C->MoxR->vWA+FGS-fold_domain*->||<-?<-?<-?<-PSE||?->FGS-fold_domain->
- **GCA_002114065.1; Streptomyces griseofuscus; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+cNMP_cyclase+Band7+HAD*->
- **GCF_000328705.1; Saccharothrix espanaensis; counts= 1; multicellularity status: TRUE**
  - EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs*->||<-METALLOPROTEASE+TPRs<-cNMP_cyclase+EAD2
- **GCF_002150735.1; Streptomyces africanus; counts= 1; multicellularity status: TRUE**
  - Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+GGDEF+EAD2+VMAP-M0+VMAP-C*->
- **GCF_002154275.1; Streptomyces castelarensis; counts= 1; multicellularity status: TRUE**
  - AB_hydrolase->CASPASE+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+TIR+cNMP_cyclase+S1COLD+EAD2*->
- **GCF_002140155.1; Micromonospora sp. NBS 11-29; counts= 1; multicellularity status: TRUE**
  - Trypco1+Trypsin+VMAP-M0+VMAP-C->MoxR->vWA+Trypsin+Coiled-coil*->Glyco_hydro_16+Ricin_B_lectin->||<-?||?->DUF397->
- **GCA_004296455.1; Calothrix sp. NIES-4101; counts= 1; multicellularity status: TRUE**
  - EAD1+Trypsin->?->EAD1+VMAP-M1+VMAP-C->||<-?||VMAP-C(partial)->MoxR->vWA+REC+CASPASE+FGS-fold_domain*->
- **GCF_002551305.1; Streptomyces sp. or20; counts= 1; multicellularity status: TRUE**
  - Trypsin+EAD2+VMAP-M0+VMAP-C->MoxR->vWA+Pkinase+APATPase+TPRs*->
- **GCA_002573955.1; Streptomyces sp. Ru87; counts= 1; multicellularity status: TRUE**
  - vWA+Pkinase+Pkinase+TPRs*->
- **GCA_002776695.1; Bradyrhizobium sp. TSA1; counts= 1; multicellularity status: TRUE**
  - AB_hydrolase->CASPASE+VMAP-M4+VMAP-C->MoxR->vWA+REC+REC+GAF+GAF+GAF+Acylphosphatase+CASPASE*->

iSTAND systems

- **GCA_001292585.1; Candidatus Magnetomorum sp. HK-1; counts= 9; multicellularity status: TRUE**
  - DRHyd+iSTAND*->
  - iSTAND*->MoxR->??+FGE-sulfatase->
  - iSTAND*->MoxR->||<-tRNA_anti-codon+tRNA-synt_2||REC+PAS+NtrC-AAA+FIS-HTH->REC+cNMP_cyclase->HAM->
  - Nucleoside_deoxyribosyltransferas?->iSTAND(fragment)*->
  - TIR+iSTAND*->MoxR->TM+TM+vWA+TM+PEGA+PEGA+FGS-fold_domain->
  - TIR+iSTAND*->STAND_NTPase->
  - TM+TM+iSTAND*->
  - TM+TM+iSTAND*->MoxR->
  - ZnR+ZnR+TIR+iSTAND*->MoxR->TM+TM+vWA+TM+FGS-fold_domain->
- **GCA_000516475.1; Candidatus Magnetoglobus multicellularis str. Araruama; counts= 5; multicellularity status: TRUE**
  - DRHyd+iSTAND*->??->GspA-ATPase(fragment)->
  - DRHyd+iSTAND*->MoxR->
  - iSTAND(fragment)*->??->??->
  - STNAD_NTPase+REase7->ZnR+ZnR+TIR+iSTAND*->MoxR->
  - TIR+iSTAND*->
- **GCA_000346485.2; Scytonema hofmannii PCC 7110; counts= 4; multicellularity status: TRUE**
  - BetaPropeller+iSTAND*->
  - Coiled-coil+iSTAND*->
  - EAD9+iSTAND*->MoxR->helical_region(leucine-richLWxKmotif)+vWA->??+CHASE+TM+TM->
  - PNP_UDP_1+EAD9->iSTAND*->MoxR->helical_region(leucine-richLWxKmotif)+vWA+FGS-fold_domain->
- **GCA_001698425.1; Oscillatoriales cyanobacterium USR001; counts= 4; multicellularity status: TRUE**
  - ??->??+HTH+iSTAND*->MoxR->
  - CASPASE+iSTAND*->MoxR->helical_region(leucine-richLWxKmotif)+vWA->Ntox45->HEPN->??->
  - EAD1+CASPASE+iSTAND*->MoxR->helical_region(leucine-richLWxKmotif)+vWA->vWA+EAD1-unk5+CASPASE->
  - HTH+iSTAND*->MoxR->
- **GCA_003242955.1; Candidatus Methyloumidiphilus alinensis; counts= 3; multicellularity status: FALSE**
  - ??->iSTAND*->MoxR->TM+TM+vWA+TM+FGE-sulfatase->
  - DrHyd+EAD9->EAD9+iSTAND*->MoxR->helical_region(leucine-richLWxKmotif)+vWA->
  - TIR+iSTAND*->MoxR->
- **GCA_003646175.1; Gammaproteobacteria bacterium; counts= 3; multicellularity status: NA**

- ??->Trypco1->||<-??||Trypsin+iSTAND*->MoxR->HTH->
- EAD-unk2->CASPASE+iSTAND*->HTH->MoxR->??->??+DUF4351->
- TM+TM+iSTAND*->

■ **GCA_000212735.1; Haliscomenobacter hydrossis DSM 1100; counts= 2; multicellularity status: TRUE**

- CASPASE+iSTAND*->MoxR->vWA+??+FGS-fold_domain+FGS-fold_domain+FGS-fold_domain+FGS-fold_domain->
- TM+TM+TM+TM+STAND_NTPase+TM+TM+TM+TM->||<-STAND_NTPase+REase<-TM||HTH->PIN+DUF3368->EADiS+iSTAND*->MoxR->||<-vWA<-??+beta-sandwich(Ig-like?)

■ **GCA_002368175.1; Calothrix sp. NIES-2098; counts= 2; multicellularity status: TRUE**

- Coiled-coil+iSTAND*->MoxR->helical_region(leucine-richLWxKmotif)+TM+Calx-beta?+TM+vWA->vWA+FGS-fold_domain->
- EAD9+iSTAND*->MoxR->helical_region(leucine-richLWxKmotif)+vWA->Cation_ATPase->Calcineurin->

■ **GCA_000300115.1; Tolypothrix sp. PCC 7601; counts= 2; multicellularity status: TRUE**

- HTH+iSTAND+HTH+IG-like+CASPASE+IG-like*->CASPASE->Pkinase+STAND_NTPase+macroglobulin-like+CASPASE->CASPASE->Coiled-coil->
- TM+DUF218->||<-??<-??||Coiled-coil+iSTAND*->MoxR->

■ **GCA_000473895.1; Rubidibacter lacunae KORDI 51-2; counts= 2; multicellularity status: TRUE**

- ??->iSTAND*->MoxR->TM+TM+vWA+TM->
- <-Trypco1||CASPASE+iSTAND*->MoxR->helical_region(leucine-richLWxKmotif)+vWA->BetaPropeller+TPRs+FGE-sulfatase->FGS-fold_domain->

■ **GCA_001314905.1; Phormidium sp. OSCR; counts= 2; multicellularity status: TRUE**

- <-Trypco1||CASPASE+iSTAND*->MoxR->helical_region(leucine-richLWxKmotif)+vWA->vWA+FGS-fold_domain->
- Coiled-coil+iSTAND*->MoxR->helical_region(leucine-richLWxKmotif)+vWA->

■ **GCA_001698435.1; Nostoc sp. MBR 210; counts= 2; multicellularity status: TRUE**

- ??+bDLD1+Trypsin->??->bDLD1+iSTAND*->MoxR->helical_region(leucine-richLWxKmotif)+vWA->
- HTH+iSTAND*->MoxR->helical_region(leucine-richLWxKmotif)+vWA->??+CASPASE->

■ **GCA_003695465.1; Bacteroidetes bacterium; counts= 2; multicellularity status: FALSE**

- Coiled-coil+iSTAND(fragment)*->
- iSTAND(fragment)*->MoxR->TM+beta-sandwich(Ig-like?)->

■ **GCA_003696835.1; Bacteroidetes bacterium; counts= 2; multicellularity status: FALSE**

- <-??||CASPASE+iSTAND*->TM+TM+vWA+??+BetaPropeller->
- REC+Alkaline_phosphatase-like->CASPASE+iSTAND*->??->Radical_SAM->

■ **GCA_900099115.2; Thiotrichales bacterium HS_08; counts= 2; multicellularity status: TRUE**

- <-PseudoU_synth||??->??+CASPASE+iSTAND*->
- Trypsin+iSTAND*->

■ **GCF_000380225.1; filamentous cyanobacterium ESFC-1; counts= 2; multicellularity status: TRUE**

- <-NfeD||??->??+iSTAND*->MoxR->
- HTH+iSTAND*->MoxR->helical_region(leucine-richLWxKmotif)+vWA->

■ **GCF_000373105.1; Lewinella persica; counts= 2; multicellularity status: TRUE**

- Coiled-coil+iSTAND*->MoxR->TM+TM+??TM+??+CASPASE->
- EADiS+iSTAND*->MoxR->

■ **GCF_900185595.1; Calothrix rhizosoleniae; counts= 2; multicellularity status: TRUE**

- EAD4+iSTAND*->MoxR->
- EAD9+iSTAND*->MoxR->helical_region(leucine-richLWxKmotif)+vWA->vWA+FGS-fold_domain->

■ **GCA_000014265.1; Trichodesmium erythraeum IMS101; counts= 1; multicellularity status: TRUE**

- iSTAND*->MoxR->TM+TM+vWA+TM+TM+TM+TM+TM+TM->

■ **GCA_000020025.1; Nostoc punctiforme PCC 73102; counts= 1; multicellularity status: TRUE**

- CASPASE+EAD9->EAD9+iSTAND*->STAND_NTPase->MoxR(fragment)->helical_region(leucine-richLWxKmotif)+vWA->??+REC->GUN4->

■ **GCA_000021825.1; Gloeothece citriformis PCC 7424; counts= 1; multicellularity status: TRUE**

- <-TM||HTH+iSTAND*->MoxR->helical_region(leucine-richLWxKmotif)+vWA->

■ **GCA_000219585.1; Nitrosomonas sp. Is79A3; counts= 1; multicellularity status: FALSE**

- TIR+iSTAND*->MoxR->TM+TM+vWA+TM+FGS-fold_domain->

■ **GCA_000316665.1; Rivularia sp. PCC 7116; counts= 1; multicellularity status: TRUE**

- Trypco1->Trypsin+iSTAND*->MoxR->helical_region(leucine-richLWxKmotif)+vWA->vWA+FGS-fold_domain->

■ **GCA_000317435.1; Calothrix sp. PCC 6303; counts= 1; multicellularity status: TRUE**

- CASPASE+iSTAND*->STAND_NTPase(fragment)->

■ **GCA_000317535.1; Cylindrospermum stagnale PCC 7417; counts= 1; multicellularity status: TRUE**

- CASPASE+EAD9->Coiled-coil+iSTAND*->

■ **GCA_001854205.1; Moorea producens JHB; counts= 1; multicellularity status: TRUE**

- Coiled-coil+iSTAND*->MoxR->helical_region(leucine-richLWxKmotif)+TM+Calx-beta?+TM+vWA->

■ **GCA_002796605.1; Sphingomonas sp. Cra20; counts= 1; multicellularity status: FALSE**

- rve_3->Trypsin+iSTAND*->MoxR->

■ **GCA_002813575.1; Nostoc flagelliforme CCNUN1; counts= 1; multicellularity status: TRUE**

- EAD9+iSTAND*->MoxR->helical_region(leucine-richLWxKmotif)+vWA->??+TM->CASPASE(fragment)->

■ **GCA_000210375.1; Arthrospira platensis NIES-39; counts= 1; multicellularity status: TRUE**

- SLH+OprB->||<-TM||RadC-like_JAB+sGTPase->Coiled-coil+iSTAND*->MoxR->helical_region(leucine-richLWxKmotif)+vWA->TA_antitoxin(DUF1902)->Ntox45->HEPN->

■ **GCA_002368215.1; Nostoc sp. NIES-2111; counts= 1; multicellularity status: TRUE**

- Pentapeptide_repeats+TM+TM+TM+TM+TM+TM+TM+Pentapeptide_repeats->Pentapeptide_repeats->STNAD_NTPase+TM+TM+TM+TM+TM+TM+TM+TM->iSTAND*->MoxR->TM+TM+vWA->||<-DDE_endonuclease<-PAIREDC-HTH||beta-rich_jelly-roll?->

■ **GCA_002368235.1; Scytonema sp. HK-05; counts= 1; multicellularity status: TRUE**

- iSTAND*->MoxR->helical_region(leucine-richLWxKmotif)+vWA->TM+Pentapeptide_repeats+TM+TM+TM+TM+TM+TM+TM+Pentapeptide_repeats->||<-TM+TM+TM+TM+TM

- **GCA_002368435.1; Scytonema sp. NIES-4073; counts= 1; multicellularity status: TRUE**
  - EAD8+Trypsin->EAD8+iSTAND*->MoxR->helical_region(leucine-richLWxKmotif)+vWA->REase->vWA+GTPase-AIG->
- **GCA_002368335.1; Nostoc sp. NIES-4103; counts= 1; multicellularity status: TRUE**
  - HTH+iSTAND*->MoxR->helical_region(leucine-richLWxKmotif)+vWA->
- **GCA_003609755.1; Planktothrix agardhii NIES-204; counts= 1; multicellularity status: TRUE**
  - ??+HTH+iSTAND*->MoxR->helical_region(leucine-richLWxKmotif)+vWA->
- **GCA_000026145.1; Bradyrhizobium sp. ORS 278; counts= 1; multicellularity status: TRUE**
  - Trypco2->Trypsin+iSTAND*->MoxR->2TM+vWA+22TM->??+TM->??->
- **GCA_000283655.1; Azospirillum lipoferum 4B; counts= 1; multicellularity status: FALSE**
  - Trypco2->Trypsin+iSTAND*->MoxR->2TM+vWA+22TM->
- **GCA_900009265.1; Planktothrix paucivesiculata PCC 9631; counts= 1; multicellularity status: TRUE**
  - Death-like.bact-prob+iSTAND*->MoxR->helical_region(leucine-richLWxKmotif)+vWA->vWA+TPRs+CASPASE->??->
- **GCA_900009145.1; Planktothrix tepida PCC 9214; counts= 1; multicellularity status: TRUE**
  - HTH+iSTAND*->MoxR->helical_region(leucine-richLWxKmotif)+vWA->
- **GCA_001458735.1; Candidatus Nitrospira nitrosa; counts= 1; multicellularity status: NA**
  - DUF805(3TM_protein)->??->DUF805(3TM_protein)->TM+TM+TM->TIR+iSTAND*->MoxR->TM+TM+vWA+TM+TM->
- **GCA_000169335.1; Crocosphaera chwakensis CCY0110; counts= 1; multicellularity status: TRUE**
  - AB_hydrolase->CASPASE+iSTAND*->MoxR->helical_region(leucine-richLWxKmotif)+vWA->vWA+FGS-fold_domain->
- **GCA_000170715.1; Beggiatoa sp. PS; counts= 1; multicellularity status: TRUE**
  - PNP_UDP_1->PNP_UDP_1(fragment)->iSTAND*->HTH->MoxR->
- **GCA_000155555.1; Coleofasciculus chthonoplastes PCC 7420; counts= 1; multicellularity status: TRUE**
  - <-TM||HTH+iSTAND*->MoxR->
- **GCA_000307915.1; Arthrospira platensis C1; counts= 1; multicellularity status: TRUE**
  - SLH+OprB->RadC-like_JAB+sGTPase->Coiled-coil+iSTAND*->MoxR->helical_region(leucine-richLWxKmotif)+vWA->TA_antitoxin(DUF1902)->HicA_toxin->Ntox45->
- **GCA_000585055.1; Candidatus Accumulibacter sp. BA-92; counts= 1; multicellularity status: FALSE**
  - TIR+iSTAND*->MoxR->TM+TM->vWA+TIR->TM+FGS-fold_domain->
- **GCA_000739535.1; Candidatus Vecturithrix granuli; counts= 1; multicellularity status: TRUE**
  - TIR+iSTAND*->GspA-ATPase(fragment)->Ploop_inactive->
- **GCA_003864295.1; Aphanothece sacrum FPU1; counts= 1; multicellularity status: TRUE**
  - HTH+iSTAND*->MoxR->

- **GCA_000710505.1; Planktothrix agardhii NIVA-CYA 126/8; counts= 1; multicellularity status: TRUE**
  - ??+HTH+iSTAND*->MoxR->vWA+FGE-sulfatase->
- **GCA_000584955.2; Candidatus Accumulibacter sp. SK-01; counts= 1; multicellularity status: FALSE**
  - iSTAND*->MoxR->
- **GCA_000817745.1; Aphanocapsa montana BDHKU210001; counts= 1; multicellularity status: TRUE**
  - iSTAND*->MoxR->??->
- **GCA_000817785.1; Hassallia byssoidea VB512170; counts= 1; multicellularity status: TRUE**
  - EAD9+iSTAND*->MoxR->??->
- **GCA_000817775.1; Lyngbya confervoides BDU141951; counts= 1; multicellularity status: TRUE**
  - TM+TM+TM+TM+TM->EAD9+iSTAND*->
- **GCA_000828075.2; Tolypothrix campylonemoides VB511288; counts= 1; multicellularity status: TRUE**
  - cyclic_phosphodiesterase->OppC_N+TM+BPD_transp_1->DRHyd+iSTAND*->
- **GCA_001399705.1; Kouleothrix aurantiaca; counts= 1; multicellularity status: TRUE**
  - STAND_NTPase->Coiled-coil+iSTAND*->STAND_NTPase->
- **GCA_001428505.1; Terrabacter sp. Root181; counts= 1; multicellularity status: TRUE**
  - CASPASE->EAD9+iSTAND*->MoxR->helical_region(leucine-richLWxKmotif)+vWA->CASPASE+Pkinase->
- **GCA_001456025.1; Mastigocoleus testarum BC008; counts= 1; multicellularity status: TRUE**
  - <-??+Coiled-coil+TM+TM<-??||CASPASE+APATPase+wTHT+TPR->CASPASE+iSTAND*->MoxR->helical_region(leucine-richLWxKmotif)+vWA->
- **GCA_001580545.1; Paraburkholderia monticola; counts= 1; multicellularity status: FALSE**
  - DUF805(3TM_protein)->TM+TM+TM->TIR+iSTAND*->MoxR->TM+TM+vWA+TM+TM->??->??->||<-??
- **GCA_001712795.1; Nostoc sp. KVJ20; counts= 1; multicellularity status: TRUE**
  - EAD1+VMAP-M1+iSTAND*->MoxR->helical_region(leucine-richLWxKmotif)+vWA->TM+sGTPase->
- **GCA_000817735.2; Scytonema millei VB511283; counts= 1; multicellularity status: TRUE**
  - HTH+iSTAND*->MoxR->helical_region(leucine-richLWxKmotif)+vWA->vWA+FGS-fold_domain->
- **GCA_001746915.1; Desertifilum sp. IPPAS B-1220; counts= 1; multicellularity status: TRUE**
  - iSTAND*->MoxR->helical_region(leucine-richLWxKmotif)+vWA+FGS-fold_domain->Four-helical-protein->RVT->
- **GCA_001899605.1; Sphingobacteriales bacterium 40-81; counts= 1; multicellularity status: NA**
  - <-??||DRHyd+iSTAND*->MoxR->TM+TM+beta-sandwich(Ig-like?)+vWA+TM+??+LRRs?->TM+ATP-synt_A->TM+TM->ATP-synt_B->
- **GCA_001904675.1; Scytonema sp. HK-05; counts= 1; multicellularity status: TRUE**
  - pJV1-spdB3?->cNMP_cyclase->??+iSTAND*->MoxR->helical_region(leucine-richLWxKmotif)+vWA->vWA+FGS-fold_domain->

- **GCA_001942495.1; Moorea bouillonii PNG; counts= 1; multicellularity status: TRUE**
  - Trypsin+iSTAND*->MoxR->helical_region(leucine-richLWxKmotif)+vWA->
- **GCA_002077945.1; Niastella vici; counts= 1; multicellularity status: TRUE**
  - DrHyd+iSTAND*->MoxR->TM+beta-sandwich(Ig-like?)+TM+vWA+TM+??->
- **GCA_002083395.1; Proteobacteria bacterium SG_bin4; counts= 1; multicellularity status: NA**
  - TIR+iSTAND*->MoxR->TM->TM+vWA+TM+FGS-fold_domain->
- **GCA_002084355.1; Bacteroidetes bacterium 4572_128; counts= 1; multicellularity status: FALSE**
  - TIR->iSTAND*->MoxR->Coiled-coil+??->??+DrHyd+APATPase+wHTH+TPR->TPRs->
- **GCA_002212985.1; Sphingobacteriales bacterium TSM_CSS; counts= 1; multicellularity status: NA**
  - TIR+iSTAND*->MoxR->TM+beta-sandwich(Ig-like?)+TM+vWA+TM+TM+TPRs+BetaPropeller->ZnR->||<-TM||MazG+MazG->
- **GCA_002289455.1; Calothrix elsteri CCALA 953; counts= 1; multicellularity status: TRUE**
  - CASPASE+EAD9->EAD9+iSTAND*->MoxR(fragment)->
- **GCA_002591745.1; Lewinellaceae bacterium SD302; counts= 1; multicellularity status: NA**
  - EADiS+iSTAND*->MoxR->beta-sandwich(Ig-like?)+TM+vWA+TM+OmpA->
- **GCA_002842325.1; Betaproteobacteria bacterium HGW-Betaproteobacteria-13; counts= 1; multicellularity status: FALSE**
  - DRHyd+iSTAND*->MoxR->vWA->??+TIR+CASPASE->
- **GCA_002893205.1; Cylindrospermopsis raciborskii S07; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+iSTAND*->MoxR->
- **GCA_003003725.1; filamentous cyanobacterium Phorm 6; counts= 1; multicellularity status: TRUE**
  - EAD1+CASPASE+iSTAND*->MoxR->
- **GCA_002212765.2; Haliangium sp. UPWRP_2; counts= 1; multicellularity status: TRUE**
  - Coiled-coil??+iSTAND*->MoxR->helical_region(leucine-richLWxKmotif)+vWA->??->EAD7+EAD7+EAD7+EAD7+VWA->||<-??
- **GCA_003017785.1; filamentous cyanobacterium CCP5; counts= 1; multicellularity status: TRUE**
  - iSTAND*->MoxR->helical_region(leucine-richLWxKmotif)+vWA->Coiled-coil->
- **GCA_003023605.1; Bacteroidetes bacterium; counts= 1; multicellularity status: FALSE**
  - EADiS+iSTAND*->MoxR->TM+beta-rich_region+TM+vWA->
- **GCA_003261315.1; Hapalosiphonaceae cyanobacterium JJU2; counts= 1; multicellularity status: TRUE**
  - HTH+iSTAND*->MoxR->
- **GCA_003577195.1; Candidatus Brocadia sp.; counts= 1; multicellularity status: NA**
  - Trypco1->Trypsin+iSTAND*->

- **GCA_003645185.1; Gammaproteobacteria bacterium; counts= 1; multicellularity status: NA**
  - iSTAND*->
- **GCA_003645315.1; Gammaproteobacteria bacterium; counts= 1; multicellularity status: NA**
  - iSTAND*->DUF4065->BECR->MoxR->helical_bundle+TM+LysM+TM+vWA+iSvmX1+TM_region
- **GCA_003696485.1; Bacteroidetes bacterium; counts= 1; multicellularity status: FALSE**
  - EADiS+iSTAND*->STAND(fragment)->
- **GCA_001544535.2; Caballeronia choica; counts= 1; multicellularity status: FALSE**
  - Trypco2->Trypsin+iSTAND*->MoxR->TM+LRRs->
- **GCA_900107745.1; Variovorax sp. YR216; counts= 1; multicellularity status: FALSE**
  - TIR+iSTAND*->MoxR->TM+TM+vWA+BetaPropeller+PASTA->
- **GCF_000314005.1; Spirulina subsalsa; counts= 1; multicellularity status: TRUE**
  - ??+iSTAND*->MoxR->helical_region(leucine-richLWxKmotif)+vWA->TM->||<-Y1_Tnp
- **GCF_000315565.1; Mastigocladopsis repens; counts= 1; multicellularity status: TRUE**
  - EAD9+iSTAND*->MoxR->helical_region(leucine-richLWxKmotif)+vWA->
- **GCF_000332355.1; Geitlerinema sp. PCC 7105; counts= 1; multicellularity status: TRUE**
  - NTP_transferase->BetaPropeller+AB_hydrolase->||<-Trypco1||CASPASE+iSTAND*->MoxR->helical_region(leucine-richLWxKmotif)+vWA->||<-HicB_lk_antitox||vWA+FGS-fold_domain->FGS-fold_domain->
- **GCF_000331305.1; Calothrix sp. PCC 7103; counts= 1; multicellularity status: TRUE**
  - Coiled-coil+iSTAND*->MoxR->helical_region(leucine-richLWxKmotif)+vWA+FGS-fold_domain->
- **GCF_000379765.1; Flexithrix dorotheae; counts= 1; multicellularity status: TRUE**
  - TIR+iSTAND*->MoxR->
- **GCF_000379805.1; Lewinella cohaerens; counts= 1; multicellularity status: TRUE**
  - EADiS+iSTAND*->MoxR->??+beta-sandwich(Ig-like?)+TM+vWA+TM+FGE-sulfatase->||<-TPRs
- **GCF_000447295.1; Fischerella sp. PCC 9431; counts= 1; multicellularity status: TRUE**
  - TIR->iSTAND*->MoxR->helical_region(leucine-richLWxKmotif)+vWA->
- **GCF_000426905.1; Dolichospermum circinale; counts= 1; multicellularity status: TRUE**
  - EAD9+iSTAND*->MoxR->TM+TM+??+Amidase->RVT->
- **GCF_000472745.1; Bradyrhizobium japonicum; counts= 1; multicellularity status: TRUE**
  - TIR+iSTAND*->MoxR->TM+TM+vWA+TM+Sel1->??->
- **GCF_000423565.1; Runella zeae; counts= 1; multicellularity status: TRUE**
  - CASPASE+iSTAND*->MoxR->vWA->CASPASE+LRRs->SUI->??->

- **GCF_000582685.1; [Scytonema hofmanni] UTEX B 1581; counts= 1; multicellularity status: TRUE**
  - EAD9+iSTAND*->MoxR->helical_region(leucine-richLWxKmotif)+vWA->
- **GCF_000828085.2; Scytonema tolypothrichoides; counts= 1; multicellularity status: TRUE**
  - TIR+iSTAND*->MoxR->
- **GCF_001597745.1; Anabaena sp. 4-3; counts= 1; multicellularity status: TRUE**
  - ??+iSTAND*->MoxR->helical_region(leucine-richLWxKmotif)+vWA->
- **GCF_001858025.1; Trichormus sp. NMC-1; counts= 1; multicellularity status: TRUE**
  - Trypco1->Trypsin+EAD9->EAD9+iSTAND*->MoxR->helical_region(leucine-richLWxKmotif)+vWA->7TMR-HDED+Beta-rich+HTH+FGS-fold_domain->
- **GCF_000526455.1; Desulfovibrio magneticus; counts= 1; multicellularity status: FALSE**
  - DRHyd+iSTAND*->MoxR->vWA->??+TIR+APATPase+TPRs+Pentapeptide_repeats->
- **GCF_000744415.1; Ghiorsea bivora; counts= 1; multicellularity status: FALSE**
  - iSTAND+McrB*->REase->||<-SLOG||??->TM->DUF262+??+DUF1524(HNH?)->
- **GCF_000759025.1; Phaeodactylibacter xiamenensis; counts= 1; multicellularity status: TRUE**
  - CASPASE+AB_hydrolase+iSTAND*->MoxR->vWA->??+SGNH_hydrolase+CASPASE->
- **GCF_002198735.1; Ideonella sp. A 288; counts= 1; multicellularity status: FALSE**
  - TIR+iSTAND*->MoxR->BetaPropeller+FGS-fold_domain->
- **GCF_900469875.1; Rhizobiales bacterium; counts= 1; multicellularity status: FALSE**
  - iSTAND*->MoxR->TM+TM+vWA+TM+Sel1->
- **GCF_003838225.1; Okeania hirsuta; counts= 1; multicellularity status: TRUE**
  - ??+iSTAND*->MoxR->

FtsH systems

- **GCA_002720785.1; Deltaproteobacteria bacterium; counts= 2; multicellularity status: NA**
  - inactive_FtsH+FtsH*->X3_analog->
  - Radical_SAM->?->X5->inactive_FtsH+FtsH*->X3_analog->?->MoxR<-?||helical_unk+vWA->
- **GCF_000331735.1; Myxococcus stipitatus; counts= 1; multicellularity status: TRUE**
  - Radical_SAM->X6->X5->inactive_FtsH+FtsH*->X3_analog->a/b_unk+NEFF1+TPR_region->MoxR->?->helical_unk+ivWA->
- **GCA_002402105.1; Candidatus Cloacimonetes bacterium; counts= 1; multicellularity status: NA**
  - Radical_SAM->?->X5->inactive_FtsH+FtsH*->X3_analog->??+NEFF1->PSE->PSE->helical_unk+ivWA->
- **GCF_000186345.1; Isosphaera pallida; counts= 1; multicellularity status: TRUE**
  - inactive_FtsH+FtsH*->X3_analog->??+TPRs+NEFF1->MoxR->helical_unk+ivWA->
- **GCA_002747355.1; Proteobacteria bacterium; counts= 1; multicellularity status: TRUE**
  - Radical_SAM->X6->X5->inactive_FtsH+FtsH*->X3_analog->a/b_unk+NEFF1+TPR_region->MoxR->helical_unk+ivWA->
- **GCF_900101905.1; Myxococcus virescens; counts= 1; multicellularity status: TRUE**
  - Radical_SAM->X6->X5->inactive_FtsH+FtsH*->X3_analog->a/b_unk+NEFF1+TPR_region->MoxR->helical_unk+ivWA->
- **GCF_002305895.1; Myxococcus macrosporus; counts= 1; multicellularity status: TRUE**
  - Radical_SAM->X6->X5->inactive_FtsH+FtsH*->X3_analog->a/b_unk+NEFF1+TPR_region->MoxR->helical_unk+ivWA->
- **GCF_006401215.1; Myxococcus xanthus; counts= 1; multicellularity status: TRUE**
  - Radical_SAM->X6->X5->inactive_FtsH+FtsH*->X3_analog->a/b_unk+NEFF1+TPR_region->MoxR->helical_unk+ivWA->
- **GCF_006400955.1; Myxococcus xanthus; counts= 1; multicellularity status: TRUE**
  - Radical_SAM->X6->X5->inactive_FtsH+FtsH*->X3_analog->a/b_unk+NEFF1+TPR_region->MoxR->helical_unk+ivWA->
- **GCF_006401635.1; Myxococcus xanthus; counts= 1; multicellularity status: TRUE**
  - Radical_SAM->X6->X5->inactive_FtsH+FtsH*->X3_analog->a/b_unk+NEFF1+TPR_region->MoxR->helical_unk+ivWA->
- **GCF_006518195.1; Myxococcus; counts= 1; multicellularity status: TRUE**
  - Radical_SAM->X6->X5->inactive_FtsH+FtsH*->X3_analog->a/b_unk+NEFF1+TPR_region->MoxR->helical_unk+ivWA->
- **GCF_006547365.1; Myxococcus sp. AB025A; counts= 1; multicellularity status: TRUE**
  - Radical_SAM->X6->X5->inactive_FtsH+FtsH*->X3_analog->a/b_unk+NEFF1+TPR_region->MoxR->helical_unk+ivWA->

- **GCF__006547355.1; Myxococcus sp. AB024B; counts= 1; multicellularity status: TRUE**
  - Radical_SAM->X6->X5->inactive_FtsH+FtsH*->X3_analog->a/b_unk+NEFF1+TPR_region->MoxR->helical_unk+ivWA->
- **GCF__000988565.1; Myxococcus fulvus; counts= 1; multicellularity status: TRUE**
  - Radical_SAM->X6->X5->inactive_FtsH+FtsH*->X3_analog->a/b_unk+NEFF1+TPR_region->MoxR->||<-?||helical_unk+ivWA->
- **GCA__003327425.1; Candidatus Ozemobacter sibiricus; counts= 1; multicellularity status: NA**
  - inactive_FtsH+FtsH*->?->?->MoxR->helical_unk+ivWA->Radical_SAM->RadSAM_pep->
- **GCA__002839435.1; Candidatus Riflebacteria bacterium HGW-Riflebacteria-2; counts= 1; multicellularity status: NA**
  - inactive_FtsH+FtsH*->?->MoxR->helical_unk+ivWA->Radical_SAM->RadSAM_pep->?->X5->
- **GCA__002343915.1; Nannocystis exedens; counts= 1; multicellularity status: TRUE**
  - Radical_SAM->?->X5->inactive_FtsH+FtsH*->X3_analog->?->MoxR->helical_unk+ivWA->
- **GCF__900112715.1; Nannocystis exedens; counts= 1; multicellularity status: TRUE**
  - Radical_SAM->?->X5->inactive_FtsH+FtsH*->X3_analog->?->MoxR->helical_unk+ivWA->
- **GCF__000012685.1; Myxococcus; counts= 1; multicellularity status: TRUE**
  - Radical_SAM->X6->X5->inactive_FtsH+FtsH*->X3_analog->a/b_unk+NEFF1+TPR_region->MoxR->?->helical_unk+ivWA->
- **GCF__000280925.3; Myxococcus hansupus; counts= 1; multicellularity status: TRUE**
  - Radical_SAM->X6->X5->inactive_FtsH+FtsH*->X3_analog->a/b_unk+NEFF1+TPR_region->MoxR->helical_unk+ivWA->
- **GCF__002305875.1; Cystobacter fuscus; counts= 1; multicellularity status: TRUE**
  - Radical_SAM->X6->X5->inactive_FtsH+FtsH*->X3_analog->a/b_unk+NEFF1+TPR_region->MoxR->helical_unk+ivWA->?->?->||<-Radical_SAM
- **GCF__000335475.2; Cystobacter fuscus; counts= 1; multicellularity status: TRUE**
  - Radical_SAM->X6->?->X5->inactive_FtsH+FtsH*->X3_analog->a/b_unk+NEFF1+TPR_region->MoxR->helical_unk+ivWA->?->?->||<-Radical_SAM
- **GCF__000219105.1; Myxococcus macrosporus; counts= 1; multicellularity status: TRUE**
  - X6->X5->inactive_FtsH+FtsH*->X3_analog->a/b_unk+NEFF1+TPR_region->MoxR->helical_unk+ivWA->?->?->||<-Radical_SAM
- **GCF__001887355.1; Cystobacter ferrugineus; counts= 1; multicellularity status: TRUE**
  - Radical_SAM->X6->X5->inactive_FtsH+FtsH*->X3_analog->a/b_unk+NEFF1+TPR_region->MoxR->helical_unk+ivWA->?->?->||<-Radical_SAM
- **GCA__002839445.1; Candidatus Riflebacteria bacterium HGW-Riflebacteria-1; counts= 1; multicellularity status: NA**
  - inactive_FtsH+FtsH*->?->MoxR->helical_unk+ivWA->Radical_SAM->RadSAM_pep->?->X5->
- **GCF__900111765.1; Myxococcus fulvus; counts= 1; multicellularity status: TRUE**
  - Radical_SAM->X6->X5->inactive_FtsH+FtsH*->X3_analog->a/b_unk+NEFF1+TPR_region->MoxR->||<-?||helical_unk+vWA->
- **GCA__002722755.1; Proteobacteria bacterium; counts= 1; multicellularity status: TRUE**
  - Radical_SAM->?->X5->inactive_FtsH+FtsH*->X3_analog->?->MoxR->??+ivWA->||<-?||STAND_NTPase->

- **GCF_004138135.1; Oscillochloris sp. Chuk17; counts= 1; multicellularity status: TRUE**
  - TPRs->?->?->??+vWA+FGS-fold_domain->inactive_FtsH+FtsH*->REase->MoxR
- **GCF_000152145.1; Oscillochloris trichoides; counts= 1; multicellularity status: TRUE**
  - TPRs->?->?->??+vWA+FGS-fold_domain->inactive_FtsH+FtsH*->MoxR->?->?->STAND_NTPase->
- **GCF_006518215.1; Myxococcus sp. AB022; counts= 1; multicellularity status: TRUE**
  - Radical_SAM->X6->X5->inactive_FtsH+FtsH*->X3_analog->a/b_unk+NEFF1+TPR_region->MoxR->||<-?||helical_unk+ivWA->
- **GCF_000255705.1; Zavarzinella formosa; counts= 1; multicellularity status: TRUE**
  - Radical_SAM->?->Radical_SAM->X6->X5->inactive_FtsH+FtsH*->X3_analog->?->a/b_unk+NEFF+TPR_region->
- **GCF_001610855.1; Gemmata sp. SH-PL17; counts= 1; multicellularity status: FALSE**
  - Radical_SAM->X6->X5->inactive_FtsH+FtsH*->X3_analog->a/b_unk+NEFF1+TPR_region->a/b_unk+NEFF1+TPR_region->
- **GCF_000720255.1; Streptomyces griseus; counts= 1; multicellularity status: TRUE**
  - EAD1+CASPASE->RING(inactive)+RING->E1+UFD->EAD1+Ubl-Nterm+Ubl+E2->JAB-N+JAB->X1->inactive_FtsH+FtsH*->MoxR->X2->X3->TPRs->low_complexity+a/b_unk+TPR_repeat<-BetaPropeller+vWA<-RadSAM_pep<-RADICAL_SAM.Ammemo
- **GCF_000317435.1; Calothrix parietina; counts= 1; multicellularity status: TRUE**
  - E1+UFD->EAD8+Trypsin->TPRs+FGS-fold_domain->EAD8+EAD1->EAD1+Ubl-Nterm+Ubl+E2->JAB-N+JAB->X1->inactive_FtsH+FtsH*->TPRs+C-type_lectin->MoxR->?->X3->TPRs+C-type_lectin->TPRs+C-type_lectin->?->Clp_N_repeats+vWA<-RADICAL_SAM.Ammemo
- **GCF_002027195.1; Streptomyces sp. GKU 895; counts= 1; multicellularity status: TRUE**
  - E1+UFD->E1+UFD->EAD1+Ubl-Nterm+Ubl+E2->JAB_N+JAB->X1->inactive_FtsH+FtsH*->MoxR->X2->X3->PSE->?->beta_propeller(frag?)
- **GCF_000716715.1; Dactylosporangium aurantiacum; counts= 1; multicellularity status: TRUE**
  - E1+UFD->EAD1+Ubl-Nterm+Ubl+E2->JAB_N+JAB->X1->inactive_FtsH+FtsH*->MoxR->X2->X3->TPRs->low_complexity+a/b_unk+TPR_repeat->BetaPropeller+vWA->||<-RadSAM_pep<-RADICAL_SAM.Ammemo
- **GCF_900100605.1; Sinosporangium album; counts= 1; multicellularity status: TRUE**
  - E1+UFD->EAD1+Ubl-Nterm+Ubl+E2->JAB_N+JAB->X1->inactive_FtsH+FtsH*->MoxR->X2->X3->TPRs->low_complexity+a/b_unk+TPR_repeat->BetaPropeller+vWA->||<-RadSAM_pep
- **GCF_000972385.1; Streptomyces sp. WM6386; counts= 1; multicellularity status: TRUE**
  - <-DO-GTPase2<-Pkinase+TM||EAD1+CASPASE->RING(inactive)+RING->E1+UFD->EAD1+Ubl-Nterm+Ubl+E2->JAB_N+JAB*->X1->inactive_FtsH+FtsH->MoxR->??->X2->X3->TPRs->low_complexity+a/b_unk+TPR_repeat->BetaPropeller+vWA->||<-RadSAM_pep<-RADICAL_SAM.Ammemo<-MPTase<-RadSAM.X1
- **GCF_000746395.1; Streptomyces mirabilis; counts= 1; multicellularity status: TRUE**
  - <-TM+??<-TM+coiled-coil<-GAP1-N2+GAP1-M+??<-DO-GTPase2<-Pkinase+TM||EAD1+CASPASE->RING(inactive)+RING->E1+UFD->EAD1+Ubl-Nterm+Ubl+E2->JAB_N+JAB->X1->inactive_FtsH+FtsH*->MoxR->X2->X3->TPRs->low_complexity+a/b_unk+TPR_repeat->BetaPropeller+vWA->||<-RadSAM_pep<-RADICAL_SAM.Ammemo<-MPTase
- **GCF_001514035.1; Streptomyces yokosukanensis; counts= 1; multicellularity status: TRUE**
  - EAD1+CASPASE->RING(inactive)+RING->E1+UFD->EAD1+Ubl-Nterm+Ubl+E2->JAB_N+JAB->X1->inactive_FtsH+FtsH*->MoxR->X2->X3->TPRs->?->BetaPropeller+vWA<-RadSAM_pep<-RADICAL_SAM.Ammemo<-MPTase
- **GCA_004345645.1; Actinocrispum wychmicini; counts= 1; multicellularity status: TRUE**
  - <-TM+??<-TM+coiled-coil<-GAP1-N2+GAP1-M+??<-DO-GTPase2<-Pkinase+TM||EAD1+CASPASE->RING(inactive)+RING->E1+UFD->EAD1+Ubl-Nterm+Ubl+E2->JAB_N+JAB->X1->inactive_FtsH+FtsH*->MoxR->X2->X3->TPRs->low_complexity+a/b_unk+TPR_repeat->BetaPropeller+vWA->||<-RadSAM_pep<-RADICAL_SAM.Ammemo
- **GCF_000384295.1; Amycolatopsis balhimycina; counts= 1; multicellularity status: TRUE**
  - EAD1+CASPASE->RING(inactive)+RING->E1+UFD->EAD1+Ubl-Nterm+Ubl+E2->JAB_N+JAB->X1->inactive_FtsH+FtsH*->MoxR->X2->X3->TPRs->low_complexity+a/b_unk+TPR_repeat->BetaPropeller+vWA->||<-RadSAM_pep<-RADICAL_SAM.Ammemo<-TM+TM

- **GCF_002234595.1; Amycolatopsis sp. H5; counts= 1; multicellularity status: TRUE**
  - EAD1+CASPASE->RING(inactive)+RING->E1+UFD->EAD1+Ubl-Nterm+Ubl+E2->JAB_N+JAB->X1->inactive_FtsH+FtsH*->MoxR->X2->X3->TPRs->low_complexity+a/b_unk+TPR_repeat->BetaPropeller+vWA->||<-RadSAM_pep<-RADICAL_SAM.Ammemo<-TM+TM
- **GCF_003955715.1; Streptomyces sp. GGCR-6; counts= 1; multicellularity status: TRUE**
  - EAD1+CASPASE->RING(inactive)+RING->E1+UFD->EAD1+Ubl-Nterm+Ubl+E2->JAB_N+JAB->X1->inactive_FtsH+FtsH*->MoxR->X2->X3->TPRs->low_complexity+a/b_unk+TPR_repeat->BetaPropeller+vWA->||<-RadSAM_pep<-RADICAL_SAM.Ammemo
- **GCF_004345645.1; Actinocrispum wychmicini; counts= 1; multicellularity status: TRUE**
  - <-TM+??<-TM+coiled-coil<-GAP1-N2+GAP1-M+??<-DO-GTPase2<-Pkinase+TM||EAD1+CASPASE->RING(inactive)+RING->E1+UFD->EAD1+Ubl-Nterm+Ubl+E2->JAB_N+JAB->X1->inactive_FtsH+FtsH*->MoxR->X2->X3->TPRs->low_complexity+a/b_unk+TPR_repeat->BetaPropeller+vWA->||<-RadSAM_pep<-RADICAL_SAM.Ammemo
- **GCF_004343295.1; Streptomyces sp. BK042; counts= 1; multicellularity status: TRUE**
  - EAD1+CASPASE->RING(inactive)+RING->E1+UFD->EAD1+Ubl-Nterm+Ubl+E2->JAB_N+JAB->X1->inactive_FtsH+FtsH*->MoxR->X2->X3->TPRs->low_complexity+a/b_unk+TPR_repeat->BetaPropeller+vWA->||<-RadSAM_pep<-RADICAL_SAM.Ammemo
- **GCF_900104725.1; Actinoplanes derwentensis; counts= 1; multicellularity status: TRUE**
  - Trypsin+EAD1->BetaPropeller+vWA->RADICAL_SAM.Ammemo->RadSAM_pep->RING(inactive)+RING->E1+UFD->EAD1+Ubl-Nterm+Ubl+E2->JAB_N+JAB->X1->inactive_FtsH+FtsH*->MoxR->X2->X3->TPRs->low_complexity+a/b_unk+TPR_repeat->CASPASE+Ploop_NTPase->BetaPropeller->ABhydrolase+TIR->EAD1+TIR->BetaPropeller+vWA->
- **GCF_000725475.1; Streptomyces durhamensis; counts= 1; multicellularity status: TRUE**
  - EAD1+CASPASE->RING(inactive)+RING->E1+UFD->EAD1+Ubl-Nterm+Ubl+E2->JAB_N+JAB->X1->inactive_FtsH+FtsH*->MoxR->X2->X3->TPRs->low_complexity+a/b_unk+TPR_repeat->BetaPropeller+vWA->||<-RadSAM_pep<-RADICAL_SAM.Ammemo<-MPTase<-RadSAM.X1
- **GCF_001280015.1; Streptomyces sp. MMG1121; counts= 1; multicellularity status: TRUE**
  - EAD1+CASPASE->RING(inactive)+RING->E1+UFD->EAD1+Ubl-Nterm+Ubl+E2->JAB_N+JAB->X1->inactive_FtsH+FtsH*->MoxR->X2->X3->TPRs->low_complexity+a/b_unk+TPR_repeat->BetaPropeller+vWA->||<-RadSAM_pep<-RADICAL_SAM.Ammemo<-MPTase<-RadSAM.X1
- **GCF_001866665.1; Streptomyces sp. MUSC 1; counts= 1; multicellularity status: TRUE**
  - EAD1+CASPASE->RING(inactive)+RING->E1+UFD->EAD1+Ubl-Nterm+Ubl+E2->JAB_N+JAB->X1->inactive_FtsH+FtsH*->MoxR->X2->X3->TPRs->low_complexity+a/b_unk+TPR_repeat->BetaPropeller+vWA->||<-RadSAM_pep<-RADICAL_SAM.Ammemo<-MPTase<-RadSAM.X1
- **GCF_001735805.1; Streptomyces puniciscabiei; counts= 1; multicellularity status: TRUE**
  - <-TM+??<-TM+coiled-coil<-GAP1-N2+GAP1-M+??<-DO-GTPase2<-Pkinase+TM||EAD1+CASPASE->RING(inactive)+RING->E1+UFD->EAD1+Ubl-Nterm+Ubl+E2->JAB_N+JAB->X1->inactive_FtsH+FtsH*->MoxR->X2->X3->TPRs->low_complexity+a/b_unk+TPR_repeat->||<-BetaPropeller+vWA<-RadSAM_pep<-RADICAL_SAM.Ammemo<-MPTase
- **GCF_000379645.1; Actinoplanes globisporus; counts= 1; multicellularity status: TRUE**
  - Clp_N_repeats+vWA->Clp_N_repeats+vWA->Clp_N_repeats+vWA->Clp_N_repeats+vWA->Clp_N_repeats+vWA->Clp_N_repeats+vWA->??->??+4TM->EAD1+CASPASE->RADICAL_SAM.Ammemo->RadSAM_pep->RING(inactive)+RING->E1+UFD->EAD1+Ubl-Nterm+Ubl+E2->JAB_N+JAB->X1->inactive_FtsH+FtsH*->MoxR->X2->?->TPRs->low_complexity+a/b_unk+TPRs->
- **GCF_004364215.1; Streptomyces sp. BK161; counts= 1; multicellularity status: TRUE**
  - EAD1+CASPASE->RING(inactive)+RING->E1+UFD->EAD1+Ubl-Nterm+Ubl+E2->JAB_N+JAB->X1->inactive_FtsH+FtsH*->MoxR->X2->X3->TPRs->low_complexity+a/b_unk+TPRs->||<-BetaPropeller+vWA<-RadSAM_pep<-RADICAL_SAM.Ammemo
- **GCA_006912135.1; Cryptosporangium sp. A-T 5661; counts= 1; multicellularity status: TRUE**
  - BetaPropeller+vWA->BetaPropeller+vWA->BetaPropeller+vWA->||<-TIR+EAD1||BetaPropeller+vWA->RADICAL_SAM.Ammemo->RadSAM_pep->RING(inactive)+RING->E1+UFD->EAD1+Ubl-Nterm+Ubl+E2->JAB_N+JAB->X1->inactive_FtsH+FtsH*->MoxR->X2->X3->TPRs->low_complexity+a/b_unk+TPRs->
- **GCF_005144585.1; Polyangium fumosum; counts= 1; multicellularity status: TRUE**
  - <-RadSAM_pep<-Radical_SAM<-BetaPropeller+vWA||Prok_Ring(degenerate)+Prok_Ring->E1+UFD->EAD1+Ubl-Nterm+Ubl+E2->JAB-N+JAB->X1->inactive_FtsH+FtsH*->MoxR->?->TPRs->low_complexity+a/b_unk+TPRs->
- **GCF_004217135.1; Micromonospora violae; counts= 1; multicellularity status: TRUE**
  - Clp_N_repeats+vWA->??->??+4TM->EAD1+CASPASE->RING(inactive)+RING->E1+UFD->EAD1+Ubl-Nterm+Ubl+E2->JAB_N+JAB->X1->inactive_FtsH+FtsH*->MoxR->TPRs->low_complexity+a/b_unk+TPR_repeat->
- **GCA_001292585.1; Candidatus Magnetomorum sp. HK-1; counts= 1; multicellularity status: TRUE**
  - TIR+??->||<-?||Ubl+E2->JAB-N+JAB->inactive_FtsH+FtsH*->E1+UFD->TPRs+FGS-fold_domain->

- **GCF_002154695.1; Nostoc sp. T09; counts= 1; multicellularity status: TRUE**
  - RadSAM_pep->RING(inactive)+RING->E1+UFD->Trypco2->TCAD4+CASPASE+EAD1->EAD1+Ubl-Nterm+Ubl+E2->JAB_N+JAB->X1->inactive_FtsH+FtsH*->TPRs+FGS-fold_domain->MoxR->?->?->FGS-fold_domain->||<-?||?->||<-BetaPropeller+vWA||RADICAL_SAM.Ammemo->
- **GCF_003143935.1; Streptomyces sp. Act143; counts= 1; multicellularity status: TRUE**
  - EAD1+CASPASE->RING(inactive)+RING->E1+UFD->EAD1+Ubl-Nterm+Ubl+E2->JAB_N+JAB->X1->inactive_FtsH+FtsH*->MoxR->X2->X3->TPRs->low_complexity+a/b_unk+TPR_repeat->||<-BetaPropeller+vWA<-RadSAM_pep<-RADICAL_SAM.Ammemo
- **GCA_000516475.1; Candidatus Magnetoglobus multicellularis str. Araruama; counts= 1; multicellularity status: TRUE**
  - inactive_FtsH+FtsH*->inactive_FtsH+FtsH->Prok_Ring+Prok_Ring->E1+UFD->TIR+??->Ubl+E2->JAB_N2->JAB->
- **GCA_900104725.1; Actinoplanes derwentensis; counts= 1; multicellularity status: TRUE**
  - Trypsin+EAD1->BetaPropeller+vWA->RADICAL_SAM.Ammemo->RadSAM_pep->RING(inactive)+RING->E1+UFD->EAD1+Ubl-Nterm+Ubl+E2->JAB_N+JAB->X1->inactive_FtsH+FtsH*->MoxR->X2->X3->TPRs->low_complexity+a/b_unk+TPR_repeat->CASPASE+Ploop_NTPase->beta_propeller->ABhydrolase+TIR->EAD1+TIR->BetaPropeller+vWA->
- **GCA_003695705.1; Planctomycetes bacterium; counts= 1; multicellularity status: NA**
  - MPTase->||<-Prok-RING+TM<-?<-Prok-RING+TM+TM<-Band7<-Band7||inactive_FtsH+FtsH*->X3_analog->
- **GCF_001767235.1; Moorea producens; counts= 1; multicellularity status: TRUE**
  - RadSAM_pep->Prok_Ring(degenerate)+Prok_Ring->X1->TPRs->inactive_FtsH+FtsH*->MoxR->?->?->TPRs+FGS-fold_domain->->||<-?||?->?->||<-RADICAL_SAM.Ammemo
- **GCF_000262465.1; Frankia sp. QA3; counts= 1; multicellularity status: TRUE**
  - E1+UFD->EAD1+Ubl-Nterm+Ubl+E2->JAB_N+JAB->X1->X1->inactive_FtsH+FtsH*->MoxR->Clathrin+DnaJ_CXXCXGXG+DnaJ_C->low_complexity+a/b_unk+TPR_repeat->||<-?<-TIR
- **GCF_900206255.1; Streptomyces sp. TLI_55; counts= 1; multicellularity status: TRUE**
  - RING(inactive)+RING->E1+UFD->EAD1+Ubl-Nterm+Ubl+E2->||<-PSE->X1->inactive_FtsH+FtsH*->MoxR->?->?->TPRs->low_complexity+a/b_unk+TPR_repeat->BetaPropeller+vWA->||<-RadSAM_pep<-RADICAL_SAM.Ammemo
- **GCF_001469165.1; Thiohalocapsa sp. ML1; counts= 1; multicellularity status: TRUE**
  - RING(inactive)+RING->E1+UFD->helical_X+TIR->EAD1+Ubl-Nterm+Ubl+E2->||<-PSE||?->inactive_FtsH+FtsH*->MoxR->BetaPropeller+vWA->X2->X3?->TPRs->low_complexity+a/b_unk+TPR_repeat->||<-?||BetaPropeller+vWA->HTH->RADICAL_SAM.Ammemo->RadSAM_pep->
- **GCF_900634715.1; Frankia symbiont of Datisca glomerata; counts= 1; multicellularity status: TRUE**
  - RadSAM_pep->RING(inactive)+RING->E1+?->TIR->||<-?<-?<-?||X1->inactive_FtsH+FtsH*->MoxR->
- **GCF_000024805.1; Haliangium ochraceum; counts= 1; multicellularity status: TRUE**
  - beta_propeller+vWA->X1->inactive_FtsH+FtsH*->MoxR->X2->X3->?->Radical_SAM->RadSAM_pep->
- **GCF_001017755.1; Frankia coriariae; counts= 1; multicellularity status: TRUE**
  - X1->inactive_FtsH+FtsH*->MoxR->X2->
- **GCA_001787855.1; Candidatus Riflebacteria bacterium GWC2_50_8; counts= 1; multicellularity status: NA**
  - inactive_FtsH+FtsH*->?->MoxR->
- **GCF_900635405.1; Frankia symbiont of Datisca glomerata; counts= 1; multicellularity status: TRUE**
  - inactive_FtsH+FtsH*->MoxR->
- **GCA_003645185.1; Gammaproteobacteria bacterium; counts= 1; multicellularity status: NA**
  - inactive_FtsH+FtsH*->?->

- **GCA_001873925.1; Deltaproteobacteria bacterium CG2_30_63_29; counts= 1; multicellularity status: NA**
  - X5->inactive_FtsH+FtsH*->
- **GCA_002789955.1; Deltaproteobacteria bacterium CG_4_9_14_3_um_filter_63_12; counts= 1; multicellularity status: NA**
  - X5->inactive_FtsH+FtsH*->
- **GCA_000821145.1; uncultured bacterium; counts= 1; multicellularity status: NA**
  - X6->X5->inactive_FtsH+FtsH*->
- **GCF_006636215.1; Myxococcus sp. AM401; counts= 1; multicellularity status: TRUE**
  - Radical_SAM->X6->X5->inactive_FtsH+FtsH*->X3_analog->a/b_unk+NEFF1+TPR_region->MoxR->
- **GCF_001854205.1; Moorea producens; counts= 1; multicellularity status: TRUE**
  - inactive_FtsH+FtsH*->MoxR->?->||<-?<-?||X2->
- **GCF_000171775.1; Gemmata obscuriglobus; counts= 1; multicellularity status: FALSE**
  - Radical_SAM->X6->X5->inactive_FtsH+FtsH*->X3_analog->a/b_unk+NEFF1+TPR_region->a/b_unk+NEFF1+TPR_region->
- **GCA_003669555.1; Planctomycetes bacterium; counts= 1; multicellularity status: NA**
  - X5->inactive_FtsH+FtsH*->X3_analog->?+NEFF+?->MoxR->
- **GCA_002716585.1; Myxococcales bacterium; counts= 1; multicellularity status: TRUE**
  - inactive_FtsH+FtsH*->X3_analog->
- **GCA_006226375.1; Deltaproteobacteria bacterium; counts= 1; multicellularity status: NA**
  - inactive_FtsH+FtsH*->X3_analog->
- **GCF_002197845.1; Fimbriiglobus ruber; counts= 1; multicellularity status: TRUE**
  - inactive_FtsH+FtsH*->X3_analog->
- **GCA_004376375.1; Planctomycetes bacterium; counts= 1; multicellularity status: NA**
  - X5->inactive_FtsH+FtsH*->?->?->X3_analog->
- **GCA_003243425.1; Archangium gephyra; counts= 1; multicellularity status: TRUE**
  - X5->inactive_FtsH+FtsH*->X3_analog->
- **GCF_000170895.1; Plesiocystis pacifica; counts= 1; multicellularity status: TRUE**
  - X5->inactive_FtsH+FtsH*->X3_analog->?->a/b_unk+NEFF+TPRs
- **GCA_003508275.1; Planctomycetales bacterium; counts= 1; multicellularity status: NA**
  - X6->X5->inactive_FtsH+FtsH*->
- **GCF_002994615.1; Enhygromyxa salina; counts= 1; multicellularity status: TRUE**
  - Radical_SAM->X6->X5->inactive_FtsH+FtsH*->

- **GCF_900635385.1; Frankia symbiont of Coriaria nepalensis; counts= 1; multicellularity status: TRUE**
  - inactive_FtsH+FtsH*->MoxR->X2->||<-?||TPRs->
- **GCF_000177615.2; Frankia; counts= 1; multicellularity status: TRUE**
  - X1->inactive_FtsH+FtsH*->MoxR->X2->||<-?||TPRs->
- **GCF_001983005.1; Frankia sp. BMG5.30; counts= 1; multicellularity status: TRUE**
  - X1->inactive_FtsH+FtsH*->MoxR->X2->?->TPRs->

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- **GCA_900104725.1; Actinoplanes derwentensis; counts= 2; multicellularity status: TRUE**
  - ??->Trypsin+EAD1->beta_propeller+helical_linker+vWA*->RADICAL_SAM.Ammemo->RadSAM_pep->?->E1+UFD->EAD1+Ubl-Nterm+Ubl+E2->
  - low_complexity+a/b_unk+TPR_repeat->CASPASE+Ploop_NTPase->BetaPropeller->a/b_hydrolase->EAD1+TIR->beta_propeller+helical_linker+vWA*->
- **GCA_000516475.1; Candidatus Magnetoglobus multicellularis str. Araruama; counts= 2; multicellularity status: TRUE**
  - vWA*->
  - vWA*->
- **GCA_001769385.1; Bacteroidetes bacterium RIFCSPLOWO2_12_FULL_35_15; counts= 1; multicellularity status: FALSE**
  - bpX4->MoxR->bpX2->extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1+Ribosomal_L12_insert*->bpX3->
- **GCA_000265505.1; Bernardetia litoralis DSM 6794; counts= 1; multicellularity status: NA**
  - bpX4->?->MoxR->?->bpX2->extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1+Ribosomal_L12_insert*->
- **GCA_002916795.1; Flavobacterium columnare; counts= 1; multicellularity status: FALSE**
  - bpX4->MoxR->bpX2->extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1+Ribosomal_L12_insert*->abpX3+2TM+TPR_region->
- **GCA_002217335.1; Flavobacterium hydatis; counts= 1; multicellularity status: FALSE**
  - bpX4->MoxR->bpX2->extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1+Ribosomal_L12_insert*->
- **GCA_900110335.1; Flavobacterium sp. fv08; counts= 1; multicellularity status: FALSE**
  - bpX4->MoxR->bpX2->extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1+Ribosomal_L12_insert*->abpX3+2TM+TPR_region->
- **GCA_001281695.1; bacterium 336/3; counts= 1; multicellularity status: NA**
  - bpX4->MoxR->bpX2->extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*->
- **GCF_004014855.1; Apibacter sp. HY041; counts= 1; multicellularity status: FALSE**
  - bpX4->MoxR->bpX2->extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*->bpX3+4TM->2TM+TPR_region->
- **GCA_003148625.1; Arcicella aurantiaca; counts= 1; multicellularity status: FALSE**
  - bpX4->MoxR->bpX2->extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*->bpX3+TPR_region->
- **GCF_000724545.1; Aureispira sp. CCB-QB1; counts= 1; multicellularity status: TRUE**
  - bpX4->MoxR->bpX2->extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*->bpX3+TPR_region->
- **GCA_003014755.1; Chitinophaga niastensis; counts= 1; multicellularity status: TRUE**
  - MoxR->bpX2->extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*->bpX3+TPR_region+beta_propeller->

- **GCA_003308995.1; Chitinophaga sp. GDMCC 1.1325; counts= 1; multicellularity status: TRUE**
  - bpX4->MoxR->bpX2->extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*->bpX3+TPR_region+beta_propeller->
- **GCA_003412465.1; Chitinophaga sp. K20C18050901; counts= 1; multicellularity status: TRUE**
  - bpX4->MoxR->bpX2->extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*->bpX3+TPR_region+beta_propeller->HTH+TetR_C->
- **GCA_003182155.1; Chitinophaga sp. S165; counts= 1; multicellularity status: TRUE**
  - bpX4->MoxR->bpX2->extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*->bpX3+TPR_region+beta_propeller->HTH+TetR_C->
- **GCA_900110995.1; Chitinophaga sp. YR573; counts= 1; multicellularity status: TRUE**
  - bpX4->MoxR->bpX2->extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*->bpX3+TPR_region+beta_propeller->HTH+TetR_C->
- **GCA_900114995.1; Chitinophaga sp. YR627; counts= 1; multicellularity status: TRUE**
  - bpX4->MoxR->bpX2->extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*->bpX3+TPR_region+beta_propeller->
- **GCA_900100115.1; Chryseobacterium soldanellicola; counts= 1; multicellularity status: FALSE**
  - MoxR->bpX2->extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*->bpX3+4TM->2TM+TPR_region->
- **GCA_000014145.1; Cytophaga hutchinsonii ATCC 33406; counts= 1; multicellularity status: FALSE**
  - bpX4->MoxR->bpX2->extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*->bpX3+TPR_region->
- **GCF_900343125.1; Dysgonomonas sp. Marseille-P4361; counts= 1; multicellularity status: FALSE**
  - bpX4->MoxR->bpX2->extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*->bpX3+TPR_region->
- **GCA_002355595.1; Filimonas lacunae; counts= 1; multicellularity status: TRUE**
  - bpX4->MoxR->bpX2->extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1-*->extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1-*>bpX3+TPR_region->
- **GCA_003097095.1; Filimonas sp. YR581; counts= 1; multicellularity status: TRUE**
  - bpX4->MoxR->bpX2->extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*->bpX3+TPR_region->
- **GCA_000814475.1; Flavihumibacter solisilvae; counts= 1; multicellularity status: FALSE**
  - bpX4->MoxR->bpX2->extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*->bpX3+TPR_region->
- **GCA_001601815.1; Flavihumibacter sp. CACIAM 22H1; counts= 1; multicellularity status: FALSE**
  - bpX4->MoxR->bpX2->extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*->bpX3+TPR_region->
- **GCA_001644645.1; Flavisolibacter tropicus; counts= 1; multicellularity status: FALSE**
  - bpX4->MoxR->bpX2->extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*->bpX3->
- **GCA_003096035.1; Flavobacterium album; counts= 1; multicellularity status: FALSE**
  - bpX4->MoxR->bpX2->extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*->abpX3+2TM+TPR_region->
- **GCF_000967805.1; Flavobacterium sp. 316; counts= 1; multicellularity status: FALSE**
  - bpX4->MoxR->bpX2->extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*->bpX3+4TM->2TM+TPR_region->

- **GCA_000212735.1; Haliscomenobacter hydrossis DSM 1100; counts= 1; multicellularity status: TRUE**
  - bpX4->MoxR->bpX2->extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*->bpX3+TPR_region+beta_propeller->
- **GCA_002797555.1; Hymenobacter chitinivorans DSM 11115; counts= 1; multicellularity status: FALSE**
  - bpX4->MoxR->bpX2->extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*->bpX3+2TM+TPR_region+beta_propeller->
- **GCA_003970915.1; Hymenobacter gummosus; counts= 1; multicellularity status: FALSE**
  - MoxR->bpX2->extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*->
- **GCA_900188255.1; Hymenobacter mucosus; counts= 1; multicellularity status: FALSE**
  - bpX4->MoxR->bpX2->extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*->bpX3+TPR_region+beta_propeller->
- **GCF_000420705.1; Hymenobacter norwichensis; counts= 1; multicellularity status: FALSE**
  - bpX4->MoxR->bpX2->extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*->
- **GCA_003944705.1; Hymenobacter sp. 9PBR-2; counts= 1; multicellularity status: FALSE**
  - MoxR->bpX2->extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*->
- **GCA_000154725.1; Kordia algicida OT-1; counts= 1; multicellularity status: FALSE**
  - bpX4->MoxR->bpX2->extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*->bpX3+4TM->2TM+TPR_region->
- **GCA_003633615.1; Mucilaginibacter gracilis; counts= 1; multicellularity status: FALSE**
  - bpX4->MoxR->bpX2->extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*->
- **GCA_000166195.3; Mucilaginibacter paludis DSM 18603; counts= 1; multicellularity status: FALSE**
  - extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*->bpX3+TPR_region+beta_propeller->
- **GCA_004005815.1; Mucilaginibacter sp. YBJ-36; counts= 1; multicellularity status: FALSE**
  - bpX4->MoxR->bpX2->extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*->bpX3+2TM+TPR_region+beta_propeller->
- **GCA_000246855.1; Niastella koreensis GR20-10; counts= 1; multicellularity status: FALSE**
  - bpX4->MoxR->bpX2->extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*->bpX3+TPR_region+beta_propeller->
- **GCA_001442625.1; Pedobacter ginsenosidimutans; counts= 1; multicellularity status: FALSE**
  - bpX4->MoxR->bpX2->extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*->bpX3+2TM+TPR_region+beta_propeller->
- **GCA_003852495.1; Taibaiella sp. KBW10; counts= 1; multicellularity status: FALSE**
  - bpX4->MoxR->bpX2->extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*->bpX3+4TM->2TM+TPR_region->
- **GCA_002967765.1; Blastopirellula marina; counts= 1; multicellularity status: TRUE**
  - bpX4->MoxR->bpX2->extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*->bpX3+TPR_region+beta_propeller->
- **GCA_002197845.1; Fimbriiglobus ruber; counts= 1; multicellularity status: TRUE**
  - bpX2->extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*->bpX3+TPR_region+beta_propeller->

- **GCA_001610855.1; Gemmata sp. SH-PL17; counts= 1; multicellularity status: FALSE**
  - bpX4->MoxR->bpX2->extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*->bpX3+TPR_region+beta_propeller->
- **GCA_003977685.1; Isosphaeraceae bacterium GM2012; counts= 1; multicellularity status: TRUE**
  - bpX4->MoxR->bpX2->extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*->
- **GCA_900113665.1; Planctomicrobium piriforme; counts= 1; multicellularity status: TRUE**
  - bpX4->MoxR->bpX2->extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*->bpX3+TPR_region+beta_propeller->
- **GCA_001610835.1; Planctomyces sp. SH-PL14; counts= 1; multicellularity status: FALSE**
  - bpX4->MoxR->bpX2->extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*->bpX3+TPR_region+beta_propeller->
- **GCA_003576915.1; Planctomycetes bacterium; counts= 1; multicellularity status: NA**
  - MoxR->bpX2->extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*->
- **GCA_003669275.1; Planctomycetes bacterium; counts= 1; multicellularity status: NA**
  - bpX4->MoxR->bpX2->extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*->bpX3+2TM+TPR_region+??->
- **GCA_002251265.1; Rhodopirellula sp. MGV; counts= 1; multicellularity status: TRUE**
  - bpX4->MoxR->bpX2->extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*->bpX3+TPR_region+beta_propeller->
- **GCF_001642915.1; Roseimaritima ulvae; counts= 1; multicellularity status: TRUE**
  - bpX4->MoxR->bpX2->extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*->bpX3+TPR_region+beta_propeller->
- **GCF_000255655.1; Schlesneria paludicola; counts= 1; multicellularity status: TRUE**
  - extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*->bpX3+TPR_region+beta_propeller->
- **GCA_900129635.1; Singulisphaera sp. GP187; counts= 1; multicellularity status: TRUE**
  - bpX4->MoxR->bpX2->extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*->bpX3+TPR_region+beta_propeller->
- **GCF_000255705.1; Zavarzinella formosa; counts= 1; multicellularity status: TRUE**
  - extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*->
- **GCF_003856375.1; Glaciecola sp. THG-3.7; counts= 1; multicellularity status: FALSE**
  - bpX4->MoxR->bpX2->extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*->bpX3+TPR_region->
- **GCA_000173075.1; Chthoniobacter flavus Ellin428; counts= 1; multicellularity status: FALSE**
  - bpX4->MoxR->bpX2->extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*->bpX3+TPR_region+beta_propeller->
- **GCA_000172555.1; Pedosphaera parvula Ellin514; counts= 1; multicellularity status: FALSE**
  - bpX4->MoxR->bpX2->extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*->?->bpX3+TPR_region+beta_propeller->
- **GCA_003315205.1; Roseimicrobium gellanilyticum; counts= 1; multicellularity status: TRUE**
  - bpX4->MoxR->bpX2->extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*->bpX3+TPR_region+beta_propeller->

- **GCA_003054695.1; Verrucomicrobia bacterium LW23; counts= 1; multicellularity status: FALSE**
  - extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*->
- **GCF_000172155.1; Verrucomicrobium spinosum; counts= 1; multicellularity status: FALSE**
  - bpX4->MoxR->bpX2->extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*->bpX3+TPR_region+beta_propeller->
- **GCF_000719695.1; Streptomyces sp. NRRL F-6131; counts= 1; multicellularity status: TRUE**
  - MoxR->bpX5->vWA+beta_propeller*->bpX6+TMs+TPRs+Betapropeller->
- **GCA_002797915.1; Yoonia maricola; counts= 1; multicellularity status: FALSE**
  - MoxR->?->vWA+beta_propeller*->
- **GCA_001707535.1; Achromobacter xylosoxidans; counts= 1; multicellularity status: FALSE**
  - MoxR->bpX5->vWA+beta_propeller*->bpX6+TPRs+Betapropeller->
- **GCA_001294205.1; Amantichitinum ursilacus; counts= 1; multicellularity status: FALSE**
  - MoxR->bpX5->vWA+beta_propeller*->bpX6+TPRs+Betapropeller->
- **GCA_900176275.1; Andreprevotia lacus DSM 23236; counts= 1; multicellularity status: FALSE**
  - MoxR->bpX5->vWA+beta_propeller*->bpX6+TMs+TPRs+Betapropeller->
- **GCA_000007705.1; Chromobacterium violaceum ATCC 12472; counts= 1; multicellularity status: FALSE**
  - MoxR->bpX5->vWA+beta_propeller*->
- **GCA_003416915.1; Duganella sp. BJB489; counts= 1; multicellularity status: FALSE**
  - MoxR->bpX5->vWA+beta_propeller*->bpX6+TMs+TPRs+Betapropeller->
- **GCA_001427305.1; Duganella sp. Root1480D1; counts= 1; multicellularity status: FALSE**
  - MoxR->bpX5->vWA+beta_propeller*->bpX6+TMs+TPRs+Betapropeller->
- **GCF_000333495.1; Herbaspirillum sp. B39; counts= 1; multicellularity status: FALSE**
  - MoxR->bpX5->vWA+beta_propeller*->?->bpX6+TPRs+Betapropeller->
- **GCA_900129765.1; Massilia sp. CF038; counts= 1; multicellularity status: FALSE**
  - MoxR->bpX5->vWA+beta_propeller*->bpX6+TMs+TPRs+Betapropeller->
- **GCA_002752675.1; Massilia violaceinigra; counts= 1; multicellularity status: FALSE**
  - MoxR->bpX5->vWA+beta_propeller-*->vWA+beta_propeller*->bpX6+TPRs+Betapropeller->
- **GCA_003269145.1; Microvirgula sp. AG722; counts= 1; multicellularity status: FALSE**
  - MoxR->bpX5->vWA+beta_propeller*->bpX6+TPRs+Betapropeller->||<-?<-BetaPropeller<-BetaPropeller
- **GCA_001653795.1; Mitsuaria sp. 7; counts= 1; multicellularity status: FALSE**
  - MoxR->bpX5->vWA+beta_propeller*->bpX6+TMs+TPRs+Betapropeller->

- **GCA_000427195.1; Ralstonia solanacearum CMR15; counts= 1; multicellularity status: FALSE**
  - MoxR->bpX5->vWA+beta_propeller*->bpX6+TMs+TPRs+Betapropeller->
- **GCA_002116905.1; Rhizobacter gummiphilus; counts= 1; multicellularity status: FALSE**
  - MoxR->bpX5->vWA+beta_propeller*->bpX6+TMs+TPRs+Betapropeller->
- **GCA_001425785.1; Rhizobacter sp. Root1221; counts= 1; multicellularity status: FALSE**
  - MoxR->bpX5->vWA+beta_propeller*->bpX6+TPRs+Betapropeller->
- **GCA_003852895.1; Rhizobacter sp. S-16; counts= 1; multicellularity status: FALSE**
  - MoxR->bpX5->vWA+beta_propeller*->bpX6+TMs+TPRs+Betapropeller->
- **GCA_900106655.1; Variovorax sp. YR634; counts= 1; multicellularity status: FALSE**
  - MoxR->bpX5->vWA+beta_propeller*->bpX6+TMs+TPRs+Betapropeller->
- **GCA_000733295.1; Archangium violaceum Cb vi76; counts= 1; multicellularity status: TRUE**
  - bpX5->vWA+beta_propeller*->bpX6+TPRs+Betapropeller->
- **GCA_003600865.1; Corallococcus sp. H22C18031201; counts= 1; multicellularity status: TRUE**
  - MoxR->bpX5->vWA+beta_propeller*->bpX6+TPRs+Betapropeller->
- **GCA_000988565.1; Myxococcus fulvus 124B02; counts= 1; multicellularity status: TRUE**
  - bpX5->vWA+beta_propeller*->
- **GCA_002305895.1; Myxococcus macrosporus DSM 14697; counts= 1; multicellularity status: TRUE**
  - MoxR->bpX5->vWA+beta_propeller*->bpX6+TPRs+Betapropeller->
- **GCA_000012685.1; Myxococcus xanthus DK 1622; counts= 1; multicellularity status: TRUE**
  - MoxR->bpX5->vWA+beta_propeller*->bpX6+TPRs+Betapropeller->
- **GCA_002141575.1; Gilliamella apicola; counts= 1; multicellularity status: FALSE**
  - MoxR->bpX5->vWA+beta_propeller*->bpX6+TMs+TPRs+Betapropeller->
- **GCA_000012985.1; Hahella chejuensis KCTC 2396; counts= 1; multicellularity status: FALSE**
  - MoxR->bpX5->vWA+beta_propeller*->bpX6+TPRs+Betapropeller->
- **GCF_000419525.1; Leucothrix mucor; counts= 1; multicellularity status: TRUE**
  - MoxR->bpX5->vWA+beta_propeller*->bpX6+TPRs+Betapropeller->
- **GCF_000336385.2; Lysobacter antibioticus; counts= 1; multicellularity status: FALSE**
  - MoxR->bpX5->vWA+beta_propeller*->
- **GCA_002355975.1; Lysobacter enzymogenes; counts= 1; multicellularity status: FALSE**
  - MoxR->bpX5->vWA+beta_propeller*->bpX6+TPRs+Betapropeller->

- **GCA_001427505.1; Lysobacter sp. Root604; counts= 1; multicellularity status: FALSE**
  - MoxR->bpX5->vWA+beta_propeller*->bpX6+TPRs+Betapropeller->
- **GCA_001427785.1; Lysobacter sp. Root690; counts= 1; multicellularity status: FALSE**
  - MoxR->bpX5->vWA+beta_propeller*->bpX6+TPRs+Betapropeller->
- **GCA_002206145.2; Proteus mirabilis; counts= 1; multicellularity status: FALSE**
  - RADICAL_SAM.Ammemo->?->MoxR->bpX5->vWA+beta_propeller*->bpX6+TPRs+Betapropeller->
- **GCA_000314895.2; Providencia sneebia DSM 19967; counts= 1; multicellularity status: FALSE**
  - bpX5->vWA+beta_propeller*->
- **GCA_000820515.1; Pseudomonas batumici; counts= 1; multicellularity status: FALSE**
  - MoxR->bpX5->vWA+beta_propeller*->bpX6+TMs+TPRs+Betapropeller->
- **GCF_003415775.1; Pseudomonas cichorii; counts= 1; multicellularity status: FALSE**
  - MoxR->bpX5->vWA+beta_propeller*->bpX6+TMs+TPRs+Betapropeller->
- **GCF_000467005.1; Pseudomonas fuscovaginae; counts= 1; multicellularity status: FALSE**
  - MoxR->PSE->vWA+beta_propeller*->?->TPRs+Betapropeller->
- **GCA_003700875.1; Pseudomonas marginalis pv. marginalis; counts= 1; multicellularity status: FALSE**
  - MoxR->bpX5->vWA+beta_propeller*->bpX6+TMs+TPRs+Betapropeller->
- **GCA_003701285.1; Pseudomonas savastanoi pv. glycinea; counts= 1; multicellularity status: FALSE**
  - vWA+beta_propeller*->
- **GCF_900582885.1; Pseudomonas sp. 286; counts= 1; multicellularity status: FALSE**
  - MoxR->bpX5->vWA+beta_propeller*->bpX6+TMs+TPRs+Betapropeller->
- **GCA_000931385.1; Pseudomonas sp. FeS53a; counts= 1; multicellularity status: FALSE**
  - MoxR->bpX5->vWA+beta_propeller*->bpX6+TMs+TPRs+Betapropeller->
- **GCF_000812405.1; Pseudomonas sp. PI1; counts= 1; multicellularity status: FALSE**
  - MoxR->bpX5->vWA+beta_propeller*->
- **GCA_001547915.1; Pseudomonas sp. St29; counts= 1; multicellularity status: FALSE**
  - MoxR->bpX5->vWA+beta_propeller*->bpX6+TMs+TPRs+Betapropeller->
- **GCA_900215525.1; Pseudomonas sp. URIL14HWK12:I9; counts= 1; multicellularity status: FALSE**
  - MoxR->bpX5->vWA+beta_propeller*->bpX6+TPRs+Betapropeller->
- **GCA_001725155.1; Xanthomonadaceae bacterium SCN 69-320; counts= 1; multicellularity status: FALSE**
  - MoxR->bpX5->vWA+beta_propeller*->bpX6+TPRs+Betapropeller->

- **GCA_002940525.1; Xanthomonas arboricola; counts= 1; multicellularity status: FALSE**
  - MoxR->bpX5->vWA+beta_propeller*->bpX6+TPRs+Betapropeller->
- **GCA_001043115.1; Xanthomonas sp. NCPPB 1128; counts= 1; multicellularity status: FALSE**
  - MoxR->bpX5->vWA+beta_propeller*->bpX6+TPRs+Betapropeller->
- **GCF_000379645.1; Actinoplanes globisporus; counts= 1; multicellularity status: TRUE**
  - ClpN_repeats+vWA->ClpN_repeats+vWA->ClpN_repeats+vWA->*ClpN_repeats+vWA*->ClpN_repeats+vWA->ClpN_repeats+vWA->?->?->EAD1+CASPASE->
- **GCA_002234595.1; Amycolatopsis sp. H5; counts= 1; multicellularity status: TRUE**
  - MoxR->?->X3->TPRs->low_complexity+TPRs->beta_propeller+helical_linker+vWA*->||<-RadSAM_pep<-RADICAL_SAM.Ammemo
- **GCF_000716715.1; Dactylosporangium aurantiacum; counts= 1; multicellularity status: TRUE**
  - MoxR->?->X3->TPRs->low_complexity+TPRs->beta_propeller+helical_linker+vWA*->||<-RadSAM_pep<-RADICAL_SAM.Ammemo
- **GCA_001017755.1; Frankia coriariae; counts= 1; multicellularity status: TRUE**
  - beta_propeller+helical_linker+vWA*->
- **GCA_900100605.1; Sinosporangium album; counts= 1; multicellularity status: TRUE**
  - TPRs->low_complexity+TPRs->beta_propeller+helical_linker+vWA*->||<-RadSAM_pep
- **GCA_003955715.1; Streptomyces sp. GGCR-6; counts= 1; multicellularity status: TRUE**
  - beta_propeller+helical_linker+vWA*->||<-RadSAM_pep<-RADICAL_SAM.Ammemo
- **GCA_001280015.1; Streptomyces sp. MMG1121; counts= 1; multicellularity status: TRUE**
  - X3->TPRs->low_complexity+TPRs->beta_propeller+helical_linker+vWA*->||<-RadSAM_pep<-RADICAL_SAM.Ammemo
- **GCA_002154695.1; Nostoc sp. T09; counts= 1; multicellularity status: TRUE**
  - X3->TPRs+C-type_lectin->||<-?||low_complexity+TPRs->beta_propeller+helical_linker+vWA*->||<-RADICAL_SAM.Ammemo
- **GCF_000024805.1; Haliangium ochraceum; counts= 1; multicellularity status: TRUE**
  - beta_propeller+helical_linker+vWA*->TPRs->
- **GCF_001469165.1; Thiohalocapsa sp. ML1; counts= 1; multicellularity status: TRUE**
  - X3->TPRs->low_complexity+TPRs->||<-?||beta_propeller+helical_linker+vWA*->
- **GCA_003645185.1; Gammaproteobacteria bacterium; counts= 1; multicellularity status: NA**
  - helical_linker+vWA*->
- **GCF_000262465.1; Frankia sp. QA3; counts= 1; multicellularity status: TRUE**
  - vWA*->
- **GCF_002156075.1; Streptomyces scabiei; counts= 1; multicellularity status: TRUE**
  - vWA*->

DOGTPase systems

■ **GCA__000175595.1; Clostridium carboxidivorans P7; counts= 3; multicellularity status: FALSE**

- Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->?->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->PSE->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->
- TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C*->GAP1-N2+GAP1-M->
- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C->GAP1-N2+GAP1-M*->

■ **GCA__000647895.1; Clostridium tetanomorphum DSM 665; counts= 3; multicellularity status: FALSE**

- Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->
- TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M*->
- ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M*->

■ **GCA__001276615.1; Achromatium sp. WMS3; counts= 3; multicellularity status: FALSE**

- GAP1-N1+GAP1-M+GAP1-C*->
- GAP1-N2+GAP1-M+GAP1-C*->
- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__002737235.1; Opitutae bacterium; counts= 3; multicellularity status: FALSE**

- FHA-like?+ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+TM+GAP1-C*->
- FHA-like?+ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+TM+GAP1-C*->
- FHA-like?+ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+TM+GAP1-C*->

■ **GCA__002794505.1; Chloroflexi bacterium; counts= 3; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->
- GAP1-N2+GAP1-M+GAP1-C*->Pkinase+helical_region+TM_region->
- GAP1-N2+GAP1-M+TM+GAP1-C*->

■ **GCA__900129635.1; Singulisphaera sp. GP187; counts= 3; multicellularity status: TRUE**

- Calcineurin+GAPEAD1->GAP2->DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->
- DO-GTPase2.1+TM->GAP1-N2+GAP1-M+GAP1-C*->
- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__000181475.1; Gimesia maris; counts= 3; multicellularity status: FALSE**

- GAP1-N2+GAP1-M+TM+GAP1-C->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+TM+GAP1-C*->??+TM+??+beta-rich??->GYF+GYF+TM+TM+TM->
- GAP1-N2+GAP1-M+TM+GAP1-C*->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+TM+GAP1-C->??+TM+??+beta-rich??->GYF+GYF+TM+TM+TM->
- GrpE->HSP70->HSP70+vWA(canonical)->DnaJ+DnaJ+DZnR+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->?->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->

■ **GCA__000242455.3; Singulisphaera acidiphila; counts= 3; multicellularity status: TRUE**

- FGS-fold_domain->ZnR+DO-GTPase2.1->GAP1-N2+GAP1-M*->
- GAP1-N2+GAP1-M+GAP1-C*->
- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_001270375.1; Clostridium sp. DMHC 10; counts= 3; multicellularity status: NA**

- Fibronectin-like_repeats+??->PSE->GAP1-N2+GAP1-M+GAP1-C(frag)->GAP1-N2+GAP1-M*->?->?->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->TM+vWA(canonical)+YtKA-like+TM+??->PSE->?->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->
- Fibronectin-like_repeats+??->PSE->GAP1-N2+GAP1-M+GAP1-C(frag)*->GAP1-N2+GAP1-M->?->?->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->TM+vWA(canonical)+YtKA-like+TM+??->PSE->?->Tubulin+coiled_coil+HTH?+??->
- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCF_001570525.1; Herbidospora sakaeratensis; counts= 3; multicellularity status: TRUE**

- GrpE->HSP70->TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM->
- GrpE->HSP70->TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+TM+GAP1-C*->
- vWA(canonical)->DO-GTPase1->GAP1-N2+GAP1-M+GAP1-C+TM+low_complexity+TM*->

■ **GCA_000025185.1; Pirellula staleyi DSM 6068; counts= 2; multicellularity status: TRUE**

- FGS-fold_domain->ZnR+DO-GTPase2.1->GAP1-N2+GAP1-M*->
- ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->??+TM+??+beta-rich??->GYF+GYF+TM+TM+TM->

■ **GCA_000092385.1; Streptomyces bingchenggensis BCW-1; counts= 2; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->
- ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->

■ **GCA_000968375.1; Clostridium scatologenes; counts= 2; multicellularity status: FALSE**

- Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->
- TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M*->

■ **GCA_001038625.1; Clostridium carboxidivorans P7; counts= 2; multicellularity status: FALSE**

- Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->
- TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->PSE->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M*->

■ **GCA_001610835.1; Planctomyces sp. SH-PL14; counts= 2; multicellularity status: FALSE**

- DO-GTPase2.2->GAP1-N2+GAP1-M+TM+GAP1-C*->??+TM+??+beta-rich??->GYF+GYF+Trypsin->
- ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+TM+GAP1-C*->??+TM+??+beta-rich??->GYF+GYF+Trypsin->Pkinase+low_complexity+TM->

■ **GCA_002189675.1; Streptomyces alboflavus; counts= 2; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->vWA(canonical)->PP2C->Pkinase+ZnR+beta-rich->||<-TPR_containing_alpha_helical+Fibronectin-like_repeats
- Pkinase->?->?->?->?->TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->?->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->

■ **GCA_002355675.1; Corynebacterium glutamicum; counts= 2; multicellularity status: FALSE**

- GrpE->HSP70->??+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->
- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA_000239075.2; Streptomyces sp. W007; counts= 2; multicellularity status: TRUE**

- *

- TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM->?->vWA(canonical)->PP2C->Pkinase+ZnR+beta-rich->||<-?<-?||GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__000295855.1; Mycolicibacterium fortuitum subsp. fortuitum DSM 46621 = ATCC 6841; counts= 2; multicellularity status: FALSE**

- HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->
- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->PSE->PSE->HRDC-like?+Fibronectin-like_repeats->PSE->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->TM+DUF4190+TM+PknH_C->

■ **GCA__000497445.1; Streptomyces roseochromogenus subsp. oscitans DS 12.976; counts= 2; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+Jelly_roll+beta-sandwich->||<-STAND_NTPase+TM+TM+TM+TM+TM+TM+TM
- Pkinase->?->?->?->?->HSP70_domain_2+low_complexity+domain_betaX->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->

■ **GCA__000524095.1; Mycobacterium kansasii 824; counts= 2; multicellularity status: FALSE**

- TM+DUF4190+TM->TM+DUF4190+TM->polar_leader+TM+TM+TM->PSE->PSE->GAP_unknown1+TM+TM+GAP_unknown2->GAP_unknown1+TM+TM+GAP_unknown2->PSE->GAP1-N2+GAP1-M+GAP1-C*->GAP1-N2+GAP1-M+GAP1-C->?->beta-rich+vWA(canonical)->
- Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C->GAP1-N2+GAP1-M+GAP1-C*->?->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA__000785145.2; Candidatus Thiomargarita nelsonii; counts= 2; multicellularity status: TRUE**

- DO-GTPase1->?->GAP1-N2+GAP1-M+GAP1-C*->DO-GTPase2?->
- ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->

■ **GCA__001898385.1; Planctomycetales bacterium 71-10; counts= 2; multicellularity status: NA**

- GAP1-N2+GAP1-M*->
- ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__001905595.1; Streptomyces sp. CB00316; counts= 2; multicellularity status: TRUE**

- TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM->vWA(canonical)->PP2C->Pkinase+ZnR+beta-rich->||<-?<-?<-?||GAP1-N2+GAP1-M+GAP1-C*->
- TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM->vWA(canonical)->PP2C->Pkinase+ZnR+beta-rich->

■ **GCA__001874765.1; Acinetobacter baumannii; counts= 2; multicellularity status: FALSE**

- GAP2->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->EAD1->
- PNP_UDP_1+EAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->EAD1->

■ **GCA__001983595.1; Streptomyces sp. IB2014 011-1; counts= 2; multicellularity status: TRUE**

- TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM->vWA(canonical)->PP2C->Pkinase+ZnR+beta-rich->
- vWA(canonical)->PP2C->Pkinase+ZnR+beta-rich->||<-?<-?<-?||GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__002003625.1; Mycobacterium kansasii; counts= 2; multicellularity status: FALSE**

- GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->GAP1-M->GAP1-N2+GAP1-M+GAP1-C->beta-rich+vWA(canonical)->??+DO-GTPase2.2->
- Tubulin+alpha_helical+??+??->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C->GAP1-M*->GAP1-N2+GAP1-M+GAP1-C->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA__002167455.1; Rhodopirellula; counts= 2; multicellularity status: TRUE**

- FGS-fold_domain->ZnR+DO-GTPase2.1->GAP1-N2+GAP1-M*->
- ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+TM+GAP1-C*->??+TM+??+beta-rich??->GYF+GYF+TM+TM+TM->

■ **GCA__002279765.1; Verrucomicrobia bacterium 12-59-8; counts= 2; multicellularity status: FALSE**

- FHA-like?+ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+TM*->

- FHA-like?+ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+TM+GAP1-C*->

■ **GCA__002401775.1; Ectothiorhodospiraceae bacterium; counts= 2; multicellularity status: TRUE**

- GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+CASPASE*->
- GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+CASPASE*->

■ **GCA__002794585.1; Chloroflexi bacterium; counts= 2; multicellularity status: TRUE**

- GAP1-N2+GAP1-M*->
- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__003002825.1; Spirosoma oryzae; counts= 2; multicellularity status: TRUE**

- GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->PNP_UDP_1+EAD1->
- ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->PNP_UDP_1+EAD1->

■ **GCA__900091795.1; Streptomyces sp. Termitarium-T10T-6; counts= 2; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C->GAP1-N2+GAP1-M+GAP1-C*->
- GAP1-N2+GAP1-M+GAP1-C*->GAP1-N2+GAP1-M+GAP1-C->

■ **GCA__900111115.1; Giesbergeria anulus; counts= 2; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->
- GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->

■ **GCA__000416365.2; Mycobacteriaceae; counts= 2; multicellularity status: FALSE**

- HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->??+DO-GTPase2.2->
- Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->TM+DUF4190+TM+PknH_C->TM+DUF4190+TM+PknH_C->

■ **GCA__000062885.1; Saccharopolyspora erythraea; counts= 2; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->
- GrpE->HSP70->TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->||<-?<-?<-HSP70<-unknown+CASPASE

■ **GCA__003149495.1; Gemmata obscuriglobus; counts= 2; multicellularity status: FALSE**

- DO-GTPase2.1->?->GAP1-N2+GAP1-M+TM+low_complexity+TM*->
- GAP1-N2+GAP1-M+TM*->

■ **GCA__000010265.1; Clostridium kluyveri; counts= 2; multicellularity status: FALSE**

- Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M->
- GAP1-N2+GAP1-M+GAP1-C->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M*->

■ **GCA__000024385.1; Thermomonospora curvata; counts= 2; multicellularity status: TRUE**

- GrpE->HSP70->TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->
- GrpE->HSP70->TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM->

■ **GCA__000143685.1; Clostridium ljungdahlii; counts= 2; multicellularity status: FALSE**

- Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->

- Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->?->?->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M*->

■ **GCA__000484505.1; Clostridium autoethanogenum; counts= 2; multicellularity status: NA**

- Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->PSE->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->
- Tubulin+coiled_coil+??->PSE->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->?->?->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M*->

■ **GCF__000619945.1; Clostridium lundense; counts= 2; multicellularity status: FALSE**

- Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->
- TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M*->

■ **GCF__000686125.1; Ruminococcus sp. NK3A76; counts= 2; multicellularity status: TRUE**

- GrpE->HSP70->HSP70+vWA(canonical)->?->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->
- HSP70->?->HSP70(frag)+vWA(canonical)->?->ZnR+ZnR+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->?->GAP1-N2+GAP1-M+GAP1-C*->

■ **GCF__000716675.1; Streptomyces; counts= 2; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->
- Pkinase->?->?->?->HSP70_domain_2+low_complexity+domain_betaX->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->

■ **GCF__000721705.1; Actinoplanes subtropicus; counts= 2; multicellularity status: TRUE**

- <-TPR_region+CASPASE||GrpE->HSP70->TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->
- ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+TM+GAP1-C*->

■ **GCF__000719065.1; Herbidospora cretacea; counts= 2; multicellularity status: TRUE**

- GrpE->HSP70->TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM->
- vWA(canonical)->DO-GTPase1->GAP1-N2+GAP1-M+GAP1-C+TM+low_complexity+TM*->

■ **GCF__000974445.1; Lechevalieria aerocolonigenes; counts= 2; multicellularity status: TRUE**

- TM+vWA(canonical)+TM->HSP70->??+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->||<-GrpE
- vWA(canonical)+beta-rich+low_complexity->Tubulin+alpha_helical+??+??->??+TM+TM+TM+TM+??->Pkinase+TM->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+SLATT+SLATT*->

■ **GCF__000718135.1; Streptomyces cyaneofuscatus; counts= 2; multicellularity status: TRUE**

- TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM->vWA(canonical)->PP2C->Pkinase+ZnR+beta-rich->||<-?<-?<-?||GAP1-N2+GAP1-M+GAP1-C*->
- TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM->vWA(canonical)->PP2C->Pkinase+ZnR+beta-rich->

■ **GCF__000718165.1; Streptomyces fulvoviolaceus; counts= 2; multicellularity status: TRUE**

- DO-GTPase1->GAP1-N2+GAP1-M+TM+GAP1-C*->?->TM+vWA(canonical)+TM+low_complexity->
- TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM->vWA(canonical)->PP2C->Pkinase+ZnR+beta-rich->

■ **GCA__001278095.1; Streptomyces sp. CFMR 7; counts= 2; multicellularity status: TRUE**

- TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM->vWA(canonical)->PP2C->Pkinase+ZnR+beta-rich->||<-?<-?<-?||GAP1-N2+GAP1-M+GAP1-C*->
- TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM->vWA(canonical)->PP2C->Pkinase+ZnR+beta-rich->

■ **GCA__001278845.1; Actinomyces sp. oral taxon 414; counts= 2; multicellularity status: NA**

- GrpE->HSP70->??+Fibronectin->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->?->??+DO-GTPase2.2->

■ **GCA_001279525.1; Nocardia sp. NRRL S-836; counts= 2; multicellularity status: TRUE**

- TM+vWA(canonical)+TM->HSP70->??+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->||<-GrpE
- vWA(canonical)+beta-rich+low_complexity->?->?->Tubulin+alpha_helical+??+??->??+TM+TM+TM+TM+??->Pkinase+TM->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C+TM+beta-rich*->?->||<-?||Pkinase+TM+Septum_form->

■ **GCA_001307545.1; Mycolicibacterium fortuitum; counts= 2; multicellularity status: FALSE**

- HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->??+DO-GTPase2.2->
- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->TM+DUF4190+TM+PknH_C->TM+DUF4190+TM+PknH_C->

■ **GCA_001317355.1; Oxobacter pfennigii; counts= 2; multicellularity status: FALSE**

- GAP1-N2+GAP1-M+GAP1-C*->
- Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF_001368795.1; Paenibacillus ihuae; counts= 2; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->PSE->PSE->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->
- TM+vWA(canonical)+YtKA-like+TM+??->PSE->PSE->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M*->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich->

■ **GCA_002102345.1; Mycolicibacterium peregrinum; counts= 2; multicellularity status: FALSE**

- HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->??+DO-GTPase2.2->
- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->TM+DUF4190+TM+PknH_C->TM+DUF4190+TM+PknH_C->

■ **GCA_001570465.1; Mycolicibacterium fortuitum; counts= 2; multicellularity status: FALSE**

- HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->??+DO-GTPase2.2->
- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->TM+DUF4190+TM+PknH_C->TM+DUF4190+TM+PknH_C->

■ **GCF_001570605.1; Herbidospora cretacea; counts= 2; multicellularity status: TRUE**

- GrpE->HSP70->TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM->
- vWA(canonical)->DO-GTPase1->GAP1-N2+GAP1-M+GAP1-C+TM+low_complexity+TM*->

■ **GCF_001570565.1; Herbidospora yilanensis; counts= 2; multicellularity status: TRUE**

- GrpE->HSP70->TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM->
- vWA(canonical)->DO-GTPase1->GAP1-N2+GAP1-M+GAP1-C+TM+low_complexity+TM*->

■ **GCF_001570585.1; Herbidospora daliensis; counts= 2; multicellularity status: TRUE**

- GrpE->HSP70->TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM->
- vWA(canonical)->DO-GTPase1->GAP1-N2+GAP1-M+GAP1-C+TM+low_complexity+TM*->

■ **GCA_001636845.1; Clostridium ljungdahlii; counts= 2; multicellularity status: FALSE**

- Fibronectin-like_repeats+??->PSE->?->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->
- TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->?->?->?->?->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M*->

■ **GCA_001636835.1; Clostridium coskatii; counts= 2; multicellularity status: FALSE**

- Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->

- TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->?->?->?->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M*->

■ **GCA_001665455.1; Mycolicibacterium fortuitum; counts= 2; multicellularity status: FALSE**

- HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->??+DO-GTPase2.2->
- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->TM+DUF4190+TM+PknH_C->TM+DUF4190+TM+PknH_C->

■ **GCA_001665415.1; Mycolicibacterium fortuitum; counts= 2; multicellularity status: FALSE**

- HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->??+DO-GTPase2.2->
- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->TM+DUF4190+TM+PknH_C->

■ **GCA_001665625.1; Mycolicibacterium peregrinum; counts= 2; multicellularity status: FALSE**

- HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->??+DO-GTPase2.2->
- TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->TM+DUF4190+TM+PknH_C->

■ **GCA_001665315.1; Mycolicibacterium fortuitum; counts= 2; multicellularity status: FALSE**

- HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->??+DO-GTPase2.2->
- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->TM+DUF4190+TM+PknH_C->

■ **GCA_001665785.1; Mycolicibacterium peregrinum; counts= 2; multicellularity status: FALSE**

- HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->??+DO-GTPase2.2->
- TM+[lc_insert+]vWA(canonical)+Fibronectin-like_repeats+TM+??+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->TM+DUF4190+TM+PknH_C->

■ **GCA_001667205.1; Mycolicibacterium peregrinum; counts= 2; multicellularity status: FALSE**

- HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->??+DO-GTPase2.2->
- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->TM+DUF4190+TM+PknH_C->TM+DUF4190+TM+PknH_C->

■ **GCA_001673325.1; Mycolicibacterium fortuitum; counts= 2; multicellularity status: FALSE**

- HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->??+DO-GTPase2.2->
- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->TM+DUF4190+TM+PknH_C->TM+DUF4190+TM+PknH_C->

■ **GCA_001673265.1; Mycolicibacterium conceptionense; counts= 2; multicellularity status: FALSE**

- GrpE->HSP70->TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->HSP70->vWA(canonical)->
- HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->??+DO-GTPase2.2->

■ **GCA_001672845.1; Mycolicibacterium fortuitum; counts= 2; multicellularity status: FALSE**

- HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->??+DO-GTPase2.2->
- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->TM+DUF4190+TM+PknH_C->TM+DUF4190+TM+PknH_C->

■ **GCA_001673275.1; Mycolicibacterium fortuitum; counts= 2; multicellularity status: FALSE**

- HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->??+DO-GTPase2.2->
- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->TM+DUF4190+TM+PknH_C->

■ **GCA_001675165.1; Clostridium ragsdalei; counts= 2; multicellularity status: FALSE**

- Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->

- TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->?->?->?->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M*->

■ **GCA_001673485.1; Mycolicibacterium fortuitum; counts= 2; multicellularity status: FALSE**

- GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->TM+DUF4190+TM+PknH_C->
- HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->??+DO-GTPase2.2->

■ **GCF_001570545.1; Herbidospora mongoliensis; counts= 2; multicellularity status: TRUE**

- GrpE->HSP70->TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM->
- vWA(canonical)->DO-GTPase1->GAP1-N2+GAP1-M+GAP1-C+TM+low_complexity+TM*->

■ **GCA_001666875.1; Mycobacterium sp. E802; counts= 2; multicellularity status: FALSE**

- GrpE->HSP70->TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->HSP70->vWA(canonical)->
- HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->??+DO-GTPase2.2->

■ **GCF_001552135.1; Actinomadura chibensis; counts= 2; multicellularity status: TRUE**

- GrpE->HSP70->TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM->
- vWA(canonical)->DO-GTPase1->GAP1-N2+GAP1-M+GAP1-C+TM*->

■ **GCA_003001795.1; Actinomadura; counts= 2; multicellularity status: TRUE**

- GrpE->HSP70->TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->?->unknown+CASPASE->HSP70->
- HSP70->TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM->

■ **GCA_002300155.1; Rhodococcus; counts= 2; multicellularity status: TRUE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->
- TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA_001905575.1; Streptomyces sp. CB00072; counts= 2; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM->vWA(canonical)->PP2C->Pkinase+ZnR+beta-rich->||<-?<-?||GAP1-N2+GAP1-M+GAP1-C*->
- TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM->vWA(canonical)->PP2C->Pkinase+ZnR+beta-rich->||<-?<-?||GAP1-N2+GAP1-M+GAP1-C->

■ **GCA_900129675.1; Bradyrhizobium erythrophlei; counts= 2; multicellularity status: TRUE**

- Calcineurin+GAPEAD1->GAP2->DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->
- GAP1-N1+GAP1-M+GAP1-C*->

■ **GCF_001610835.1; Planctomyces sp. SH-PL14; counts= 2; multicellularity status: FALSE**

- DO-GTPase2.2->GAP1-N2+GAP1-M+TM+GAP1-C*->??+TM+??+beta-rich??->GYF+GYF+Trypsin->
- ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+TM+GAP1-C*->??+TM+??+beta-rich??->GYF+GYF+Trypsin->Pkinase+low_complexity+TM->

■ **GCA_001954035.1; Mycolicibacterium fortuitum; counts= 2; multicellularity status: FALSE**

- HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->??+DO-GTPase2.2->
- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA_001956985.1; Paludisphaera borealis; counts= 2; multicellularity status: TRUE**

- GAP1-N2+GAP1-M*->

- ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->??+TM+??+beta-rich??->

■ **GCA__002197845.1; Fimbriiglobus ruber; counts= 2; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+TM+GAP1-C*->
- GAP1-N2+GAP1-M+TM+low_complexity+TM*->

■ **GCA__002224125.1; Streptomyces sp. NBS 14/10; counts= 2; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->
- PP2C->Pkinase->?->?->?->HSP70_domain_2+low_complexity+domain_betaX->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->

■ **GCA__900091865.1; Streptomyces sp. DvalAA-19; counts= 2; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C->||<-PSE||vWA(canonical)->PP2C->Pkinase+ZnR+beta-rich->PSE->||<-?<-?<-?||GAP1-N2+GAP1-M+GAP1-C*->
- TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->||<-PSE||vWA(canonical)->PP2C->Pkinase+ZnR+beta-rich->PSE->||<-?<-?<-?||GAP1-N2+GAP1-M+GAP1-C->

■ **GCA__002251265.1; Rhodopirellula; counts= 2; multicellularity status: TRUE**

- FGS-fold_domain->ZnR+DO-GTPase2.1->GAP1-N2+GAP1-M*->
- ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+TM+GAP1-C*->??+TM+??+beta-rich??->GYF+GYF+TM+TM+TM->

■ **GCA__002289565.1; Rhodopirellula sp. SM50; counts= 2; multicellularity status: TRUE**

- FGS-fold_domain->ZnR+DO-GTPase2.1->GAP1-N2+GAP1-M*->
- ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+TM+GAP1-C*->??+TM+??+beta-rich??->GYF+GYF+TM+TM+TM->

■ **GCF__002551465.1; Streptomyces sp. b84; counts= 2; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM->vWA(canonical)->PP2C->Pkinase+ZnR+beta-rich->||<-?<-?||GAP1-N2+GAP1-M+GAP1-C*->
- TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM->vWA(canonical)->PP2C->Pkinase+ZnR+beta-rich->||<-?<-?||GAP1-N2+GAP1-M+GAP1-C->

■ **GCA__000025345.1; Geodermatophilus obscurus DSM 43160; counts= 1; multicellularity status: TRUE**

- Pkinase+TM->TM->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->?->||<-?<-?||?->Pkinase+low_complexity->

■ **GCA__000190575.1; Bacteroides salanitronis DSM 18170; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->?->DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA__000221965.1; Xanthomonas campestris pv. raphani 756C; counts= 1; multicellularity status: FALSE**

- GAP2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->

■ **GCA__000283295.1; Mycolicibacterium smegmatis MC2 155; counts= 1; multicellularity status: FALSE**

- HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->??+DO-GTPase2.2->

■ **GCA__002603685.1; Leptospira phage vb__LkmZ__Bejolso9-LE1; counts= 1; multicellularity status: FALSE**

- GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->PNP_UDP_1+EAD1->

■ **GCA__000739375.1; Comamonas testosteroni TK102; counts= 1; multicellularity status: FALSE**

- GAP2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->

■ **GCA__000828015.1; Corynebacterium glutamicum; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA_000833575.1; Corynebacterium singulare; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->polar_leader+TM+TM+TM->

■ **GCA_000959345.1; Burkholderia pseudomallei PB08298010; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_001040905.1; Streptomyces sp. PBH53; counts= 1; multicellularity status: TRUE**

- TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM->vWA(canonical)->Pkinase+ZnR+beta-rich->

■ **GCA_001447315.1; Paenibacillus sp. IHB B 3084; counts= 1; multicellularity status: TRUE**

- Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_001447865.2; Corynebacterium glutamicum; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA_001518935.2; Corynebacterium glutamicum; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA_001610875.1; Pirellula sp. SH-Sr6A; counts= 1; multicellularity status: TRUE**

- GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->||<-EAD1+Trypsin

■ **GCA_001643015.1; Corynebacterium crudilactis; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->

■ **GCA_001865855.1; Nocardia seriolae; counts= 1; multicellularity status: TRUE**

- Pkinase+TM->?->ZnR+DO-GTPase2.1->GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_001874405.2; Paenibacillus polymyxa; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_001874425.2; Paenibacillus polymyxa; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->PSE->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_001931635.1; Streptomyces sp. Tue 6075; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_001936195.1; Corynebacterium glutamicum; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA_002094995.1; Streptomyces sp. S8; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_002220305.1; Burkholderia sp. AD24; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA__003431825.1; Blastomonas fulva; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA__002814075.1; Polaribacter sejongensis; counts= 1; multicellularity status: TRUE**

- GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+PNP_UDP_1*->

■ **GCA__002943525.1; Kitasatospora sp. MMS16-BH015; counts= 1; multicellularity status: TRUE**

- PP2C->Pkinase->?->?->?->HSP70_domain_2+low_complexity+domain_betaX->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->

■ **GCA__000011325.1; Corynebacterium glutamicum ATCC 13032; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA__000010225.1; Corynebacterium glutamicum R; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA__000010605.1; Streptomyces griseus subsp. griseus NBRC 13350; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__000010805.1; Rhodococcus opacus B4; counts= 1; multicellularity status: TRUE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA__002355155.1; Corynebacterium glutamicum; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA__002355915.1; Actinomyces naeslundii; counts= 1; multicellularity status: TRUE**

- HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__003966365.1; Acetobacter orientalis; counts= 1; multicellularity status: FALSE**

- AB_hydrolase+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA__003609795.1; Sphingobium sp. YG1; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA__000196335.1; Corynebacterium glutamicum ATCC 13032; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA__001046875.1; Tetrasphaera jenkinsii Ben 74; counts= 1; multicellularity status: TRUE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->?->??+DO-GTPase2.2->

■ **GCA__000431615.1; Firmicutes bacterium CAG:41; counts= 1; multicellularity status: FALSE**

- GAP1-N2+GAP1-M+TM+GAP1-C*->

■ **GCA__000433415.1; Clostridium sp. CAG:448; counts= 1; multicellularity status: NA**

- GAP1-N2+GAP1-M+TM+GAP1-C*->

■ **GCA__000437175.1; Ruminococcus sp. CAG:330; counts= 1; multicellularity status: TRUE**

- HSP70(frag)+vWA(canonical)->?->DO-GTPase2.1->GAP1-N2+GAP1-M+TM+GAP1-C*->

■ **GCA__000438015.1; Coraliomargarita sp. CAG:312; counts= 1; multicellularity status: FALSE**

- FHA-like?+ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+TM+GAP1-C*->

■ **GCA__000982975.1; Halomonas sp. A3H3; counts= 1; multicellularity status: FALSE**

- GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->

■ **GCA__001160225.1; Mycobacterium tuberculosis; counts= 1; multicellularity status: FALSE**

- TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM->

■ **GCA__001152565.1; Yersinia pekkanenii; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA__001261935.1; Corynebacterium striatum; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->polar_leader+TM+TM+TM->

■ **GCA__001319925.1; Yersinia intermedia; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA__001405915.1; Prevotella copri; counts= 1; multicellularity status: FALSE**

- DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA__000016505.1; Clostridium kluyveri DSM 555; counts= 1; multicellularity status: FALSE**

- TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M*->

■ **GCA__000173655.1; Corynebacterium amycolatum SK46; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA__000167995.1; Yersinia mollaretii ATCC 43969; counts= 1; multicellularity status: FALSE**

- DO-GTPase2.1(fragment)->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA__000156475.1; Streptomyces albus J1074; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__000158855.1; Streptomyces sp. SPB78; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__000158895.1; Streptomyces sp. C; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__000158915.1; Streptomyces himastatinicus ATCC 53653; counts= 1; multicellularity status: TRUE**

- TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM->vWA(canonical)->PP2C->Pkinase+ZnR+beta-rich->

■ **GCA__000208635.2; Gluconacetobacter sp. SXCC-1; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA__000224315.2; Corynebacterium glutamicum S9114; counts= 1; multicellularity status: FALSE**

- TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA__000245555.2; Paenibacillus dendritiformis C454; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA__000271305.1; Hydrocarboniphaga effusa AP103; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA__000278565.1; Pseudomonas sp. Ag1; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA__000243895.3; Leptospira interrogans str. FPW2026; counts= 1; multicellularity status: FALSE**

- GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA__000244275.3; Leptospira interrogans str. UI 12621; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA__000244135.3; Leptospira interrogans serovar Grippotyphosa str. UI 08368; counts= 1; multicellularity status: FALSE**

- GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA__000344825.1; Salmonella enterica subsp. enterica serovar Newport str. SH111077; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA__000364445.1; Methylobacterium mesophilicum SR1.6/6; counts= 1; multicellularity status: TRUE**

- CASPASE+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA__000368445.1; Acinetobacter sp. CIP 56.2; counts= 1; multicellularity status: FALSE**

- GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->EAD1->CASPASE+EAD1->

■ **GCA__000414115.1; Streptomyces aurantiacus JA 4570; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->vWA(canonical)->

■ **GCA__001856845.1; Thermoplasmatales archaeon Gpl; counts= 1; multicellularity status: FALSE**

- TM+TM+TM+TM+TM+TM+DO-GTPase2.1->GAP1-N2+GAP1-M+GAP1-C*->??->TM_region+DO-GTPase1->

■ **GCA__000448385.1; Saccharopolyspora erythraea D; counts= 1; multicellularity status: TRUE**

- ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__000481145.1; Pseudomonas aeruginosa BWHPSA028; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_000502855.1; Mesorhizobium sp. L2C067A000; counts= 1; multicellularity status: TRUE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_000508425.1; Actinomyces urogenitalis DORA_12; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C(frag)*->

■ **GCA_000516475.1; Candidatus Magnetoglobus multicellularis str. Araruama; counts= 1; multicellularity status: TRUE**

- GrpE->?->?->GrpE->DO-GTPase2.1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_000517865.1; Paenibacillus sp. FSL R7-269; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->?->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_000517905.1; Paenibacillus sp. FSL H7-689; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_000517965.1; Paenibacillus sp. FSL R7-277; counts= 1; multicellularity status: TRUE**

- Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->?->?->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_000568155.1; Enterobacter sp. DC3; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_000349585.1; Dietzia sp. UCD-THP; counts= 1; multicellularity status: FALSE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_000739515.1; Candidatus Moduliflexus flocculans; counts= 1; multicellularity status: TRUE**

- DO-GTPase2.1->GAP1-N2+GAP1-M+low_complexity+TM+TM*->

■ **GCA_000974725.1; Methylobacterium sp. ME121; counts= 1; multicellularity status: TRUE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_001570725.1; Paenibacillus amylolyticus; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_001894745.1; Paenibacillus sp. NAIST15-1; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_002003445.1; Corynebacterium glutamicum; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA_000698985.1; Bordetella bronchiseptica MBORD731; counts= 1; multicellularity status: FALSE**

- DO-GTPase2.1(fragment)->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_000694595.1; Klebsiella variicola; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA__000698455.1; Rhodococcus qingshengii; counts= 1; multicellularity status: TRUE**

- GrpE->TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->?->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->??->HSP70->vWA(canonical)->

■ **GCA__000705615.1; Rhizobium leguminosarum bv. phaseoli CCGM1; counts= 1; multicellularity status: TRUE**

- Calcineurin+GAPEAD1->GAP2->DO-GTPase2.1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA__000219495.2; Medicago truncatula; counts= 1; multicellularity status: FALSE**

- DO-GTPase2+DO-GTPase1+GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA__000584955.2; Candidatus Accumulibacter sp. SK-01; counts= 1; multicellularity status: FALSE**

- GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->

■ **GCA__000741785.1; Bifidobacterium stellenboschense; counts= 1; multicellularity status: FALSE**

- TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->GrpE->HSP70->HSP70+vWA(canonical)->DnaJ+DnaJ+ZnR+ZnR+coiled_coil+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__000758965.1; Corynebacterium freneyi DNF00450; counts= 1; multicellularity status: FALSE**

- TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->??+DO-GTPase2.2->

■ **GCA__000812585.1; Chromobacterium piscinae; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA__000817655.1; Streptomyces sp. RSD-27; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__000818175.1; Streptomyces sp. AcH 505; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__000819915.1; Corynebacterium glutamicum; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA__000834545.1; Pseudomonas fluorescens; counts= 1; multicellularity status: FALSE**

- GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->

■ **GCA__000878385.1; Methylobacterium radiotolerans; counts= 1; multicellularity status: TRUE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA__000932205.1; Streptomyces sp. MBRL 601; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__000961745.1; Rhodospirillaceae bacterium BRH_c57; counts= 1; multicellularity status: FALSE**

- GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->

■ **GCA__000961795.1; Hyphomonas sp. BRH_c22; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_000966975.1; Streptomyces katrae; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_000966985.1; Streptomyces sp. NRRL S-444; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_001038505.1; Puniceibacterium sp. IMCC21224; counts= 1; multicellularity status: FALSE**

- DO-GTPase2.2->GAP1-N2+GAP1-M+TM+GAP1-C*->

■ **GCA_001047325.1; Streptomyces viridochromogenes; counts= 1; multicellularity status: TRUE**

- GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->

■ **GCA_001047335.1; Streptomyces regensis; counts= 1; multicellularity status: TRUE**

- TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->vWA(canonical)->Pkinase+ZnR+beta-rich->

■ **GCA_001187725.1; Brevibacillus reuszeri; counts= 1; multicellularity status: FALSE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_001270675.1; Streptomyces griseus subsp. rhodochrous; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_001275645.1; Bacillus sp. FJAT-18019; counts= 1; multicellularity status: NA**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_001277345.1; Paenibacillus solani; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_001277855.1; Paenibacillus polymyxa; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_001279425.1; Streptomyces sp. NRRL F-2295; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_001279735.1; Streptomyces sp. MMG1522; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_001280045.1; Streptomyces sp. NRRL WC-3723; counts= 1; multicellularity status: TRUE**

- TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->vWA(canonical)->Pkinase+ZnR+beta-rich->

■ **GCA_001280595.1; Paenibacillus sp. A59; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_001280885.1; Streptomyces sp. XY332; counts= 1; multicellularity status: TRUE**

- TPR_containing_alpha_helical+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM->vWA(canonical)->PP2C->Pkinase+ZnR+beta-rich->

- **GCA__001298555.1; Actinobacteria bacterium OV450; counts= 1; multicellularity status: NA**
  - Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->
- **GCA__001304075.1; candidate division BRC1 bacterium SM23__51; counts= 1; multicellularity status: NA**
  - ZnR+DO-GTPase2.1->GAP1-N2+GAP1-M+TM+GAP1-C*->
- **GCA__001400775.1; Pseudomonas congelans; counts= 1; multicellularity status: FALSE**
  - Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->GAP1-N1+GAP1-M+GAP1-C*->
- **GCA__001426045.1; Methylobacterium sp. Leaf94; counts= 1; multicellularity status: TRUE**
  - GAP1-N1+GAP1-M+GAP1-C*->
- **GCA__001425705.1; Pelomonas sp. Root1217; counts= 1; multicellularity status: FALSE**
  - Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->
- **GCA__001514305.1; Streptomyces sp. RV15; counts= 1; multicellularity status: TRUE**
  - TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM->vWA(canonical)->PP2C->Pkinase+ZnR+beta-rich->
- **GCA__001526225.1; Burkholderia ubonensis; counts= 1; multicellularity status: FALSE**
  - Calcineurin+GAPEAD1->GAP2->||<-?||DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->
- **GCA__001527385.1; Burkholderia ubonensis; counts= 1; multicellularity status: FALSE**
  - Calcineurin+GAPEAD1->GAP2->||<-?||DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->
- **GCA__001528875.1; Burkholderia ubonensis; counts= 1; multicellularity status: FALSE**
  - Calcineurin+GAPEAD1->GAP2->DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->
- **GCA__001546485.1; Gardnerella vaginalis; counts= 1; multicellularity status: FALSE**
  - TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->?->HSP70->HSP70+vWA(canonical)->DnaJ+DnaJ+ZnR+ZnR+coiled_coil+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->
- **GCA__001560865.1; Pseudomonas aeruginosa; counts= 1; multicellularity status: FALSE**
  - GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->
- **GCA__001567085.1; Chloroflexi bacterium OLB15; counts= 1; multicellularity status: TRUE**
  - GAP1-N2+GAP1-M+GAP1-C*->
- **GCA__001589295.1; Sorangium cellulosum; counts= 1; multicellularity status: TRUE**
  - GAP1-N1+GAP1-M+GAP1-C*->||<-DO-GTPase1<-ZnR+DO-GTPase2.1<-GAP2
- **GCA__001613855.1; Thalassospira xiamenensis; counts= 1; multicellularity status: FALSE**
  - Calcineurin+GAPEAD1->GAP2->ZnR(fragment)+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->
- **GCA__001636565.1; Frankia sp. EI5c; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C+ZnR+DO-GTPase2*->

■ **GCA_001644415.1; Planctomycetaceae bacterium SCGC AG-212-F19; counts= 1; multicellularity status: NA**

- GAP1-N2+GAP1-M+TM+low_complexity*->

■ **GCA_001705105.1; Bradyrhizobium sp. UASWS1016; counts= 1; multicellularity status: TRUE**

- DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_001723765.1; Candidatus Scalindua rubra; counts= 1; multicellularity status: NA**

- DO-GTPase2.1->GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_001807225.1; Corynebacterium sp. HMSC05E07; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->polar_leader+TM+TM+TM->

■ **GCA_001807025.1; Corynebacterium sp. HMSC11E11; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->polar_leader+TM+TM+TM->

■ **GCA_001767115.1; Acidobacteria bacterium RIFCSPLOWO2_12_FULL_59_11; counts= 1; multicellularity status: FALSE**

- DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_001772075.1; Burkholderiales bacterium RIFCSPHIGHO2_02_FULL_64_19; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_001804865.1; Lentisphaerae bacterium GWF2_57_35; counts= 1; multicellularity status: FALSE**

- FHA-like+??+ZnR+ZnR+DO-GTPase2.2+??->GAP1-N2+GAP1-M+TM+GAP1-C*->

■ **GCA_001803235.1; Lentisphaerae bacterium RIFOXYA12_64_32; counts= 1; multicellularity status: FALSE**

- GAP1-N2+GAP1-M*->??+TM+??+beta-rich??->

■ **GCA_001828265.1; Planctomycetes bacterium RBG_13_63_9; counts= 1; multicellularity status: NA**

- FGS-fold_domain->ZnR+DO-GTPase2.1->GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_001828305.1; Planctomycetes bacterium RBG_16_64_10; counts= 1; multicellularity status: NA**

- FGS-fold_domain->ZnR+DO-GTPase2.1->GAP1-N2+GAP1-M+GAP1-C(frag)*->

■ **GCA_001828335.1; Planctomycetes bacterium RBG_16_64_12; counts= 1; multicellularity status: NA**

- ZnR+DO-GTPase2.1->GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_001830395.1; Pseudomonadales bacterium RIFCSPLOWO2_12_59_9; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_001831115.1; Verrucomicrobia bacterium GWF2_62_7; counts= 1; multicellularity status: FALSE**

- GAP1-N2+GAP1-M+TM+GAP1-C*->

■ **GCA_001854655.1; Frankia sp. Cc1.17; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C+ZnR+DO-GTPase2*->

■ **GCA__001898335.1; Mucilaginibacter sp. 44-25; counts= 1; multicellularity status: FALSE**

- TIR+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA__001897835.1; Bacteroidetes bacterium 46-16; counts= 1; multicellularity status: FALSE**

- GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->PNP_UDP_1+EAD1->

■ **GCA__001898665.1; Burkholderiales bacterium 68-20; counts= 1; multicellularity status: FALSE**

- GAP2->DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->

■ **GCA__001905305.1; Mycobacterium sp. SWH-M5; counts= 1; multicellularity status: FALSE**

- HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C(frag)*->

■ **GCA__001905065.1; Saccharothrix sp. CB00851; counts= 1; multicellularity status: TRUE**

- HSP70->||<-?||GrpE->HSP70->TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->

■ **GCA__001905525.1; Streptomyces sp. TSRI0395; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__001905905.1; Streptomyces sp. CB02366; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__001912755.2; Corynebacterium glutamicum; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA__001912725.1; Corynebacterium glutamicum; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA__001917305.1; Verrucomicrobia bacterium CAG:312_58_20; counts= 1; multicellularity status: FALSE**

- FHA-like?+ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+TM+GAP1-C*->

■ **GCA__001921865.1; Pseudomonas chlororaphis; counts= 1; multicellularity status: FALSE**

- GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->

■ **GCA__001955985.1; Paenibacillus pabuli; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA__001956035.1; Paenibacillus amylolyticus; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA__001956835.1; Paenibacillus macerans; counts= 1; multicellularity status: TRUE**

- TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA__001974825.1; Corchorus olitorius; counts= 1; multicellularity status: NA**

- TM+TM+TM+vWA+TM+TM+TM+ZnR+GTPase+GAP1-N2+GAP1-M+GAP1-C+ATP_grasp+ATP_grasp+Rossmann-like+thioredoxin_fold*->

■ **GCA_002083655.1; Proteobacteria bacterium ST_bin14; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_002085445.1; Beggiatoa sp. 4572_84; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->||<-HSP70<-GrpE

■ **GCA_002086865.1; Mycobacterium kansasii; counts= 1; multicellularity status: FALSE**

- TM+DUF4190+TM->TM+DUF4190+TM->polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA_002086855.1; Mycobacterium kansasii; counts= 1; multicellularity status: FALSE**

- TM+DUF4190+TM->TM+DUF4190+TM->polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA_002086925.1; Mycobacterium kansasii; counts= 1; multicellularity status: FALSE**

- TM+DUF4190+TM->TM+DUF4190+TM->polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA_002086935.1; Mycobacterium kansasii; counts= 1; multicellularity status: FALSE**

- TM+DUF4190+TM->TM+DUF4190+TM->polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA_002104865.1; Streptomyces sp. BF-3; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_001432265.1; Acinetobacter baumannii; counts= 1; multicellularity status: FALSE**

- GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_002159375.1; Alistipes sp. An54; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->?->DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_002170515.1; Verrucomicrobia bacterium TMED71; counts= 1; multicellularity status: FALSE**

- FHA-like?+ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+low_complexity+TM+TM*->

■ **GCA_002170435.1; Verrucomicrobiaceae bacterium TMED76; counts= 1; multicellularity status: NA**

- FHA-like?+ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+TM+beta-rich+??*->??+TM+??->

■ **GCA_002200935.1; Rhizobium yanglingense; counts= 1; multicellularity status: TRUE**

- GAPEAD1->GAP2->GAP1-N1+GAP1-M+GAP1-C*->?->Calcineurin->

■ **GCA_002204655.1; Cuniculiplasma sp. C_DKE; counts= 1; multicellularity status: TRUE**

- TM+TM+TM+TM+TM+TM+DO-GTPase2.1->GAP1-N2+GAP1-M+GAP1-C*->??->TM_region+DO-GTPase1->

■ **GCA_002242735.1; Streptomyces sp. 2R; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_002254715.1; archaeon ex4484_74; counts= 1; multicellularity status: NA**

- GAP1-N2+GAP1-M*->

- **GCA__002279215.1; Planctomycetia bacterium 21-64-5; counts= 1; multicellularity status: NA**
  - ??+GAP1-N2+GAP1-M+??+TM+TM*->
- **GCA__002280395.1; Flavobacteriales bacterium 32-35-8; counts= 1; multicellularity status: FALSE**
  - GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->??+EAD1->EAD1+Trypsin->
- **GCA__002281555.1; Hydrogenophilales bacterium 28-61-23; counts= 1; multicellularity status: FALSE**
  - Calcineurin+EAD1->||<-?||GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->
- **GCA__002264305.1; Paenibacillus taichungensis; counts= 1; multicellularity status: TRUE**
  - ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->
- **GCA__002286935.1; Bifidobacterium criceti; counts= 1; multicellularity status: FALSE**
  - TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->GrpE->HSP70->HSP70+vWA(canonical)->DnaJ+DnaJ+ZnR+ZnR+coiled_coil+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->
- **GCA__002304375.1; Opitutae bacterium Tous-C2FEB; counts= 1; multicellularity status: FALSE**
  - ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+TM+GAP1-C*->
- **GCA__002290585.1; Opitutae bacterium AMD-G3; counts= 1; multicellularity status: FALSE**
  - FHA-like?+ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+TM+GAP1-C*->
- **GCA__002290595.1; Opitutae bacterium AMD-G1; counts= 1; multicellularity status: FALSE**
  - FHA-like?+ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+TM+GAP1-C*->
- **GCA__002401295.1; SAR324 cluster bacterium; counts= 1; multicellularity status: NA**
  - GAP2->DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+PNP_UDP_1*->
- **GCA__002401655.1; Gammaproteobacteria bacterium; counts= 1; multicellularity status: NA**
  - GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->
- **GCA__002733575.1; Blastopirellula sp.; counts= 1; multicellularity status: TRUE**
  - FGS-fold_domain->ZnR+DO-GTPase2.1->GAP1-N2+GAP1-M+GAP1-C*->
- **GCA__002735695.1; Chitinimonas sp. BJB300; counts= 1; multicellularity status: FALSE**
  - Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->
- **GCA__002735705.1; Janthinobacterium sp. BJB426; counts= 1; multicellularity status: FALSE**
  - GAP2->DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->
- **GCA__002737185.1; Opitutae bacterium; counts= 1; multicellularity status: FALSE**
  - FHA-like?+ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+TM+GAP1-C*->
- **GCA__002737585.1; Planctomycetaceae bacterium; counts= 1; multicellularity status: NA**

- ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+TM*->

■ **GCA__002748445.1; candidate division KSB3 bacterium; counts= 1; multicellularity status: NA**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__002754535.1; Streptomyces sp. 61; counts= 1; multicellularity status: TRUE**

- TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM->?->vWA(canonical)->PP2C->Pkinase+ZnR+beta-rich->

■ **GCA__002750415.1; Paenibacillus sp. LK1; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA__002760695.1; Acinetobacter baumannii; counts= 1; multicellularity status: FALSE**

- PNP_UDP_1+EAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA__002760725.1; Acinetobacter baumannii; counts= 1; multicellularity status: FALSE**

- PNP_UDP_1+EAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA__002760715.1; Acinetobacter baumannii; counts= 1; multicellularity status: FALSE**

- PNP_UDP_1+EAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA__002760785.1; Acinetobacter baumannii; counts= 1; multicellularity status: FALSE**

- PNP_UDP_1+EAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA__002760765.1; Acinetobacter baumannii; counts= 1; multicellularity status: FALSE**

- GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA__002760825.1; Acinetobacter baumannii; counts= 1; multicellularity status: FALSE**

- ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA__002760895.1; Acinetobacter baumannii; counts= 1; multicellularity status: FALSE**

- GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA__002775095.1; Corynebacterium striatum; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->PSE->PSE->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C(frag)*->?->beta-rich+vWA(canonical)->??+DO-GTPase2.2->polar_leader+TM+TM+TM->

■ **GCA__002775105.1; Corynebacterium striatum; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->PSE->PSE->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->polar_leader+TM+TM+TM->

■ **GCA__002794595.1; Chloroflexi bacterium; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__002808645.1; Streptomyces albidoflavus; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__002813225.1; Streptomyces sp. Ag109__G2-1; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

- **GCA__002836235.1; Psychrobacter sp. Choline-02u-13; counts= 1; multicellularity status: FALSE**
  - DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->
- **GCA__001896795.2; Thermomonospora sp. CIF 1; counts= 1; multicellularity status: TRUE**
  - GrpE->HSP70->TPR__containing__alpha__helical+Fibronectin-like__repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM->
- **GCA__002840095.1; Gammaproteobacteria bacterium HGW-Gammaproteobacteria-1; counts= 1; multicellularity status: FALSE**
  - Calcineurin+GAPEAD1->GAP2->DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->
- **GCA__002841525.1; Firmicutes bacterium HGW-Firmicutes-17; counts= 1; multicellularity status: FALSE**
  - DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->
- **GCA__002842145.1; Betaproteobacteria bacterium HGW-Betaproteobacteria-6; counts= 1; multicellularity status: FALSE**
  - Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->PSE->GAP1-N1+GAP1-M+GAP1-C*->
- **GCA__002842665.1; Bacteroidetes bacterium HGW-Bacteroidetes-11; counts= 1; multicellularity status: FALSE**
  - GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->PNP__UDP__1+EAD1->
- **GCA__002843035.1; Actinobacteria bacterium HGW-Actinobacteria-5; counts= 1; multicellularity status: NA**
  - ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+low__complexity*->
- **GCA__002860365.1; Bifidobacterium parmae; counts= 1; multicellularity status: FALSE**
  - TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->GrpE->HSP70->HSP70+vWA(canonical)->DnaJ+DnaJ+ZnR+ZnR+coiled__coil+Fibronectin-like__repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->
- **GCA__002863645.1; Psychrobacter sp. MES7-P7E; counts= 1; multicellularity status: FALSE**
  - GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->
- **GCA__002873265.1; Vibrio lentus; counts= 1; multicellularity status: FALSE**
  - Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->
- **GCA__002878555.1; Vibrio splendidus; counts= 1; multicellularity status: FALSE**
  - PNP__UDP__1+EAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->SLATT->
- **GCA__003002065.1; Pseudosporangium ferrugineum; counts= 1; multicellularity status: TRUE**
  - GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->PNP__UDP__1+EAD1->
- **GCA__003010405.1; Acidobacteria bacterium; counts= 1; multicellularity status: FALSE**
  - DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->
- **GCA__900084005.1; Klebsiella oxytoca; counts= 1; multicellularity status: FALSE**
  - Calcineurin+GAPEAD1->GAP2->DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->
- **GCA__900086575.1; Komagataeibacter rhaeticus; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_900091315.1; Streptomyces sp. DI166; counts= 1; multicellularity status: TRUE**

- TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_900091875.1; Streptomyces sp. BpilaLS-43; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_900091755.1; Streptomyces sp. TverLS-915; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_900091715.1; Streptomyces sp. DpondAA-F4a; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_900091895.1; Streptomyces sp. IgraMP-1; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_900091965.1; Streptomyces sp. Ncost-T6T-2b; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_900090155.1; Streptomyces sp. ScaeMP-e48; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_900101545.1; Variovorax sp. CF079; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_900101225.1; Paenibacillus sp. CF095; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_900101405.1; Bradyrhizobium sp. R5; counts= 1; multicellularity status: TRUE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_900103785.1; Geodermatophilus siccatus; counts= 1; multicellularity status: TRUE**

- Pkinase+TM->TM->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->?->||<-?<-?||?->Pkinase+low_complexity->

■ **GCA_900104025.1; Geodermatophilus sp. DSM 45219; counts= 1; multicellularity status: TRUE**

- Pkinase+TM->TM->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->?->||<-?<-?||?->Pkinase+low_complexity->

■ **GCA_900103225.1; Pseudomonas congelans; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_900101695.1; Pseudomonas sp. UC 17F4; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_900106525.1; Lysobacter enzymogenes; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_900107105.1; Geodermatophilus africanus; counts= 1; multicellularity status: TRUE**

- Pkinase+TM->TM->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->?->||<-?<-?||?->Pkinase+low_complexity->

■ **GCA_900107345.1; Pseudomonas syringae; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_900107605.1; Acidovorax soli; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_900105705.1; Streptomyces griseus; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_900104845.1; Paraburkholderia caballeronis; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_900105265.1; Streptomyces sp. 3213.3; counts= 1; multicellularity status: TRUE**

- TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM->?->vWA(canonical)->PP2C->Pkinase+ZnR+beta-rich->

■ **GCA_900107975.1; Paenibacillus sp. UNC499MF; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+Cadherin-like*->

■ **GCA_900108175.1; Actinomadura echinospora; counts= 1; multicellularity status: TRUE**

- GrpE->HSP70->TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM->

■ **GCA_900108335.1; Nonomuraea solani; counts= 1; multicellularity status: TRUE**

- GrpE->HSP70->TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM->

■ **GCA_900109515.1; Paenibacillus sp. OK003; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_900110055.1; Paenibacillus sp. OK076; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_900110775.1; Litorimicrobium taeanense; counts= 1; multicellularity status: NA**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_900111175.1; Actinokineospora terrae; counts= 1; multicellularity status: TRUE**

- CASPASE+TPR_region->?->GAP1-N2+GAP1-M*->

■ **GCA_900111455.1; Geodermatophilus poikilotrophus; counts= 1; multicellularity status: TRUE**

- Pkinase+TM->TM->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->?->||<-?<-?||?->Pkinase+low_complexity->

■ **GCA_900111565.1; Paenibacillus sp. NFR01; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_900112015.1; Azotobacter beijerinckii; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->SLATT->

■ **GCA_900112815.1; Blastococcus sp. DSM 46838; counts= 1; multicellularity status: TRUE**

- Calcineurin+GAPEAD1->GAP2->DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_900114385.1; Geodermatophilus ruber; counts= 1; multicellularity status: TRUE**

- Pkinase+TM->TM->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_900115095.1; Actinomadura madurae; counts= 1; multicellularity status: TRUE**

- GrpE->HSP70->TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM->

■ **GCA_900116845.1; Pseudomonas sp. OV546; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_900130065.1; Sporobacter termitidis DSM 10068; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_900143215.1; Geodermatophilus obscurus; counts= 1; multicellularity status: TRUE**

- Pkinase+TM->TM->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->?->||<-?<-?||?->Pkinase+low_complexity->

■ **GCA_900134035.1; Mycobacteroides abscessus subsp. abscessus; counts= 1; multicellularity status: FALSE**

- HSP70->TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_900083515.1; Cuniculiplasma divulgatum; counts= 1; multicellularity status: TRUE**

- TM+TM+TM+TM+TM+TM+DO-GTPase2.1->GAP1-N2+GAP1-M+GAP1-C*->??->TM_region+DO-GTPase1->

■ **GCA_900143625.1; Nocardiopsis sp. JB363; counts= 1; multicellularity status: TRUE**

- TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->

■ **GCA_900156185.1; Pseudomonas putida; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_900163685.1; Corynebacterium glutamicum; counts= 1; multicellularity status: FALSE**

- TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA_900132645.1; Mycobacteroides abscessus subsp. abscessus; counts= 1; multicellularity status: FALSE**

- GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_900174015.1; Klebsiella pneumoniae; counts= 1; multicellularity status: FALSE**

- GAPEAD1->GAP2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_900177425.1; Paenibacillus uliginis N3/975; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA__900188375.1; Geodermatophilus pulveris; counts= 1; multicellularity status: TRUE**

- Pkinase+TM->TM->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->Pkinase+low_complexity->

■ **GCA__900221015.1; Ornithinimicrobium pekingense; counts= 1; multicellularity status: FALSE**

- Pkinase+TM_region->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+TM+GAP1-C+TM*->

■ **GCA__900215445.1; Serratia sp. JKS296; counts= 1; multicellularity status: FALSE**

- GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->

■ **GCA__000216135.3; Leptospira interrogans; counts= 1; multicellularity status: FALSE**

- GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->PNP_UDP_1+EAD1->

■ **GCA__000306495.2; Leptospira interrogans; counts= 1; multicellularity status: FALSE**

- GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->PNP_UDP_1+EAD1->

■ **GCA__000164015.3; Pseudomonas savastanoi; counts= 1; multicellularity status: FALSE**

- GAP2->DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE(frag)->PSE->CASPASE+EAD1->

■ **GCA__000153105.1; Blastopirellula marina; counts= 1; multicellularity status: TRUE**

- FGS-fold_domain->ZnR+DO-GTPase2.1->GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__000219535.3; Brevibacillus laterosporus; counts= 1; multicellularity status: FALSE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA__000237005.2; Brevibacillus laterosporus; counts= 1; multicellularity status: FALSE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA__000353565.1; Brevibacillus borstelensis; counts= 1; multicellularity status: FALSE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA__000271785.1; Rhizobium leguminosarum; counts= 1; multicellularity status: TRUE**

- Calcineurin+GAPEAD1->GAP2->DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA__002243555.1; Corynebacterium; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA__000177175.2; Streptomyces sp. ACT-1; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__000364245.1; Clostridium sp. ASF502; counts= 1; multicellularity status: NA**

- HSP70->HSP70+vWA(canonical)->DnaJ+DnaJ+ZnR+ZnR+coiled_coil+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->?->?->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TPR_region->

■ **GCA__000738065.1; Bacteroides; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->?->DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA__000350485.1; [Clostridium] termitidis; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA__000368665.1; Acinetobacter junii; counts= 1; multicellularity status: FALSE**

- GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->

■ **GCA__000342125.1; Streptomyces mobaraensis; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__001896005.1; Acinetobacter; counts= 1; multicellularity status: FALSE**

- PNP_UDP_1+EAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->

■ **GCA__000241345.2; Gordonia amarae; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA__000599545.1; Rhodococcus opacus; counts= 1; multicellularity status: TRUE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA__000369745.1; Acinetobacter; counts= 1; multicellularity status: FALSE**

- PNP_UDP_1+EAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->

■ **GCA__000159595.1; Corynebacterium glucuronolyticum; counts= 1; multicellularity status: FALSE**

- GrpE->HSP70->TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->

■ **GCA__000164155.2; Rhodococcus hoagii; counts= 1; multicellularity status: TRUE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA__000158635.1; Corynebacterium matruchotii; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->polar_leader+TM+TM+TM->

■ **GCA__000175375.1; Corynebacterium matruchotii; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->polar_leader+TM+TM+TM->

■ **GCA__000159135.1; Corynebacterium striatum; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->polar_leader+TM+TM+TM->

■ **GCA__001404375.1; Bacteroides; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->?->DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA__000175235.1; Acidovorax delafieldii; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA__000328345.1; Brevibacillus agri; counts= 1; multicellularity status: FALSE**

- Tubulin+coiled_coil+??->PSE->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_000178455.1; Brevibacterium mcbrellneri; counts= 1; multicellularity status: FALSE**

- TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->?->??+DO-GTPase2.2->?->||<-?<-?<-TM+TM+vWA(canonical)+TM<-TM+TM+vWA(canonical)+TM

■ **GCA_000239695.1; Actinomyces graevenitzii; counts= 1; multicellularity status: TRUE**

- GrpE->HSP70->TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->

■ **GCA_000156455.1; Streptomyces filamentosus; counts= 1; multicellularity status: TRUE**

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■ **GCF_000243415.2; Mycolicibacterium tusciae; counts= 1; multicellularity status: FALSE**

- GrpE->HSP70->TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->?->?->?->?->HSP70->vWA(canonical)->

■ **GCA_000315235.1; Paenibacillus popilliae; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_000297155.2; Streptomyces tsukubensis; counts= 1; multicellularity status: TRUE**

- ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->

■ **GCA_000177675.1; Frankia sp. EUN1f; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C+ZnR+DO-GTPase2*->

■ **GCA_000159035.1; Actinomyces urogenitalis; counts= 1; multicellularity status: TRUE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->?->??+DO-GTPase2.2->

■ **GCA_000236965.2; Rhodococcus pyridinivorans; counts= 1; multicellularity status: TRUE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->PSE->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA_000190755.3; Methylobacter tundripaludum; counts= 1; multicellularity status: TRUE**

- PNP_UDP_1+EAD1->GAP2->||<-?||GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->

■ **GCA_000350545.1; Desulfotignum phosphitoxidans; counts= 1; multicellularity status: FALSE**

- ??+PNP_UDP_1+EAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->?->EAD1->

■ **GCA_000307875.1; Bacillus bataviensis; counts= 1; multicellularity status: FALSE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_000164135.1; Mycobacterium; counts= 1; multicellularity status: FALSE**

- TM+DUF4190+TM->TM+DUF4190+TM->polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C(frag)*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA_002966555.1; Pseudomonas syringae group genomosp. 3; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_000241305.2; Gordonia effusa; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA_000241265.2; Gordonia araii; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA_000245715.1; Paenibacillus sp. Aloe-11; counts= 1; multicellularity status: TRUE**

- Tubulin+coiled_coil+??->PSE->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_000282075.1; Brevibacillus sp. BC25; counts= 1; multicellularity status: FALSE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_000282095.2; Rhizobium sp. CF080; counts= 1; multicellularity status: TRUE**

- GAP2->PSE->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->

■ **GCA_000222105.4; Mycobacterium colombiense; counts= 1; multicellularity status: FALSE**

- TM+DUF4190+TM->TM+DUF4190+TM->polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->PSE->PSE->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->TM+DUF4190+TM+PknH_C->TM+DUF4190+TM+PknH_C->?->?->TM+DUF4190+TM+PknH_C->

■ **GCA_000282015.1; Brevibacillus sp. CF112; counts= 1; multicellularity status: FALSE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_000213055.1; Streptomyces sp. Tu6071; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_000174195.1; Roseburia inulinivorans; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_000155695.1; Verrucomicrobiae bacterium DG1235; counts= 1; multicellularity status: NA**

- FHA-like?+ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+TM+GAP1-C*->

■ **GCA_000297435.1; Microcystis sp. T1-4; counts= 1; multicellularity status: TRUE**

- ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM+beta-sandwich+NTF-like->GrpE->

■ **GCA_000344135.1; Gordonia malaquae; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA_000299175.2; Streptomyces; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_000333955.1; Rhodococcus sp. AW25M09; counts= 1; multicellularity status: TRUE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA_000296275.1; Actinomyces massiliensis; counts= 1; multicellularity status: TRUE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->?->??+DO-GTPase2.2->

■ **GCA_000230835.1; Clostridium sp. DL-VIII; counts= 1; multicellularity status: NA**

- Calcineurin+GAPEAD1->GAP2->DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA__000296815.2; Fibrisoma limi; counts= 1; multicellularity status: TRUE**

- GAP2->DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->PNP__UDP__1+EAD1->

■ **GCA__000280725.1; Rhodococcus sp. JVH1; counts= 1; multicellularity status: TRUE**

- polar__leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like__repeats+TM+beta-rich+lc__tail->Tubulin+alpha__helical+??+??->GAP__unknown1+TM+TM+GAP__unknown2->HRDC-like?+Fibronectin-like__repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA__000314635.1; Acinetobacter baumannii; counts= 1; multicellularity status: FALSE**

- GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->

■ **GCA__000238095.2; Peptoanaerobacter stomatis; counts= 1; multicellularity status: FALSE**

- TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->GrpE->HSP70->HSP70+vWA(canonical)->DnaJ+DnaJ+ZnR+ZnR+coiled__coil+Fibronectin-like__repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->?->?->?->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->

■ **GCA__000293035.1; Peptoanaerobacter stomatis; counts= 1; multicellularity status: FALSE**

- HSP70->HSP70+vWA(canonical)->DnaJ+DnaJ+ZnR+ZnR+coiled__coil+Fibronectin-like__repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->?->?->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->

■ **GCA__000204455.2; Paenibacillus sp. HGF5; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled__coil+??->Tubulin+coiled__coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar__tail->Fibronectin-like__repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar__tail+TM+beta-rich*->

■ **GCA__000278725.1; Actinomyces sp. ICM47; counts= 1; multicellularity status: NA**

- GrpE->HSP70->TPR__containing__alpha__helical+Fibronectin-like__repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->??->?->?->?->HSP70->vWA(canonical)->

■ **GCA__000214295.2; Paenibacillus; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled__coil+??->Tubulin+coiled__coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar__tail->Fibronectin-like__repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar__tail+TM+Cadherin-like*->

■ **GCA__000262465.1; Frankia sp. QA3; counts= 1; multicellularity status: TRUE**

- GrpE->HSP70->TPR__containing__alpha__helical+Fibronectin-like__repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->??->HSP70->

■ **GCA__000220835.1; Actinomyces sp. oral taxon 448; counts= 1; multicellularity status: NA**

- polar__leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like__repeats+TM+beta-rich+lc__tail->Tubulin+alpha__helical+??+??->PSE->HRDC-like?+Fibronectin-like__repeats->GAP1-N2+GAP1-M+GAP1-C*->?->??+DO-GTPase2.2->

■ **GCA__000022905.1; Corynebacterium aurimucosum; counts= 1; multicellularity status: FALSE**

- polar__leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like__repeats+TM+beta-rich+lc__tail->Tubulin+alpha__helical+??+??->GAP__unknown1+TM+TM+GAP__unknown2->HRDC-like?+Fibronectin-like__repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->polar__leader+TM+TM+TM->

■ **GCF__000177455.1; Pseudomonas syringae group genomosp. 3; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCF__000179195.1; Streptomyces sp. SA3__actG; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCF__000236805.1; Paenibacillus peoriae; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled__coil+??->Tubulin+coiled__coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar__tail->Fibronectin-like__repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar__tail+TM+beta-rich*->

■ **GCF__000213315.1; Paenibacillus elgii; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->?->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+Cadherin-like*->

■ **GCF_000255655.1; Schlesneria paludicola; counts= 1; multicellularity status: TRUE**

- ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+TM+GAP1-C*->??+TM+??+beta-rich??->GYF+GYF+ZnR+TM+TM+TM->

■ **GCA_002846475.1; Saccharopolyspora spinosa; counts= 1; multicellularity status: TRUE**

- GrpE->HSP70->TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->HSP70->vWA(canonical)->

■ **GCA_000364265.1; Parabacteroides; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->?->DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCF_000011325.1; Corynebacterium glutamicum; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCF_000007805.1; Pseudomonas syringae group genomosp. 3; counts= 1; multicellularity status: FALSE**

- DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_000014165.1; Mycobacterium; counts= 1; multicellularity status: FALSE**

- HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->??+DO-GTPase2.2->

■ **GCA_000014565.1; Rhodococcus jostii; counts= 1; multicellularity status: TRUE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA_000014925.1; Paenarthrobacter aurescens; counts= 1; multicellularity status: FALSE**

- PP2C->?->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+TM+GAP1-C+TM+TM*->

■ **GCA_000016005.1; Mycobacteriaceae; counts= 1; multicellularity status: FALSE**

- HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->??+DO-GTPase2.2->

■ **GCA_000012825.1; Bacteroides vulgatus; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->?->DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_000017645.1; Xanthobacter autotrophicus; counts= 1; multicellularity status: FALSE**

- GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->

■ **GCA_000020045.1; Paraburkholderia phymatum; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_000196495.1; Aliivibrio salmonicida; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->?->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_000009225.1; Pseudomonas fluorescens; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_000024165.1; Candidatus Accumulibacter phosphatis; counts= 1; multicellularity status: FALSE**

- GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA__000146875.2; Paenibacillus polymyxa; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA__000164985.2; Paenibacillus polymyxa; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA__000186345.1; Isosphaera pallida; counts= 1; multicellularity status: TRUE**

- FGS-fold_domain->ZnR+DO-GTPase2.1->GAP1-N2+GAP1-M*->

■ **GCA__000176855.2; Acidovorax avenae; counts= 1; multicellularity status: FALSE**

- GAP2->DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->

■ **GCA__000178835.2; Cellulosilyticum lentocellum; counts= 1; multicellularity status: FALSE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+TM+polar_tail+beta-rich*->

■ **GCA__000218915.1; Paenibacillus mucilaginosus; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+Cadherin-like*->

■ **GCA__000179395.2; Corynebacterium variabile; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA__000177195.2; Streptomyces; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__000176115.2; Streptomyces pratensis; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__000235585.1; Paenibacillus terrae; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA__000250655.1; Paenibacillus mucilaginosus; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->PSE->PSE->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+Cadherin-like*->

■ **GCA__000252445.1; Deinococcus gobiensis; counts= 1; multicellularity status: FALSE**

- GAP2->DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA__000237145.1; Actinoplanes; counts= 1; multicellularity status: TRUE**

- GrpE->HSP70->TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->

■ **GCA__000294515.1; Nocardiopsis alba; counts= 1; multicellularity status: TRUE**

- TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->

■ **GCA__000299395.1; Nitrosopumilus; counts= 1; multicellularity status: FALSE**

- GAP1-N2+GAP1-M+TM+low_complexity*->

■ **GCA__000311765.1; Gluconobacter oxydans; counts= 1; multicellularity status: FALSE**

- CASPASE+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA__000320385.2; Sinorhizobium meliloti; counts= 1; multicellularity status: TRUE**

- GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->

■ **GCA__000359525.1; Streptomyces; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__000364805.1; Streptomyces sp. PAMC 26508; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__000385945.1; Streptomyces fulvissimus; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__000344785.1; Corynebacterium callunae; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__000349325.1; Streptomyces davaonensis; counts= 1; multicellularity status: TRUE**

- TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM->vWA(canonical)->PP2C->Pkinase+ZnR+beta-rich->

■ **GCA__000214355.1; Treponema azotonutricium; counts= 1; multicellularity status: FALSE**

- TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->?->HSP70->HSP70+vWA(canonical)->?->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__000024685.1; Paenibacillus sp. Y412MC10; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->?->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA__000010165.1; Brevibacillus brevis; counts= 1; multicellularity status: FALSE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA__000401235.1; Bacillus nealsonii; counts= 1; multicellularity status: FALSE**

- GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA__000258535.2; Paenibacillus mucilaginosus; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+Cadherin-like*->

■ **GCA__000411315.1; Streptomyces sp. HGB0020; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->vWA(canonical)->PP2C->Pkinase+ZnR+beta-rich->||<-TPR_containing_alpha_helical+Fibronectin-like_repeats

■ **GCA__001184755.1; Bacillales; counts= 1; multicellularity status: NA**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA__000597985.1; Paenibacillus polymyxa; counts= 1; multicellularity status: TRUE**

- Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF_000263875.1; Rhodococcus sp. DK17; counts= 1; multicellularity status: TRUE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA_000287135.2; Vibrio ordalii; counts= 1; multicellularity status: FALSE**

- PNP_UDP_1+EAD1->GAP2->ZnR(fragment)+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->SLATT->

■ **GCF_000269805.1; Actinomyces massiliensis; counts= 1; multicellularity status: TRUE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->?->??+DO-GTPase2.2->

■ **GCA_000296715.2; Brevibacillus brevis; counts= 1; multicellularity status: FALSE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF_000302595.1; Pedobacter arcticus; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_000307675.1; Paenibacillus polymyxa; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF_000341225.1; Nocardiopsis alba; counts= 1; multicellularity status: TRUE**

- TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->

■ **GCF_000341265.1; Nocardiopsis prasina; counts= 1; multicellularity status: TRUE**

- GrpE->HSP70->TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->??->

■ **GCF_000340945.1; Nocardiopsis synnemataformans; counts= 1; multicellularity status: TRUE**

- TPR_containing_alpha_helical+Fibronectin-like_repeats+extended_insert+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+ZnR+ZnR+DO-GTPase2.2->

■ **GCF_000341065.1; Nocardiopsis halotolerans; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCF_000340965.1; Nocardiopsis kunsanensis; counts= 1; multicellularity status: TRUE**

- HSP70->TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->

■ **GCF_000340985.1; Nocardiopsis valliformis; counts= 1; multicellularity status: TRUE**

- GrpE->HSP70->TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->??->HSP70->vWA(canonical)->

■ **GCF_000341085.1; Nocardiopsis ganjiahuensis; counts= 1; multicellularity status: TRUE**

- TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->

■ **GCF_000341005.1; Nocardiopsis alkaliphila; counts= 1; multicellularity status: TRUE**

- TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->

■ **GCF_000341145.1; Nocardiopsis xinjiangensis; counts= 1; multicellularity status: TRUE**

- HSP70->PSE->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->

■ **GCF_000346635.1; Paenibacillus sp. A9; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF_000372385.1; Corynebacterium ciconiae; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->polar_leader+TM+TM+TM->

■ **GCF_000372445.1; Corynebacterium ulceribovis; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->?->TM+TM+TM->

■ **GCF_000375725.1; Streptomyces; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_001445835.1; Streptomyces vitaminophilus; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->vWA(canonical)->PSE->Pkinase+ZnR+beta-rich->||<-TPR_containing_alpha_helical+Fibronectin-like_repeats

■ **GCA_003688775.1; Streptomyces sp. LaPpAH-202; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCF_000373645.1; Streptomyces sp. ATexAB-D23; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCF_000374145.1; Neomegalonema perideroedes; counts= 1; multicellularity status: TRUE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCF_000374305.1; Actinomadura flavalba; counts= 1; multicellularity status: TRUE**

- GrpE->HSP70->TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM->

■ **GCA_002706795.1; Brevibacillus laterosporus; counts= 1; multicellularity status: FALSE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF_000374445.1; Actinokineospora enzanensis; counts= 1; multicellularity status: TRUE**

- GrpE->HSP70->TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->HSP70->vWA(canonical)->

■ **GCF_000374845.1; Paenibacillus terrigena; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF_000377505.1; Paenibacillus massiliensis; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF_000377545.1; Streptomyces sp. CNY228; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCF_000378145.1; Saccharibacillus kuerlensis; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF__000367365.1; Streptomyces prunicolor; counts= 1; multicellularity status: TRUE**

- GrpE->HSP70->TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+Jelly_roll+beta-sandwich->||<-STAND_NTPase+TM+TM+TM+TM+TM+TM+TM

■ **GCF__000376565.1; Streptomyces hokutonensis; counts= 1; multicellularity status: TRUE**

- TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM->vWA(canonical)->PP2C->Pkinase+ZnR+beta-rich->

■ **GCF__000283315.1; Paenibacillus sp. OSY-SE; counts= 1; multicellularity status: TRUE**

- TM+TM+TM+vWA+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C+polar_tail*->

■ **GCA__000317305.3; Mycobacteriaceae; counts= 1; multicellularity status: FALSE**

- TM+DUF4190+TM->TM+DUF4190+TM->polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->PSE->TM+DUF4190+TM+PknH_C->TM+DUF4190+TM+PknH_C->

■ **GCA__000473765.1; Rhodonellum; counts= 1; multicellularity status: FALSE**

- GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+PNP_UDP_1*->

■ **GCF__000381685.1; Nocardiopsis sp. CNS-639; counts= 1; multicellularity status: TRUE**

- TPR_containing_alpha_helical+Fibronectin-like_repeats+extended_insert+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->

■ **GCF__000381885.1; Actinomadura atramentaria; counts= 1; multicellularity status: TRUE**

- GrpE->HSP70->TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM->

■ **GCF__000381905.1; Paenibacillus fonticola; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA__900454525.1; Paenibacillus polymyxa; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF__000374185.1; Paenibacillus sp. HW567; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF__000383615.1; Streptomyces canus; counts= 1; multicellularity status: TRUE**

- GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->

■ **GCA__000767055.1; Corynebacterium doosanense; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->TM+TM+TM->

■ **GCA__000418365.1; Corynebacterium terpenotabidum; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA__000018005.1; Frankia sp. EAN1pec; counts= 1; multicellularity status: TRUE**

- HSP70->TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->

■ **GCF__000255705.1; Zavarzinella formosa; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCF_000379525.1; Lamprocystis purpurea; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCF_000379645.1; Actinoplanes globisporus; counts= 1; multicellularity status: TRUE**

- HSP70->||<-?||GrpE->HSP70->TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->

■ **GCF_000377165.1; Streptomyces sp. CNY243; counts= 1; multicellularity status: TRUE**

- PP2C->Pkinase->?->?->?->HSP70_domain_2+low_complexity+domain_betaX->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->

■ **GCF_000378385.1; Paenibacillus daejeonensis; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->?->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_002234385.1; Amycolatopsis alba; counts= 1; multicellularity status: TRUE**

- GrpE->HSP70->TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->?->HSP70->vWA(canonical)->||<-?<-?<-HSP70

■ **GCF_000377105.1; Streptomyces sp. CNQ766; counts= 1; multicellularity status: TRUE**

- PP2C->Pkinase->?->?->?->HSP70_domain_2+low_complexity+domain_betaX->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->

■ **GCF_000377125.1; Streptomyces sp. CNS335; counts= 1; multicellularity status: TRUE**

- PP2C->Pkinase->?->?->?->HSP70_domain_2+low_complexity+domain_betaX->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->

■ **GCA_000442645.1; Corynebacterium maris; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->TM+TM+TM->

■ **GCA_000444875.1; Streptomyces collinus; counts= 1; multicellularity status: TRUE**

- *

■ **GCA_000455705.1; Pseudomonas aeruginosa; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_000465875.3; Alcaligenes sp. EGD-AK7; counts= 1; multicellularity status: FALSE**

- GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->

■ **GCA_001039615.1; Crocosphaera watsonii; counts= 1; multicellularity status: TRUE**

- DnaJ+DnaJ+ZnR+ZnR+coiled_coil+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2(frag)->?->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM+beta-sandwich+NTF-like->GrpE->HSP70->?->?->HSP70+vWA(canonical)->

■ **GCA_000472325.2; Brevibacillus laterosporus; counts= 1; multicellularity status: FALSE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF_000412185.1; Euryhalocaulis caribicus; counts= 1; multicellularity status: FALSE**

- GAP2->DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+DNA-glycosylase+EAD1*->CASPASE+EAD1->

■ **GCA_000157895.2; Mycobacterium kansasii; counts= 1; multicellularity status: FALSE**

- TM+DUF4190+TM->TM+DUF4190+TM->polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA__000495755.1; Streptomyces sp. PVA 94-07; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__000495635.1; Streptomyces sp. GBA 94-10; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__000497425.1; Streptomyces niveus; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->vWA(canonical)->PP2C->Pkinase+ZnR+beta-rich->||<-TPR_containing_alpha_helical+Fibronectin-like_repeats

■ **GCA__000503775.1; Brevibacillus panacihumi; counts= 1; multicellularity status: FALSE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA__000502415.1; Mesorhizobium sp. LNHC229A00; counts= 1; multicellularity status: TRUE**

- GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA__000502395.1; Mesorhizobium sp. LNHC220B00; counts= 1; multicellularity status: TRUE**

- Calcineurin+GAPEAD1->GAP2->DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA__000502375.1; Mesorhizobium sp. L48C026A00; counts= 1; multicellularity status: TRUE**

- Calcineurin+GAPEAD1->GAP2->ZnR(fragment)+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA__000502895.1; Mesorhizobium sp. L2C085B000; counts= 1; multicellularity status: TRUE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA__000507785.1; Ruminococcus lactaris; counts= 1; multicellularity status: TRUE**

- ??->??+HTH?+GrpE->HSP70->DnaJ+DnaJ+ZnR+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->?->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->

■ **GCA__000509425.1; Paenibacillus sp. JCM 10914; counts= 1; multicellularity status: TRUE**

- Tubulin+coiled_coil+??->PSE->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA__000507205.2; Paenibacillus polymyxa; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA__000508325.2; Bacillus vireti; counts= 1; multicellularity status: NA**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF__000344825.1; Salmonella enterica; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->DO-GTPase2.1(fragment)->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA__000156695.2; Streptomyces filamentosus; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCF__000440555.1; Streptococcus suis; counts= 1; multicellularity status: FALSE**

- HSP70->?->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->

■ **GCF_000470535.1; Streptomyces sp. AW19M42; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_000499205.1; Paenibacillus; counts= 1; multicellularity status: TRUE**

- TM+TM+TM+vWA+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C+polar_tail*->

■ **GCF_000452545.1; Pseudomonas syringae; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCF_000612185.1; Brevibacillus borstelensis; counts= 1; multicellularity status: FALSE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_002074835.1; Leptospira interrogans; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_000612505.1; Paenibacillus sabinae; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_000582515.1; Yersinia similis; counts= 1; multicellularity status: FALSE**

- GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->

■ **GCF_000490295.1; Vibrio parahaemolyticus; counts= 1; multicellularity status: FALSE**

- GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->

■ **GCF_000520695.1; Paenibacillus massiliensis; counts= 1; multicellularity status: TRUE**

- Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF_000520795.1; Paenibacillus polymyxa; counts= 1; multicellularity status: TRUE**

- Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C+polar_tail*->

■ **GCF_000520815.1; Paenibacillus sp. 1-49; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF_000520735.1; Paenibacillus forsythiae; counts= 1; multicellularity status: TRUE**

- TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF_000520755.1; Paenibacillus sp. 1-18; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF_000520775.1; Paenibacillus polymyxa; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF_000526555.1; Bacteroides sp. 14(A); counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->?->DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCF_000612125.1; Brevibacillus agri; counts= 1; multicellularity status: FALSE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF_000612225.1; Paenibacillus chimensis; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->?->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+Cadherin-like*->

■ **GCF_000425065.1; Actinomadura rifamycini; counts= 1; multicellularity status: TRUE**

- GrpE->HSP70->TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM->

■ **GCF_000429225.1; Actinomyces dentalis; counts= 1; multicellularity status: TRUE**

- GrpE->HSP70->??+Fibronectin->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->

■ **GCF_000518265.1; Actinomadura oligospora; counts= 1; multicellularity status: TRUE**

- GrpE->HSP70->TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->

■ **GCF_000482865.1; Actinokineospora inagensis; counts= 1; multicellularity status: TRUE**

- vWA(canonical)+beta-rich+low_complexity->?->?->Tubulin+alpha_helical+??+??->??+TM+TM+TM+TM+??->Pkinase+TM->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C+TM+beta-rich*->

■ **GCF_000470975.1; Bacillus sp. NSP2.1; counts= 1; multicellularity status: NA**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF_000686805.1; Bacillus sp. UNC41MFS5; counts= 1; multicellularity status: NA**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF_000515315.1; Asinibacterium sp. OR53; counts= 1; multicellularity status: FALSE**

- GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->PNP_UDP_1+EAD1->

■ **GCF_000428805.1; Corynebacterium freiburgense; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCF_000427865.1; Corynebacterium sputi; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->||<-?||TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCF_000428945.1; Hamadaea tsunoensis; counts= 1; multicellularity status: TRUE**

- TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->

■ **GCA_900177315.1; Pseudomonas; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCF_000514995.1; Streptomyces sp. CNT371; counts= 1; multicellularity status: TRUE**

- PP2C->Pkinase->?->?->?->HSP70_domain_2+low_complexity+domain_betaX->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->

■ **GCF_000514715.1; Streptomyces sp. CNH099; counts= 1; multicellularity status: TRUE**

- PP2C->Pkinase->?->?->?->HSP70_domain_2+low_complexity+domain_betaX->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->

■ **GCF_000424765.1; Streptomyces sp. CNT318; counts= 1; multicellularity status: TRUE**

- PP2C->Pkinase->?->?->?->HSP70_domain_2+low_complexity+domain_betaX->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->

■ **GCF_000424805.1; Streptomyces sp. CNQ865; counts= 1; multicellularity status: TRUE**

- PP2C->Pkinase->?->?->?->HSP70_domain_2+low_complexity+domain_betaX->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->

■ **GCF_000621585.1; [Eubacterium] cellulosolvens; counts= 1; multicellularity status: FALSE**

- TM+vWA(canonical)+YtKA-like+IG-like+TM+??->Tubulin+coiled_coil+??->?->?->ZnR+insert+ZnR+DO-GTPase2.2+ZnR->GAP1-N2+GAP1-M+low_complexity+TM+TM*->

■ **GCA_004001485.1; Sinorhizobium meliloti; counts= 1; multicellularity status: TRUE**

- GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->

■ **GCF_000686945.1; Selenomonas sp. AE3005; counts= 1; multicellularity status: FALSE**

- TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->GrpE->HSP70->HSP70+vWA(canonical)->?->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_000807315.1; Bradyrhizobium japonicum; counts= 1; multicellularity status: TRUE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCF_000647875.1; Streptomyces sp. SolWspMP-sol2th; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_900091745.1; Streptomyces; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCF_000621765.1; Ruminococcaceae bacterium AB4001; counts= 1; multicellularity status: NA**

- TM+vWA(canonical)+YtKA-like+IG-like+TM+??->Tubulin+coiled_coil+??->?->?->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C*->?->?->?->Tubulin+coiled_coil+??->

■ **GCA_900116035.1; Paenibacillus; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF_000425125.1; Paenibacillus taiwanensis; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF_000620645.1; Nocardioides sp. URHA0032; counts= 1; multicellularity status: TRUE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->?->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->?->??+DO-GTPase2.2->

■ **GCF_000423605.1; Saccharospirillum impatiens; counts= 1; multicellularity status: FALSE**

- DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_002591785.1; Budvicia aquatica; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCF_000426065.1; Mycobacterium sp. URHD0025; counts= 1; multicellularity status: FALSE**

- HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->??+DO-GTPase2.2->

■ **GCF_000455145.1; Mycobacterium sp. UM_WWY; counts= 1; multicellularity status: FALSE**

- TM+DUF4190+TM->polar_leader+TM+TM+TM->PSE->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->TM+DUF4190+TM+PknH_C->TM+DUF4190+TM+PknH_C->TM+DUF4190+TM+PknH_C->

■ **GCA_003941845.1; Paenibacillus polymyxa; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF_000716815.1; Streptomyces; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCF_000718255.1; Spirillospora albida; counts= 1; multicellularity status: TRUE**

- GrpE->HSP70->TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM->

■ **GCA_003073355.1; Streptomyces scopuliridis; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCF_000717925.1; Streptomyces sp. NRRL S-241; counts= 1; multicellularity status: TRUE**

- TPR_containing_alpha_helical+Fibronectin-like_repeats->PSE->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM->vWA(canonical)->PP2C->Pkinase+ZnR+beta-rich->

■ **GCF_000720535.1; Streptomyces; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCF_000720395.1; Streptomyces flavovirens; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCF_000721105.1; Streptomyces cellulosae; counts= 1; multicellularity status: TRUE**

- GrpE->HSP70->TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+Jelly_roll+beta-sandwich->||<-STAND_NTPase+TM+TM+TM+TM+TM+TM+TM

■ **GCF_000720325.1; Streptomyces sp. NRRL B-1347; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->vWA(canonical)->PP2C->Pkinase+ZnR+beta-rich->

■ **GCF_000719495.1; Streptomyces griseus; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_003989035.1; Streptomyces griseus; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCF_000718935.1; Streptomyces sp. NRRL S-237; counts= 1; multicellularity status: TRUE**

- TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->PSE->vWA(canonical)->PP2C->Pkinase+ZnR+beta-rich->

■ **GCF_000718955.1; Streptomyces sp. NRRL S-575; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->||<-PSE||vWA(canonical)->PP2C->Pkinase+ZnR+beta-rich->

■ **GCF_000719435.1; Streptomyces griseus; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

- **GCF_000717945.1; Streptomyces sp. NRRL S-920; counts= 1; multicellularity status: TRUE**
  - GAP1-N2+GAP1-M+GAP1-C*->vWA(canonical)->PP2C->Pkinase+ZnR+beta-rich->||<-TPR_containing_alpha_helical+Fibronectin-like_repeats
- **GCF_000721685.1; Streptomyces mediolani; counts= 1; multicellularity status: TRUE**
  - GAP1-N2+GAP1-M+GAP1-C*->
- **GCF_000721305.1; Streptomyces sp. NRRL S-1868; counts= 1; multicellularity status: TRUE**
  - GAP1-N2+GAP1-M+GAP1-C*->PSE->?->||<-TPR_containing_alpha_helical+Fibronectin-like_repeats
- **GCF_000720405.1; Streptomyces sp. NRRL B-24051; counts= 1; multicellularity status: TRUE**
  - GAP1-N2+GAP1-M+GAP1-C*->
- **GCF_000721445.1; Streptomyces sp. NRRL F-5053; counts= 1; multicellularity status: TRUE**
  - GAP1-N2+GAP1-M+GAP1-C*->PSE->?->||<-TPR_containing_alpha_helical+Fibronectin-like_repeats
- **GCF_000721265.1; Streptomyces sp. NRRL F-5126; counts= 1; multicellularity status: TRUE**
  - GAP1-N2+GAP1-M+GAP1-C*->
- **GCF_000720795.1; Streptomyces sp. NRRL S-515; counts= 1; multicellularity status: TRUE**
  - GAP1-N2+GAP1-M+GAP1-C*->||<-PSE||vWA(canonical)->PP2C->Pkinase+ZnR+beta-rich->
- **GCF_000721715.1; Streptomyces sp. NRRL B-24720; counts= 1; multicellularity status: TRUE**
  - GAP1-N2+GAP1-M+GAP1-C*->
- **GCF_000719575.1; Streptomyces sp. NRRL S-1824; counts= 1; multicellularity status: TRUE**
  - GAP1-N2+GAP1-M+GAP1-C*->
- **GCF_000719475.1; Streptomyces sp. NRRL F-5630; counts= 1; multicellularity status: TRUE**
  - GAP1-N2+GAP1-M+GAP1-C*->
- **GCF_000721935.1; Streptomyces sp. NRRL WC-3549; counts= 1; multicellularity status: TRUE**
  - GAP1-N2+GAP1-M+GAP1-C*->
- **GCA_001294345.1; Streptomyces; counts= 1; multicellularity status: TRUE**
  - GAP1-N2+GAP1-M+GAP1-C*->
- **GCF_000725635.1; Streptomyces sp. NRRL B-3253; counts= 1; multicellularity status: TRUE**
  - GAP1-N2+GAP1-M+GAP1-C*->
- **GCF_000725655.1; Streptomyces; counts= 1; multicellularity status: TRUE**
  - TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->PSE->vWA(canonical)->PP2C->Pkinase+ZnR+beta-rich->
- **GCF_000735775.1; Paenibacillus polymyxa; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF__000725465.1; Streptomyces bicolor; counts= 1; multicellularity status: TRUE**

- TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM->vWA(canonical)->PP2C->Pkinase+ZnR+beta-rich->

■ **GCF__001076885.1; Bacillus; counts= 1; multicellularity status: NA**

- GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA__000738785.1; Brevibacillus borstelensis; counts= 1; multicellularity status: FALSE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA__003096175.1; Clostridium drakei; counts= 1; multicellularity status: FALSE**

- TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M*->

■ **GCF__000760995.1; Rhodococcus fascians; counts= 1; multicellularity status: TRUE**

- GAP2->?->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->PNP_UDP_1+EAD1->PNP_UDP_1->

■ **GCF__000761035.1; Rhodococcus fascians; counts= 1; multicellularity status: TRUE**

- GAP2->?->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->PNP_UDP_1+EAD1->PNP_UDP_1->

■ **GCA__000261345.2; Streptomyces globisporus; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__000743295.1; Streptomyces sp. JS01; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCF__000167995.1; Yersinia mollaretii; counts= 1; multicellularity status: FALSE**

- DO-GTPase2.1(fragment)->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCF__000278565.1; Pseudomonas sp. Ag1; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCF__000720725.1; Streptomyces rimosus; counts= 1; multicellularity status: TRUE**

- TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM->vWA(canonical)->PP2C->Pkinase+ZnR+beta-rich->

■ **GCA__002356035.1; Nocardia seriolae; counts= 1; multicellularity status: TRUE**

- Pkinase+TM->ZnR+DO-GTPase2.1->GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__000702925.2; Methylomonas sp. LW13; counts= 1; multicellularity status: FALSE**

- PNP_UDP_1+EAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->

■ **GCF__000716685.1; Streptomyces virginiae; counts= 1; multicellularity status: TRUE**

- TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->PSE->vWA(canonical)->PP2C->Pkinase+ZnR+beta-rich->

■ **GCF__000717375.1; Streptomyces griseus; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCF_000716605.1; Streptomyces sp. NRRL F-525; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCF_000717025.1; Streptomyces atroolivaceus; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCF_000716805.1; Streptomyces yerevanensis; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->vWA(canonical)->PP2C->Pkinase+ZnR+beta-rich->||<-TPR_containing_alpha_helical+Fibronectin-like_repeats

■ **GCF_000716715.1; Dactylosporangium aurantiacum; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->||<-HSP70_domain_1

■ **GCF_000716595.1; Saccharothrix sp. NRRL B-16314; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCF_000698985.1; Bordetella bronchiseptica; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCF_000797385.1; Streptomyces sp. CNQ431; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_000758745.1; Actinomyces urogenitalis; counts= 1; multicellularity status: TRUE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->?->??+DO-GTPase2.2->

■ **GCA_000522425.1; Candidatus Entotheonella palauensis; counts= 1; multicellularity status: TRUE**

- HSP70+vWA(canonical)->DnaJ+DnaJ+ZnR+ZnR+coiled_coil+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->

■ **GCF_000702965.1; Butyrivibrio sp. AE2032; counts= 1; multicellularity status: FALSE**

- TM+vWA(canonical)+YtKA-like+IG-like+TM+??->Tubulin+coiled_coil+??->?->?->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C*->?->?->?->Tubulin+coiled_coil+??->Tubulin+coiled_coil+??->

■ **GCF_000741785.1; Bifidobacterium stellenboschense; counts= 1; multicellularity status: FALSE**

- TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->GrpE->HSP70->HSP70+vWA(canonical)->DnaJ+DnaJ+ZnR+ZnR+coiled_coil+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_000767255.1; Corynebacterium auriscanis; counts= 1; multicellularity status: FALSE**

- Tubulin+alpha_helical+??+??->?->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->?->?->??+DO-GTPase2.2->

■ **GCA_000601455.1; Fervidicella metallireducens; counts= 1; multicellularity status: FALSE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_000576325.1; Bacillus sp. JCM 19045; counts= 1; multicellularity status: NA**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_000576345.1; Bacillus sp. JCM 19046; counts= 1; multicellularity status: NA**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__000737695.1; Flavobacterium hydatis; counts= 1; multicellularity status: FALSE**

- GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->??+EAD1->EAD1+Trypsin->

■ **GCF__000744785.1; Kitasatospora azatica; counts= 1; multicellularity status: TRUE**

- TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM->vWA(canonical)->PP2C->Pkinase+ZnR+beta-rich->

■ **GCA__000761485.1; Modestobacter caceresii; counts= 1; multicellularity status: TRUE**

- Pkinase+TM->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__000723385.1; Mycolicibacterium farcinogenes; counts= 1; multicellularity status: FALSE**

- HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->??+DO-GTPase2.2->

■ **GCA__000612825.1; Mycolicibacterium mageritense; counts= 1; multicellularity status: FALSE**

- TM+DUF4190+TM->polar_leader+TM+TM+TM->PSE->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->TM+DUF4190+TM+PknH_C->TM+DUF4190+TM+PknH_C->

■ **GCA__000612885.1; Mycolicibacterium; counts= 1; multicellularity status: FALSE**

- HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->??+DO-GTPase2.2->

■ **GCA__000583715.2; Nocardia seriolae; counts= 1; multicellularity status: TRUE**

- Pkinase+TM->ZnR+DO-GTPase2.1->GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__000517945.1; Paenibacillus sp. FSL H8-457; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA__000517845.1; Paenibacillus; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA__000722545.1; Paenibacillus tyrfis; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->?->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+Cadherin-like*->

■ **GCA__000695255.1; Photobacterium galatheae; counts= 1; multicellularity status: FALSE**

- PNP_UDP_1+EAD1->GAP2->ZnR(fragment)+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->SLATT->

■ **GCA__003150695.1; Rhizobium; counts= 1; multicellularity status: TRUE**

- Calcineurin+GAPEAD1->GAP2->DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+??*->

■ **GCF__000585395.1; Saccharibacillus sacchari; counts= 1; multicellularity status: TRUE**

- Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C+polar_tail*->

■ **GCF__000716535.1; Streptomyces; counts= 1; multicellularity status: TRUE**

- TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->PSE->vWA(canonical)->PP2C->Pkinase+ZnR+beta-rich->

■ **GCF__000414115.1; Streptomyces aurantiacus; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->vWA(canonical)->

■ **GCA_002803845.1; Streptomyces lavendulae; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCF_000745675.1; Streptomyces atratus; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCF_000745715.1; Streptomyces mirabilis; counts= 1; multicellularity status: TRUE**

- TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM->vWA(canonical)->PP2C->Pkinase+ZnR+beta-rich->

■ **GCF_000746395.1; Streptomyces mirabilis; counts= 1; multicellularity status: TRUE**

- TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM->vWA(canonical)->PP2C->Pkinase+ZnR+beta-rich->

■ **GCA_004217635.1; Streptomyces sp. CNQ-525; counts= 1; multicellularity status: TRUE**

- PP2C->Pkinase->?->?->?->HSP70_domain_2+low_complexity+domain_betaX->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->

■ **GCF_000721595.1; Streptomyces sp. NRRL S-325; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCF_000721455.1; Streptomyces sp. NRRL F-6628; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_000698495.1; Streptomyces sp. NTK 937; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCF_000717895.1; Streptomyces sp. NRRL WC-3744; counts= 1; multicellularity status: TRUE**

- TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->PSE->vWA(canonical)->PP2C->Pkinase+ZnR+beta-rich->

■ **GCF_900091485.1; Streptomyces; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_000788395.1; Pseudoalteromonas piratica; counts= 1; multicellularity status: FALSE**

- PNP_UDP_1+EAD1->GAP2->ZnR(fragment)+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->SLATT->

■ **GCA_000747525.1; Sphingobacterium sp. ML3W; counts= 1; multicellularity status: FALSE**

- GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->?->??+EAD1->EAD1+Trypsin->

■ **GCA_000773415.1; Burkholderia pseudomallei; counts= 1; multicellularity status: FALSE**

- GAP2->DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->

■ **GCA_000812465.1; Cupriavidus sp. IDO; counts= 1; multicellularity status: FALSE**

- GAP2->DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->

■ **GCF_000813415.1; Plesiomonas shigelloides; counts= 1; multicellularity status: FALSE**

- PNP_UDP_1+EAD1->GAP2->ZnR(fragment)+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->SLATT->

■ **GCA_000714835.1; Paenibacillus polymyxa; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_000805375.1; Mycolicibacterium setense; counts= 1; multicellularity status: FALSE**

- HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->??+DO-GTPase2.2->

■ **GCA_000805385.1; Mycolicibacterium setense; counts= 1; multicellularity status: FALSE**

- HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->??+DO-GTPase2.2->

■ **GCA_000749915.1; Pectobacterium polaris; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_000746665.1; Vibrio vulnificus; counts= 1; multicellularity status: FALSE**

- PNP_UDP_1+EAD1->GAP2->ZnR(fragment)+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->SLATT->

■ **GCA_000817905.1; Pseudomonas fluorescens; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCF_000180155.1; Actinomyces oris; counts= 1; multicellularity status: FALSE**

- Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->?->??+DO-GTPase2.2->

■ **GCA_000758625.1; Paenibacillus sp. FSL R7-0273; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->||<-?||TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF_000364445.1; Methylobacterium mesophilicum; counts= 1; multicellularity status: TRUE**

- CASPASE+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_002762195.1; Acetobacteraceae; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_000819665.1; Paenibacillus polymyxa; counts= 1; multicellularity status: TRUE**

- Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C+polar_tail*->

■ **GCF_000820765.1; Candidatus Soleaferrea massiliensis; counts= 1; multicellularity status: FALSE**

- ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+TM+GAP1-C+TM*->

■ **GCF_900143195.1; Butyricicoccus pullicaecorum; counts= 1; multicellularity status: FALSE**

- GAP1-N2+GAP1-M+TM+GAP1-C*->||<-Pkinase

■ **GCF_000173655.1; Corynebacterium amycolatum; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCF_000305495.1; Bacillus psychrosaccharolyticus; counts= 1; multicellularity status: FALSE**

- TM+vWA(canonical)+YtKA-like+TM+??->PSE->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF_000271305.1; Hydrocarboniphaga effusa; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCF_000308695.1; Nocardia takedensis; counts= 1; multicellularity status: TRUE**

- GrpE->HSP70->TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->?->HSP70->vWA(canonical)->

■ **GCF_000308815.1; Nocardia concava; counts= 1; multicellularity status: TRUE**

- Pkinase+TM->ZnR+DO-GTPase2.1->GAP1-N2+GAP1-M+GAP1-C*->

■ **GCF_000308655.1; Nocardia niigatensis; counts= 1; multicellularity status: TRUE**

- Pkinase+TM->ZnR+DO-GTPase2.1->GAP1-N2+GAP1-M+GAP1-C*->

■ **GCF_000025345.1; Geodermatophilus obscurus; counts= 1; multicellularity status: TRUE**

- Pkinase+TM->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->||<-?<-?||?->Pkinase+low_complexity->

■ **GCF_000190575.1; Bacteroides salanitronis; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->?->DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_003028645.1; Paraburkholderia caribensis; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCF_000818175.1; Streptomyces sp. AcH 505; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_004117095.1; Paenibacillus chitinolyticus; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+Cadherin-like*->

■ **GCF_000710955.1; Nocardiopsis alba; counts= 1; multicellularity status: TRUE**

- TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->

■ **GCA_000759795.1; Pseudescherichia vulneris; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCF_000720295.1; Streptomyces sp. NRRL WC-3725; counts= 1; multicellularity status: TRUE**

- TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->PSE->vWA(canonical)->PP2C->Pkinase+ZnR+beta-rich->

■ **GCF_000721515.1; Streptomyces sp. NRRL F-5193; counts= 1; multicellularity status: TRUE**

- TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM->?->vWA(canonical)->PP2C->Pkinase+ZnR+beta-rich->

■ **GCA_000733295.1; Archangium violaceum; counts= 1; multicellularity status: TRUE**

- GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCF_000092385.1; Streptomyces bingchenggensis; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__000785985.1; Actinoplanes utahensis; counts= 1; multicellularity status: TRUE**

- DO-GTPase1->GAP1-N2+GAP1-M+TM+GAP1-C*->?->?->TM+vWA(canonical)+TM+low_complexity->CASPASE+low_complexity->TPR_region+CASPASE->

■ **GCF__000410615.1; Novosphingobium sp. B-7; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA__001643285.1; Aeromonas salmonicida; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCF__000613125.1; Bacillus sp. EB01; counts= 1; multicellularity status: NA**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA__000935305.1; Pseudomonas oryzihabitans; counts= 1; multicellularity status: FALSE**

- GAP2->DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->

■ **GCA__000661085.1; Mycobacterium colombiense; counts= 1; multicellularity status: FALSE**

- TM+DUF4190+TM->TM+DUF4190+TM->polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->TM+DUF4190+TM+PknH_C->TM+DUF4190+TM+PknH_C->TM+DUF4190+TM+PknH_C->TM+DUF4190+TM+PknH_C->TM+DUF4190+TM+PknH_C->

■ **GCF__000455325.1; Mycolicibacterium septicum; counts= 1; multicellularity status: FALSE**

- HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->??+DO-GTPase2.2->

■ **GCA__000943545.1; Paenibacillus terrae; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA__000943535.1; Paenibacillus polymyxa; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA__000955955.1; Lechevalieria aerocolonigenes; counts= 1; multicellularity status: TRUE**

- vWA(canonical)+beta-rich+low_complexity->Tubulin+alpha_helical+??+??->??+TM+TM+TM+TM+??->Pkinase+TM->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+SLATT+SLATT*->

■ **GCF__000818335.1; Vibrio campbellii; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCF__000818715.1; Vibrio jasicida; counts= 1; multicellularity status: FALSE**

- ZnR(fragment)+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->SLATT->

■ **GCF__000818475.1; Vibrio hyugaensis; counts= 1; multicellularity status: FALSE**

- PNP_UDP_1+EAD1->GAP2->ZnR(fragment)+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->SLATT->

■ **GCA__000960765.1; Desulfosporosinus sp. I2; counts= 1; multicellularity status: FALSE**

- GAP1-N1+GAP1-M+GAP1-C*->

■ **GCF__000959835.1; Vibrio vulnificus; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCF_000962825.1; Actinoplanes rectilineatus; counts= 1; multicellularity status: TRUE**

- TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_000938735.2; Sphingobacterium sp. PM2-P1-29; counts= 1; multicellularity status: FALSE**

- DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->??+EAD1->EAD1+Trypsin->

■ **GCA_000967665.1; Marinomonas sp. S3726; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_000968575.1; Pseudomonas kilonensis; counts= 1; multicellularity status: FALSE**

- GAP2->DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->

■ **GCA_000968555.1; Sinorhizobium meliloti; counts= 1; multicellularity status: TRUE**

- Calcineurin+GAPEAD1->GAP2->ZnR(fragment)+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_002871755.1; Corynebacterium kroppenstedtii; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->?->?->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCF_000971855.1; Corynebacterium kroppenstedtii; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCF_000971965.1; Paenibacillus wulumuqiensis; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF_000971985.1; Paenibacillus dauci; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_000972385.1; Streptomyces sp. WM6386; counts= 1; multicellularity status: TRUE**

- TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM->vWA(canonical)->PP2C->Pkinase+ZnR+beta-rich->

■ **GCA_000980905.1; Pseudomonas syringae group genomosp. 3; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_000988105.2; Leptospira santarosai; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCF_000988945.1; Streptomyces europaeiscabiei; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->vWA(canonical)->PP2C->Pkinase+ZnR+beta-rich->

■ **GCA_001981455.1; Leptospira santarosai; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_001012795.1; Mycolicibacterium; counts= 1; multicellularity status: FALSE**

- HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->??+DO-GTPase2.2->

■ **GCA__006540185.1; Brevibacillus formosus; counts= 1; multicellularity status: FALSE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA__001013325.1; Vibrio vulnificus; counts= 1; multicellularity status: FALSE**

- PNP_UDP_1+EAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->SLATT->

■ **GCA__001014595.1; Streptomyces sp. KE1; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCF__000800535.1; Streptomyces sp. M10; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCF__000798835.1; Shewanella sp. ZOR0012; counts= 1; multicellularity status: FALSE**

- GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->

■ **GCA__001029205.1; Paenibacillus sp. VT-400; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF__001029525.1; Nocardiopsis sp. RV163; counts= 1; multicellularity status: TRUE**

- TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__001029855.1; Bacillus circulans; counts= 1; multicellularity status: FALSE**

- GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA__001039275.2; Brevibacillus brevis; counts= 1; multicellularity status: FALSE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA__000978965.1; Methanosarcina mazei; counts= 1; multicellularity status: TRUE**

- TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->GrpE->HSP70->HSP70+vWA(canonical)->DnaJ+DnaJ+ZnR+ZnR+coiled_coil+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__000979335.1; Methanosarcina mazei; counts= 1; multicellularity status: TRUE**

- TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->GrpE->HSP70->HSP70+vWA(canonical)->DnaJ+DnaJ+ZnR+ZnR+coiled_coil+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__001043915.1; Methylobacterium aquaticum; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+TM+GAP1-C*->

■ **GCA__001045445.1; Chryseobacterium sp. BLS98; counts= 1; multicellularity status: FALSE**

- GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->??+EAD1->EAD1+Trypsin->

■ **GCF__001047325.1; Streptomyces viridochromogenes; counts= 1; multicellularity status: TRUE**

- GAP2->DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->

■ **GCF__001054325.1; Corynebacterium vitaeruminis; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCF_001059615.1; Corynebacterium aurimucosum; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->polar_leader+TM+TM+TM->

■ **GCF_001152565.1; Yersinia pekkanenii; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCF_001187435.1; Streptomyces caatingaensis; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCF_006540225.1; Brevibacillus reuszeri; counts= 1; multicellularity status: FALSE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_001187505.1; Mycolicibacterium goodii; counts= 1; multicellularity status: FALSE**

- HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->??+DO-GTPase2.2->

■ **GCF_000455265.1; Paenibacillus antibioticophila; counts= 1; multicellularity status: TRUE**

- Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C+polar_tail*->

■ **GCA_000698945.1; Streptomyces wadayamensis; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCF_000739635.1; Verrucomicrobium sp. BvORR034; counts= 1; multicellularity status: FALSE**

- GrpE->HSP70->||<-?||HSP70+vWA(canonical)->DnaJ+DnaJ+ZnR+ZnR+coiled_coil+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->?->TM+TM+ZnR+ZnR+DO-GTPase2.2+TM+PDZ+PDZ->

■ **GCA_001046895.1; Pseudarthrobacter siccitolerans; counts= 1; multicellularity status: FALSE**

- GrpE->HSP70->TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->??->HSP70->vWA(canonical)->

■ **GCF_001140765.1; Yersinia; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_001136465.1; Yersinia pseudotuberculosis; counts= 1; multicellularity status: FALSE**

- GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_001189515.2; Olsenella sp. oral taxon 807; counts= 1; multicellularity status: FALSE**

- TM+vWA(canonical)+YtKA-like+IG-like+TM+??->Tubulin+coiled_coil+??->?->?->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C*->??+Pkinase->?->Tubulin+coiled_coil+??->Tubulin+coiled_coil+??->

■ **GCA_001189025.1; Streptomyces europaeiscabiei; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_001319605.1; Yersinia mollaretii; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCF_000452605.1; Pseudomonas syringae; counts= 1; multicellularity status: FALSE**

- GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->

■ **GCF_000498935.1; Streptomyces sp. HCCB10043; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCF_000502855.1; Mesorhizobium sp. L2C067A000; counts= 1; multicellularity status: TRUE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCF_001244405.1; Eubacterium sp. SB2; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCF_000245555.1; Paenibacillus dendritiformis; counts= 1; multicellularity status: TRUE**

- TM+TM+TM+vWA+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C+polar_tail*->

■ **GCF_000316035.1; Paenibacillus sp. PAMC 26794; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF_000423085.1; Granulicoccus phenolivorans; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->||<-?||Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCF_000422445.1; Paenibacillus assamensis; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->?->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF_000422505.1; Paenibacillus pinihumi; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF_000426545.1; Paenibacillus panacisoli; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF_000497205.1; Saccharopolyspora rectivirgula; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_000517665.1; Rhodococcus rhodochrous; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCF_000517905.1; Paenibacillus sp. FSL H7-689; counts= 1; multicellularity status: TRUE**

- Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C+polar_tail*->

■ **GCA_001632305.1; Paenibacillus; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF_000517965.1; Paenibacillus sp. FSL R7-277; counts= 1; multicellularity status: TRUE**

- Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->?->?->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF_000524095.1; Mycobacterium kansasii; counts= 1; multicellularity status: FALSE**

- TM+DUF4190+TM->TM+DUF4190+TM->polar_leader+TM+TM+TM->PSE->PSE->GAP_unknown1+TM+TM+GAP_unknown2->GAP_unknown1+TM+TM+GAP_unknown2->PSE->GAP1-N2+GAP1-M+GAP1-C->GAP1-N2+GAP1-M+GAP1-C*->?->beta-rich+vWA(canonical)->

■ **GCA_000517925.1; Paenibacillus; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF_000517865.1; Paenibacillus sp. FSL R7-269; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->?->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF_000686845.1; Paenibacillus sp. UNC451MF; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+Cadherin-like*->

■ **GCF_000710755.1; Saccharopolyspora rectivirgula; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCF_000719555.1; Streptomyces sp. NRRL F-5727; counts= 1; multicellularity status: TRUE**

- ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM->?->vWA(canonical)->PP2C->Pkinase+ZnR+beta-rich->

■ **GCA_000949305.1; Rhodococcus; counts= 1; multicellularity status: TRUE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCF_000719505.1; Streptomyces sp. NRRL B-3229; counts= 1; multicellularity status: TRUE**

- PP2C->Pkinase->?->?->?->HSP70_domain_2+low_complexity+domain_betaX->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->PSE->||<-TPR_region+CASPASE

■ **GCA_000695625.1; Amycolatopsis rifamycinica; counts= 1; multicellularity status: TRUE**

- GrpE->HSP70->TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->?->HSP70->vWA(canonical)->?->||<-HSP70<-unknown+CASPASE

■ **GCF_000716435.1; Streptomyces xylophagus; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_000746875.1; Paenibacillus macerans; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_000576305.1; Paenibacillus pini; counts= 1; multicellularity status: TRUE**

- Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->PSE->GAP1-N2+GAP1-M*->

■ **GCF_000758775.1; Actinomyces sp. S4-C9; counts= 1; multicellularity status: NA**

- GrpE->HSP70->TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->?->?->?->HSP70->vWA(canonical)->

■ **GCA_002259145.1; Rhodococcus; counts= 1; multicellularity status: TRUE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCF_000758965.1; Corynebacterium freneyi; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->||<-?||HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->polar_leader+TM+TM+TM->

■ **GCF_000760815.1; Rhodococcus fascians; counts= 1; multicellularity status: TRUE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCF_000757885.1; Paenibacillus wynnii; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF_000758525.1; Paenibacillus sp. FSL H7-0357; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF_000758725.1; Paenibacillus odorifer; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF_000758685.1; Paenibacillus stellifer; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_000787385.1; Paenibacillus sp. P1XP2; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->PSE->PSE->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_001263755.1; Corynebacterium riegelii; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->?->??+DO-GTPase2.2->?->||<-?<-?<-HSP70

■ **GCF_000812585.1; Chromobacterium piscinae; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_900478045.1; Corynebacterium minutissimum; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->polar_leader+TM+TM+TM->

■ **GCF_000455485.1; Gorillibacterium massiliense; counts= 1; multicellularity status: FALSE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF_000612665.1; Bacillus dielmoensis; counts= 1; multicellularity status: FALSE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF_000612625.1; Bacillus; counts= 1; multicellularity status: NA**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF_000723885.1; Paenibacillus camerounensis; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->||<-?||TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF_000758545.1; Paenibacillus sp. FSL H7-0737; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF_000756615.1; Paenibacillus durus; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF_000758585.1; Paenibacillus sp. FSL R5-0345; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF__000758705.1; Paenibacillus graminis; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF__000758605.1; Paenibacillus sp. FSL R5-0912; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF__000758645.1; Paenibacillus sp. FSL R7-0331; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF__000758565.1; Paenibacillus sp. FSL P4-0081; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF__000758665.1; Paenibacillus borealis; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF__000787775.1; Streptacidiphilus carbonis; counts= 1; multicellularity status: TRUE**

- TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+DO-GTPase2->vWA(canonical)->PP2C->Pkinase+ZnR+beta-rich->

■ **GCA__000819445.1; Corynebacterium humireducens; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->polar_leader+TM+TM+TM->

■ **GCF__000818195.1; Streptomyces sp. 150FB; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCF__000876225.1; Micromonospora carbonacea; counts= 1; multicellularity status: TRUE**

- GrpE->HSP70->TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->

■ **GCA__002221455.1; Methylobacterium radiotolerans; counts= 1; multicellularity status: TRUE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA__001610855.1; Gemmata sp. SH-PL17; counts= 1; multicellularity status: FALSE**

- GAP1-N2+GAP1-M+TM*->

■ **GCF__000193415.1; Paenibacillus vortex; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF__000949425.1; Paenibacillus sp. IHBB 10380; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA__900112925.1; Paenibacillus algorifonticola; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA__000981585.1; Paenibacillus riograndensis; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF__000993825.1; Paenibacillus durus; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF__000802655.2; Paenibacillus sp. IHB B 3415; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->?->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA__001263295.1; Agrobacterium sp. SUL3; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA__001020985.1; Corynebacterium mustelae; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+low_complexity+TM+TM*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->polar_leader+TM+TM+TM->

■ **GCF__000702505.1; Thermogemmatispora carboxidivorans; counts= 1; multicellularity status: TRUE**

- ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->

■ **GCF__001015055.1; Aneurinibacillus tyrosinisolvens; counts= 1; multicellularity status: FALSE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail(frag)->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF__000988225.1; Corynebacterium striatum; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->PSE->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->polar_leader+TM+TM+TM->

■ **GCA__002803965.1; Corynebacterium striatum; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->polar_leader+TM+TM+TM->

■ **GCF__001059955.1; Corynebacterium striatum; counts= 1; multicellularity status: FALSE**

- GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->polar_leader+TM+TM+TM->

■ **GCF__001058455.1; Corynebacterium striatum; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->polar_leader+TM+TM+TM->

■ **GCA__001270565.1; Streptomyces virginiae; counts= 1; multicellularity status: TRUE**

- TPR_containing_alpha_helical+Fibronectin-like_repeats->PSE->GAP1-N2+GAP1-M+GAP1-C*->PSE->vWA(canonical)->PP2C->Pkinase+ZnR+beta-rich->

■ **GCA__001270635.1; Streptomyces antibioticus; counts= 1; multicellularity status: TRUE**

- TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->PSE->vWA(canonical)->PP2C->Pkinase+ZnR+beta-rich->

■ **GCF__001270375.1; Clostridium sp. DMHC 10; counts= 1; multicellularity status: NA**

- TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->TM+vWA(canonical)+YtKA-like+TM+??->PSE->?->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M*->

■ **GCA__001272655.2; Paenibacillus peoriae; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF__001273715.1; Vibrio alginolyticus; counts= 1; multicellularity status: FALSE**

- PNP_UDP_1+EAD1->GAP2->ZnR(fragment)+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->SLATT->

■ **GCF_001273905.1; Paenibacillus sp. FJAT-27812; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_001275655.1; Bacillus sp. FJAT-21945; counts= 1; multicellularity status: NA**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_001275735.1; Pseudomonas coronafaciens; counts= 1; multicellularity status: FALSE**

- GAP2->DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->

■ **GCF_001275645.1; Bacillus sp. FJAT-18019; counts= 1; multicellularity status: NA**

- Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C+polar_tail*->

■ **GCF_001278535.1; Caballeronia cordobensis; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_001279585.1; Nocardiopsis sp. NRRL B-16309; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCF_000347295.2; Gordonia sp. NB4-1Y; counts= 1; multicellularity status: FALSE**

- Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C(frag)*->?->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCF_001280595.1; Paenibacillus sp. A59; counts= 1; multicellularity status: TRUE**

- TM+TM+TM+vWA+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C+polar_tail*->

■ **GCA_900099955.1; Halomonas; counts= 1; multicellularity status: FALSE**

- GAP2->DO-GTPase2.1->PSE->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->

■ **GCF_001280845.1; Bacillus sp. FJAT-28004; counts= 1; multicellularity status: NA**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF_001292845.1; Rhodococcus jostii; counts= 1; multicellularity status: TRUE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA_001302585.1; Kibdelosporangium phytohabitans; counts= 1; multicellularity status: TRUE**

- Pkinase+TM->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M*->

■ **GCF_001277345.1; Paenibacillus solani; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_001306465.1; Frankia sp. R43; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C+ZnR+DO-GTPase2*->

■ **GCF_001312305.1; Paenibacillus pinihumi; counts= 1; multicellularity status: TRUE**

- Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->

■ **GCF_001310955.1; Marinifilum fragile; counts= 1; multicellularity status: TRUE**

- GrpE->HSP70->DnaJ+DnaJ+ZnR+ZnR+coiled_coil+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->?->TM+TM+ZnR+ZnR+DO-GTPase2.2+TM+SH3->FGS-fold_domain->

■ **GCF_001310595.1; Bacillus sp. JCM 19035; counts= 1; multicellularity status: NA**

- GAP1-N2+GAP1-M+GAP1-C(frag)*->

■ **GCA_001399685.1; Paenibacillus sp. A3; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->?->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+Cadherin-like*->

■ **GCF_001403875.1; Paenibacillus ihumii; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF_001373335.1; Ralstonia solanacearum; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCF_001418465.1; Streptomyces kanamyceticus; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->vWA(canonical)->PP2C->Pkinase+ZnR+beta-rich->||<-TPR_containing_alpha_helical+Fibronectin-like_repeats

■ **GCF_001419745.1; Streptomyces silaceus; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->vWA(canonical)->PP2C->Pkinase+ZnR+beta-rich->

■ **GCA_001420695.1; Brevibacillus choshinensis; counts= 1; multicellularity status: FALSE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_001422685.1; Paenibacillus sp. Leaf72; counts= 1; multicellularity status: TRUE**

- Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C+polar_tail*->

■ **GCF_001426045.1; Methylobacterium sp. Leaf94; counts= 1; multicellularity status: TRUE**

- GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_001422775.1; Methylobacterium sp. Leaf87; counts= 1; multicellularity status: TRUE**

- GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->

■ **GCA_001428625.1; Hydrogenophaga sp. Root209; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->PSE->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_001423865.2; Brevibacillus sp. Leaf182; counts= 1; multicellularity status: FALSE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_001428245.1; Paenibacillus sp. Soil522; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->HRDC-like?+Fibronectin-like_repeats->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_001420595.1; Bacillus solani; counts= 1; multicellularity status: FALSE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA__001421665.1; Sphingobium sp. Leaf26; counts= 1; multicellularity status: FALSE**

- GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->

■ **GCA__001426325.1; Streptomyces; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__001426865.1; Paenibacillus sp. Root52; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA__001428565.1; Nocardioides sp. Root190; counts= 1; multicellularity status: TRUE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->?->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->?->??+DO-GTPase2.2->

■ **GCA__001426615.1; Streptomyces; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__001429505.1; Bosea sp. Root483D1; counts= 1; multicellularity status: NA**

- EAD1-M1+GAP1-C*->

■ **GCF__001425705.1; Pelomonas sp. Root1217; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA__001401405.1; Pseudomonas syringae group genomosp. 3; counts= 1; multicellularity status: FALSE**

- GAP2->DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->

■ **GCA__001401265.1; Pseudomonas amygdali; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA__001431425.1; Stenotrophomonas nitritireducens; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA__001434355.1; Streptomyces anulatus; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCF__001439605.1; Bacillus praedii; counts= 1; multicellularity status: FALSE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA__001444405.1; Pseudoalteromonas phenolica; counts= 1; multicellularity status: FALSE**

- PNP_UDP_1+EAD1->GAP2->ZnR(fragment)+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->SLATT->

■ **GCA__001457595.1; Mycolicibacterium smegmatis; counts= 1; multicellularity status: FALSE**

- HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->??+DO-GTPase2.2->

■ **GCA__001458375.1; Tropicibacter naphthalenivorans; counts= 1; multicellularity status: FALSE**

- GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->

■ **GCF_001457415.1; Gorillibacterium timonense; counts= 1; multicellularity status: FALSE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_001467145.1; Pseudomonas; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_001467105.1; Pseudomonas syringae; counts= 1; multicellularity status: FALSE**

- GAP2->DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->

■ **GCF_001469165.1; Thiohalocapsa sp. ML1; counts= 1; multicellularity status: TRUE**

- GrpE->HSP70->HSP70+vWA(canonical)->?->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->?->TIR->TM+ZnR+ZnR+DO-GTPase2.2+PEGA+PEGA->

■ **GCA_001476655.1; Microbacterium testaceum; counts= 1; multicellularity status: FALSE**

- GrpE->HSP70->TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->

■ **GCA_002872435.1; Paenibacillus; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_004219785.1; Salmonella enterica; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCF_001049835.1; Paenibacillus; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF_001493375.1; Streptomyces specialis; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCF_001485495.1; Gordonia desulfuricans; counts= 1; multicellularity status: FALSE**

- Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA_001482305.1; Leucobacter sp. G161; counts= 1; multicellularity status: TRUE**

- GrpE->HSP70->TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->?->?->HSP70->vWA(canonical)->

■ **GCA_001499965.1; Mycobacterium sp. GA-2829; counts= 1; multicellularity status: FALSE**

- HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->??+DO-GTPase2.2->

■ **GCA_001500125.1; Mycobacterium sp. IS-1742; counts= 1; multicellularity status: FALSE**

- HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->??+DO-GTPase2.2->

■ **GCA_001499995.1; Mycobacterium sp. IS-1496; counts= 1; multicellularity status: FALSE**

- HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->??+DO-GTPase2.2->

■ **GCA_001509565.1; Streptomyces griseus; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_001511815.1; Streptomyces reticuli; counts= 1; multicellularity status: TRUE**

- TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM->vWA(canonical)->PP2C->Pkinase+ZnR+beta-rich->

■ **GCA_001522865.1; Burkholderia sp. TSV86; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_001522035.1; Burkholderia ubonensis; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_001526205.1; Burkholderia cepacia; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_001528175.1; Burkholderia ubonensis; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCF_001528875.1; Burkholderia ubonensis; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_001527825.1; Burkholderia stagnalis; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_001529865.1; Burkholderia ubonensis; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->||<-?||DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_001533325.1; Burkholderia ubonensis; counts= 1; multicellularity status: FALSE**

- GAP2->DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->

■ **GCA_001532865.1; Burkholderia ubonensis; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_001535945.1; Pseudomonas syringae; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_001421015.2; Paenibacillus bovis; counts= 1; multicellularity status: TRUE**

- Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->||<-?||TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->?->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M*->

■ **GCA_001012825.2; Paenibacillus etheri; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF_001465325.1; Rhodococcus pyridinivorans; counts= 1; multicellularity status: TRUE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA_001541145.1; Streptomyces albus; counts= 1; multicellularity status: TRUE**

- TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM->vWA(canonical)->PP2C->Pkinase+ZnR+beta-rich->

■ **GCA_001544575.2; Caballeronia cordobensis; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCF_001546065.1; Paenibacillus riograndensis; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF_001550375.1; Streptomyces europaeiscabiei; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->vWA(canonical)->PP2C->Pkinase+ZnR+beta-rich->

■ **GCA_001552955.1; Corynebacterium kroppenstedtii; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA_001553935.1; Actinomyces oris; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->?->??+DO-GTPase2.2->

■ **GCA_001555475.1; Rhodococcus sp. SC4; counts= 1; multicellularity status: TRUE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCF_001568445.1; Leptospira borgpetersenii; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCF_001569365.1; Leptospira weilii; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_001577385.1; Streptomyces albus; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_001583455.1; Rhodococcus sp. LB1; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA_900445325.1; Bacillus circulans; counts= 1; multicellularity status: FALSE**

- GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_001593085.1; Paenibacillus polymyxa; counts= 1; multicellularity status: TRUE**

- Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C+polar_tail*->

■ **GCA_001425445.1; Devosia sp. Leaf420; counts= 1; multicellularity status: FALSE**

- GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->CASPASE+??->

■ **GCA_001579275.1; Corynebacterium; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->polar_leader+TM+TM+TM->

■ **GCA_001586215.1; Corynebacterium simulans; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->polar_leader+TM+TM+TM->

■ **GCA_001586235.1; Corynebacterium simulans; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->polar_leader+TM+TM+TM->

■ **GCA_001513975.1; Streptomyces curacoi; counts= 1; multicellularity status: TRUE**

- TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM->vWA(canonical)->PP2C->Pkinase+ZnR+beta-rich->

■ **GCF_001514495.1; Paenibacillus pabuli; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF_001546055.1; Paenibacillus jilunlii; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->?->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF_000971455.1; Lysinimicrobium rhizosphaerae; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA_001509505.1; Streptomyces sp. NRRL S-1521; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->vWA(canonical)->PP2C->Pkinase+ZnR+beta-rich->||<-TPR_containing_alpha_helical+Fibronectin-like_repeats

■ **GCA_003634525.1; Williamsia muralis; counts= 1; multicellularity status: TRUE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA_001570425.1; Mycolicibacterium brisbanense; counts= 1; multicellularity status: FALSE**

- TM+DUF4190+TM->polar_leader+TM+TM+TM->PSE->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->TM+DUF4190+TM+PknH_C->TM+DUF4190+TM+PknH_C->TM+DUF4190+TM+PknH_C->

■ **GCF_001570725.1; Paenibacillus amylolyticus; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_003326775.1; Thalassospira xiamenensis; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->DO-GTPase2.1(fragment)->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCF_900075065.1; Enterobacteriaceae; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_001619725.1; Paenibacillus elgii; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->?->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+Cadherin-like*->

■ **GCA_001619755.1; Paenibacillus jamilae; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_001619605.1; Brevibacillus parabrevis; counts= 1; multicellularity status: FALSE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_001633025.1; Paenibacillus glucanolyticus; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF_001636635.1; Paenibacillus sp. O199; counts= 1; multicellularity status: TRUE**

- Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF_001650215.1; Streptomyces sp. RTd22; counts= 1; multicellularity status: TRUE**

- TPR_containing_alpha_helical+Fibronectin-like_repeats->?->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM->vWA(canonical)->PP2C->Pkinase+ZnR+beta-rich->

■ **GCF_001418335.1; Streptomyces aurantiacus; counts= 1; multicellularity status: TRUE**

- TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM->vWA(canonical)->PP2C->Pkinase+ZnR+beta-rich->

■ **GCA_001639025.1; Corynebacterium afermentans; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->?->||<-?<-?<-HSP70<-GrpE

■ **GCA_001643175.1; Dietzia cinnamea; counts= 1; multicellularity status: FALSE**

- GrpE->HSP70->TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->?->HSP70->vWA(canonical)->

■ **GCA_001645205.1; Brevibacillus sp. SKDU10; counts= 1; multicellularity status: FALSE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_900455725.1; Rhodococcus gordoniae; counts= 1; multicellularity status: TRUE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA_002152295.1; Klebsiella; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCF_001649505.1; Brevibacillus brevis; counts= 1; multicellularity status: FALSE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF_001546485.1; Gardnerella vaginalis; counts= 1; multicellularity status: FALSE**

- TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->?->HSP70->HSP70+vWA(canonical)->DnaJ+DnaJ+ZnR+ZnR+coiled_coil+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_001659845.1; Paenibacillus sp. AD87; counts= 1; multicellularity status: TRUE**

- TM+TM+TM+vWA+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C+polar_tail*->

■ **GCA_001663525.1; Enterobacter asburiae; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_001663585.1; Paenibacillus polymyxa; counts= 1; multicellularity status: TRUE**

- Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C+polar_tail*->

■ **GCA_001665445.1; Mycolicibacterium setense; counts= 1; multicellularity status: FALSE**

- HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->??+DO-GTPase2.2->

■ **GCA_001665825.1; Mycobacterium sp. 852013-50142_SCH4511227; counts= 1; multicellularity status: FALSE**

- HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->??+DO-GTPase2.2->

■ **GCA__001665335.1; Mycolicibacterium conceptionense; counts= 1; multicellularity status: FALSE**

- HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->??+DO-GTPase2.2->

■ **GCA__001666795.1; Mycolicibacterium fortuitum; counts= 1; multicellularity status: FALSE**

- HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->??+DO-GTPase2.2->

■ **GCA__001667465.1; Mycobacterium sp. 852002-10379_SCH5584320; counts= 1; multicellularity status: FALSE**

- HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->??+DO-GTPase2.2->

■ **GCA__001666985.1; Mycolicibacterium fortuitum; counts= 1; multicellularity status: FALSE**

- HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->??+DO-GTPase2.2->

■ **GCA__001665685.1; Mycobacterium sp. 852013-50091_SCH5140682; counts= 1; multicellularity status: FALSE**

- TM+DUF4190+TM->polar_leader+TM+TM+TM->PSE->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->TM+DUF4190+TM+PknH_C->TM+DUF4190+TM+PknH_C->TM+DUF4190+TM+PknH_C->

■ **GCA__001662815.1; Paenibacillus polymyxa; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA__001672365.1; Mesorhizobium loti; counts= 1; multicellularity status: TRUE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA__001672855.1; Mycolicibacterium fortuitum; counts= 1; multicellularity status: FALSE**

- HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->??+DO-GTPase2.2->

■ **GCA__001672755.1; Mycobacterium colombiense; counts= 1; multicellularity status: FALSE**

- TM+DUF4190+TM->TM+DUF4190+TM->polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->TM+DUF4190+TM+PknH_C->TM+DUF4190+TM+PknH_C->TM+DUF4190+TM+PknH_C->TM+DUF4190+TM+PknH_C->

■ **GCF__900079515.1; Shewanella sp. Alg231_23; counts= 1; multicellularity status: FALSE**

- PNP_UDP_1+EAD1->GAP2->ZnR(fragment)+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->SLATT->

■ **GCA__001680695.1; Paenibacillus sp. KS1; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->PSE->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA__001682715.1; Actinomyces oris; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->?->??+DO-GTPase2.2->

■ **GCA__001682865.1; Bacillus sp. FJAT-26390; counts= 1; multicellularity status: NA**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA__001686835.1; Mycolicibacterium vulneris; counts= 1; multicellularity status: FALSE**

- HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->??+DO-GTPase2.2->

■ **GCA__001686755.1; Mycolicibacterium vulneris; counts= 1; multicellularity status: FALSE**

- HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->??+DO-GTPase2.2->

■ **GCA__001686675.1; Mycolicibacterium vulneris; counts= 1; multicellularity status: FALSE**

- HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->??+DO-GTPase2.2->

■ **GCA__001698815.1; Pseudomonas syringae; counts= 1; multicellularity status: FALSE**

- GAP2->DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->

■ **GCF__001700505.1; Streptomyces mutomycini; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__001701025.1; Lentzea guizhouensis; counts= 1; multicellularity status: TRUE**

- GrpE->HSP70->TPR_containing_alpha_helical+Fibronectin-like_repeats->TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->?->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->HSP70->?->?->?->||<-PSE<-unknown+CASPASE

■ **GCF__001591665.1; Bacillus soli; counts= 1; multicellularity status: FALSE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->||<-?||Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF__001591805.1; Bacillus novalis; counts= 1; multicellularity status: FALSE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA__900078705.1; Bordetella ansorpii; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA__001685025.1; Bacillus sp. FJAT-27225; counts= 1; multicellularity status: NA**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF__001556295.1; Blastomonas sp. CCH5-A3; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCF__001685485.1; Formosa haliotis; counts= 1; multicellularity status: FALSE**

- GAP2->PSE->PSE->GAP1-N1+GAP1-M+GAP1-C*->EAD1->?->??+EAD1->EAD1+Trypsin->

■ **GCF__001571225.1; Hydrogenophaga palleronii; counts= 1; multicellularity status: FALSE**

- GAP2->DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->

■ **GCA__001529295.1; Flavobacterium sp. TAB 87; counts= 1; multicellularity status: FALSE**

- PNP_UDP_1+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCF__001510715.1; Bacillus sp. FJAT-29814; counts= 1; multicellularity status: NA**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA__001682855.1; Bacillus sp. FJAT-27264; counts= 1; multicellularity status: NA**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF__001661965.1; Croceicoccus mobilis; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_001665575.1; Mycobacterium sp. 852013-51886_SCH5428379; counts= 1; multicellularity status: FALSE**

- HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->??+DO-GTPase2.2->

■ **GCA_001672995.1; Mycobacterium sp. 1482292.6; counts= 1; multicellularity status: FALSE**

- GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->TM+DUF4190+TM+PknH_C->TM+DUF4190+TM+PknH_C->TM+DUF4190+TM+PknH_C->TM+DUF4190+TM+PknH_C->TM+DUF4190+TM+PknH_C->

■ **GCA_001673055.1; Mycobacterium sp. 1245801.1; counts= 1; multicellularity status: FALSE**

- GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->TM+DUF4190+TM+PknH_C->TM+DUF4190+TM->

■ **GCF_001700515.1; Streptomyces lushanensis; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_001513965.1; Streptomyces cellostaticus; counts= 1; multicellularity status: TRUE**

- TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM->vWA(canonical)->PP2C->Pkinase+ZnR+beta-rich->

■ **GCA_001673415.1; Mycobacterium; counts= 1; multicellularity status: FALSE**

- GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->TM+DUF4190+TM+PknH_C->TM+DUF4190+TM+PknH_C->TM+DUF4190+TM+PknH_C->PSE->?->TM+DUF4190+TM+PknH_C->

■ **GCA_001636945.1; Streptomyces sp. FXJ1.172; counts= 1; multicellularity status: TRUE**

- GrpE->HSP70->||<-PSE||ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+Jelly_roll+beta-sandwich->||<-STAND_NTPase+TM+TM+TM+TM+TM+TM+TM

■ **GCA_001665875.1; Mycobacterium sp. 852002-40037_SCH5390672; counts= 1; multicellularity status: FALSE**

- TM+DUF4190+TM->TM+DUF4190+TM->polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->TM+DUF4190+TM+PknH_C->TM+DUF4190+TM+PknH_C->TM+DUF4190+TM+PknH_C->TM+DUF4190+TM+PknH_C->

■ **GCA_001667145.1; Mycobacterium sp. 852002-51971_SCH5477799-a; counts= 1; multicellularity status: FALSE**

- TM+DUF4190+TM->TM+DUF4190+TM->polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->TM+DUF4190+TM+PknH_C->TM+DUF4190+TM+PknH_C->TM+DUF4190+TM+PknH_C->

■ **GCA_001669335.1; Mycobacterium sp. 1245852.3; counts= 1; multicellularity status: FALSE**

- GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->TM+DUF4190+TM+PknH_C->

■ **GCA_001673555.1; Mycobacterium sp. 1165178.9; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->TM+DUF4190+TM+PknH_C->TM+DUF4190+TM+PknH_C->TM+DUF4190+TM+PknH_C->

■ **GCA_004195765.1; Streptomyces sampsonii; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCF_001552215.1; Actinomadura macra; counts= 1; multicellularity status: TRUE**

- GrpE->HSP70->TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM->

■ **GCF_001552635.1; Actinomadura hibisca; counts= 1; multicellularity status: TRUE**

- GrpE->HSP70->TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM->

- **GCF_001613405.1; Nocardia crassostreae; counts= 1; multicellularity status: TRUE**
  - Pkinase+TM->ZnR+DO-GTPase2.1->GAP1-N2+GAP1-M+GAP1-C*->
- **GCF_001625085.1; Nocardia acidivorans; counts= 1; multicellularity status: TRUE**
  - Pkinase+TM->ZnR+DO-GTPase2.1->GAP1-N2+GAP1-M+GAP1-C*->
- **GCF_001570765.1; Nocardiopsis listeri; counts= 1; multicellularity status: TRUE**
  - TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->
- **GCF_001552195.1; Actinomadura latina; counts= 1; multicellularity status: TRUE**
  - GrpE->HSP70->TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM->
- **GCF_001612885.1; Nocardia harenae; counts= 1; multicellularity status: TRUE**
  - GrpE->HSP70->TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->?->HSP70->vWA(canonical)->
- **GCF_001613145.1; Nocardia jejuensis; counts= 1; multicellularity status: TRUE**
  - Pkinase+TM->ZnR+DO-GTPase2.1->GAP1-N2+GAP1-M+GAP1-C*->
- **GCA_001683795.1; Akkermansia glycaniphila; counts= 1; multicellularity status: FALSE**
  - FHA-like?+ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->
- **GCF_001552155.1; Actinomadura formosensis; counts= 1; multicellularity status: TRUE**
  - GrpE->HSP70->TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM->
- **GCA_001667505.1; Mycobacterium sp. ACS1612; counts= 1; multicellularity status: FALSE**
  - TM+DUF4190+TM->TM+DUF4190+TM->polar_leader+TM+TM+TM->PSE->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->?->TM+DUF4190+TM+PknH_C->
- **GCF_001552175.1; Actinomadura kijaniata; counts= 1; multicellularity status: TRUE**
  - GrpE->HSP70->TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM->
- **GCA_001667835.1; Mycobacterium sp. E3078; counts= 1; multicellularity status: FALSE**
  - TM+DUF4190+TM->TM+DUF4190+TM->polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->TM+DUF4190+TM+PknH_C->TM+DUF4190+TM+PknH_C->TM+DUF4190+TM+PknH_C->TM+DUF4190+TM+PknH_C->
- **GCA_001545135.1; Mycolicibacterium wolinskyi; counts= 1; multicellularity status: FALSE**
  - HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->??+DO-GTPase2.2->
- **GCA_001667865.1; Mycobacterium; counts= 1; multicellularity status: FALSE**
  - TM+DUF4190+TM->TM+DUF4190+TM->polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->TM+DUF4190+TM+PknH_C->TM+DUF4190+TM+PknH_C->TM+DUF4190+TM+PknH_C->TM+DUF4190+TM+PknH_C->
- **GCA_001666755.1; Mycobacterium; counts= 1; multicellularity status: FALSE**
  - Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->
- **GCF_001642915.1; Roseimaritima ulvae; counts= 1; multicellularity status: TRUE**

- FGS-fold_domain->ZnR+DO-GTPase2.1->GAP1-N2+GAP1-M*->

■ **GCA_001667265.1; Mycobacterium sp. ACS4331; counts= 1; multicellularity status: FALSE**

- Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->TM+DUF4190+TM+PknH_C->

■ **GCA_001667995.1; Mycobacterium sp. E2660; counts= 1; multicellularity status: FALSE**

- TM+DUF4190+TM->TM+DUF4190+TM->polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->TM+DUF4190+TM+PknH_C->TM+DUF4190+TM+PknH_C->TM+DUF4190+TM+PknH_C->TM+DUF4190+TM+PknH_C->

■ **GCA_001672685.1; Mycobacterium sp. E2462; counts= 1; multicellularity status: FALSE**

- Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->TM+DUF4190+TM+PknH_C->TM+DUF4190+TM+PknH_C->TM+DUF4190+TM+PknH_C->TM+DUF4190+TM+PknH_C->

■ **GCA_001610895.1; Planctomyces sp. SH-PL62; counts= 1; multicellularity status: NA**

- GAP1-N2+GAP1-M*->

■ **GCF_001705305.1; Paenibacillus kribbensis; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_001637205.1; Paenibacillus glacialis; counts= 1; multicellularity status: TRUE**

- Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->?->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C+polar_tail*->

■ **GCA_001637165.1; Paenibacillus macquariensis; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_001637215.1; Paenibacillus macquariensis; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF_900086655.1; Paenibacillus tuaregi; counts= 1; multicellularity status: TRUE**

- Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C+polar_tail*->

■ **GCA_001637225.1; Paenibacillus antarcticus; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_001857945.1; Paenibacillus crassostreae; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_001675045.1; Paenibacillus oryzae; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_001517085.1; Paenibacillus sp. DMB5; counts= 1; multicellularity status: TRUE**

- TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF_900069005.1; Paenibacillus sp. GM2; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF_001696705.1; Brevibacillus laterosporus; counts= 1; multicellularity status: FALSE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_001707685.1; Paenibacillus; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_001709135.1; Paenibacillus polymyxa; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_001708695.1; Mesorhizobium sp. SEMIA 3007; counts= 1; multicellularity status: TRUE**

- GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCF_001715295.1; Streptomyces griseus; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_001719045.1; Paenibacillus polymyxa; counts= 1; multicellularity status: TRUE**

- Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C+polar_tail*->

■ **GCA_001721045.1; Paenibacillus sp. TI45-13ar; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_001722515.1; Dietzia alimentaria; counts= 1; multicellularity status: FALSE**

- GrpE->HSP70->TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->?->HSP70_domain_1->HSP70->vWA(canonical)->

■ **GCA_001727475.1; Vibrio parahaemolyticus; counts= 1; multicellularity status: FALSE**

- PNP_UDP_1+EAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->SLATT->

■ **GCA_001729525.1; Brevibacterium linens; counts= 1; multicellularity status: FALSE**

- TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCF_001723055.1; Streptomyces niveus; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->vWA(canonical)->PP2C->Pkinase+ZnR+beta-rich->||<-TPR_containing_alpha_helical+Fibronectin-like_repeats

■ **GCF_001746285.1; Streptomyces sp. EN16; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCF_001748185.1; Brevibacillus brevis; counts= 1; multicellularity status: FALSE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF_001748305.1; Streptomyces luteocolor; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->vWA(canonical)->PP2C->Pkinase+ZnR+beta-rich->||<-TPR_containing_alpha_helical+Fibronectin-like_repeats

■ **GCA_001751375.1; Streptomyces; counts= 1; multicellularity status: TRUE**

- PP2C->Pkinase->?->?->?->HSP70_domain_2+low_complexity+domain_betaX->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->

■ **GCA_900079405.3; Streptomyces sp. F-1; counts= 1; multicellularity status: TRUE**

- PP2C->Pkinase->?->?->?->HSP70_domain_2+low_complexity+domain_betaX->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->

■ **GCA__001756795.1; Mycolicibacterium sp. (ex Dasyatis americana); counts= 1; multicellularity status: FALSE**

- HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->??+DO-GTPase2.2->

■ **GCA__001758225.1; Humibacillus sp. DSM 29435; counts= 1; multicellularity status: FALSE**

- TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->?->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->?->??+DO-GTPase2.2->

■ **GCA__001751305.1; Streptomyces nanshensis; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__001807295.1; Corynebacterium sp. HMSC06C06; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->polar_leader+TM+TM+TM->

■ **GCA__001807315.1; Corynebacterium sp. HMSC06D04; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->polar_leader+TM+TM+TM->

■ **GCA__001807205.1; Corynebacterium sp. HMSC05D03; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->polar_leader+TM+TM+TM->

■ **GCA__001810285.1; Corynebacterium; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->PSE->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->polar_leader+TM+TM+TM->

■ **GCA__001806945.1; Corynebacterium sp. HMSC30G07; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->?->??+DO-GTPase2.2->?->||<-?<-?<-HSP70

■ **GCA__001807365.1; Corynebacterium sp. HMSC06G04; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->polar_leader+TM+TM+TM->

■ **GCA__001807215.1; Corynebacterium sp. HMSC05D08; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->polar_leader+TM+TM+TM->

■ **GCA__001811545.1; Corynebacteriaceae; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->polar_leader+TM+TM+TM->

■ **GCA__001811515.1; Turicella sp. HMSC076G08; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->polar_leader+TM+TM+TM->

■ **GCF__001807025.1; Corynebacterium sp. HMSC11E11; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->polar_leader+TM+TM+TM->

■ **GCA__001811845.1; Corynebacteriaceae; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->polar_leader+TM+TM+TM->

■ **GCA__001808885.1; Corynebacterium sp. HMSC074E01; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->polar_leader+TM+TM+TM->

■ **GCA_001811255.1; Corynebacteriaceae; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->polar_leader+TM+TM+TM->

■ **GCA_001808895.1; Corynebacterium sp. HMSC070E08; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->polar_leader+TM+TM+TM->

■ **GCA_001810085.1; Corynebacterium sp. HMSC072A02; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->polar_leader+TM+TM+TM->

■ **GCA_001811565.1; Corynebacterium; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->polar_leader+TM+TM+TM->

■ **GCA_001812965.1; Actinomyces; counts= 1; multicellularity status: TRUE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->?->??+DO-GTPase2.2->

■ **GCA_001812805.1; Corynebacterium sp. HMSC078H07; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->polar_leader+TM+TM+TM->

■ **GCA_001815175.1; Turicella sp. HMSC034H07; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->polar_leader+TM+TM+TM->

■ **GCA_001813425.1; Corynebacterium sp. HMSC056E09; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->polar_leader+TM+TM+TM->

■ **GCA_001814395.1; Turicella sp. HMSC059E07; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->polar_leader+TM+TM+TM->

■ **GCA_001814885.1; Corynebacterium sp. HMSC068G04; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->polar_leader+TM+TM+TM->

■ **GCA_001814945.1; Corynebacterium sp. HMSC066C02; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->polar_leader+TM+TM+TM->

■ **GCA_001813815.1; Corynebacterium sp. HMSC076D02; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->PSE->PSE->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->polar_leader+TM+TM+TM->

■ **GCA_001836165.1; Corynebacterium sp. HMSC036D02; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->polar_leader+TM+TM+TM->

■ **GCA_001836185.1; Corynebacterium sp. HMSC036D03; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->polar_leader+TM+TM+TM->

■ **GCA_001853525.1; Mycobacterium sp. 24999; counts= 1; multicellularity status: FALSE**

- HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->??+DO-GTPase2.2->

■ **GCA__001854695.1; Frankia sp. NRRL B-16219; counts= 1; multicellularity status: TRUE**

- HSP70->TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->

■ **GCA__001860525.1; Paenibacillus sp. LC231; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF__001865165.1; Mycolicibacterium llatzerense; counts= 1; multicellularity status: FALSE**

- GrpE->HSP70->TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->??->HSP70->vWA(canonical)->

■ **GCF__001865795.1; Streptomyces albidoflavus; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__001866665.1; Streptomyces sp. MUSC 1; counts= 1; multicellularity status: TRUE**

- ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->

■ **GCA__001813755.1; Corynebacterium sp. HMSC074H12; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->polar_leader+TM+TM+TM->

■ **GCA__001877055.1; Nocardiopsis dassonvillei; counts= 1; multicellularity status: TRUE**

- TPR_containing_alpha_helical+Fibronectin-like_repeats+extended_insert+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->

■ **GCF__001885705.1; Streptomyces cinnamoneus; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__900101595.1; Paenibacillus; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+Cadherin-like*->

■ **GCA__900114875.1; Chryseobacterium limigenitum; counts= 1; multicellularity status: FALSE**

- GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->PNP_UDP_1+EAD1->

■ **GCA__900103235.1; Ruminococcus; counts= 1; multicellularity status: TRUE**

- GrpE->HSP70->ZnR+ZnR+DO-GTPase2.2->?->?->GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__900119365.1; Streptomyces atratus; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCF__900128415.1; Anaerococcus mediterraneensis; counts= 1; multicellularity status: TRUE**

- TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->GrpE->HSP70->HSP70+vWA(canonical)->DnaJ+DnaJ+ZnR+ZnR+coiled_coil+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->

■ **GCF__001894745.1; Paenibacillus sp. NAIST15-1; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA__900143165.1; Paenibacillus sp. ov031; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF_001895005.1; Rhodococcus yunnanensis; counts= 1; multicellularity status: TRUE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA_900101735.1; Rhodococcus tukisamuensis; counts= 1; multicellularity status: TRUE**

- Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA_900105905.1; Rhodococcus koreensis; counts= 1; multicellularity status: TRUE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA_900143025.1; Ruminococcus flavefaciens; counts= 1; multicellularity status: TRUE**

- HSP70->HSP70+vWA(canonical)->?->?->DnaJ+DnaJ+ZnR+ZnR+coiled_coil+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_900141915.1; Tessaracoccus bendigoensis; counts= 1; multicellularity status: TRUE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->?->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->?->??+DO-GTPase2.2->

■ **GCF_001895105.1; Streptomyces sp. NBRC 110465; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_900141985.1; Nocardiopsis flavescens; counts= 1; multicellularity status: TRUE**

- GrpE->HSP70->TPR_containing_alpha_helical+Fibronectin-like_repeats+extended_insert+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->

■ **GCA_001902295.1; Clostridium kluyveri; counts= 1; multicellularity status: FALSE**

- Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->

■ **GCA_001905145.1; Nocardiopsis sp. TSRI0078; counts= 1; multicellularity status: TRUE**

- TPR_containing_alpha_helical+Fibronectin-like_repeats+extended_insert+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->

■ **GCA_001905125.1; Streptomyces sp. TSRI0281; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_001905365.1; Streptomyces sp. CB02488; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_001905645.1; Streptomyces sp. CB02115; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_001905505.1; Streptomyces sp. CB02058; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_001905005.1; Streptomyces sp. CB02923; counts= 1; multicellularity status: TRUE**

- TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM->vWA(canonical)->PP2C->Pkinase+ZnR+beta-rich->

■ **GCA_001905405.1; Streptomyces sp. TSRI0445; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__001905795.1; Streptomyces sp. CB01580; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__001905785.1; Streptomyces sp. CB02130; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__001905755.1; Amycolatopsis sp. CB00013; counts= 1; multicellularity status: TRUE**

- vWA(canonical)+beta-rich+low_complexity->Tubulin+alpha_helical+??+??->??+TM+TM+TM+TM+??->Pkinase+TM->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C+TM*->

■ **GCA__001905735.1; Streptomyces sp. CB01249; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__900015285.1; Corynebacterium variabile; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA__001905825.1; Streptomyces sp. CB02009; counts= 1; multicellularity status: TRUE**

- TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM->vWA(canonical)->PSE->Pkinase+ZnR+beta-rich->

■ **GCA__001907615.1; Mycobacterium sp. SWH-M3; counts= 1; multicellularity status: FALSE**

- GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->TM+DUF4190+TM+PknH_C->TM+DUF4190+TM+PknH_C->

■ **GCA__001905705.1; Streptomyces sp. CB02460; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__001909085.1; Paenibacillus sp. P32E; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA__001908275.1; Paenibacillus xylanexedens; counts= 1; multicellularity status: TRUE**

- Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C+polar_tail*->

■ **GCA__001909045.1; Paenibacillus sp. P3E; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA__001909055.1; Paenibacillus sp. P26E; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA__001909095.1; Paenibacillus sp. P46E; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF__900129635.1; Singulisphaera sp. GP187; counts= 1; multicellularity status: TRUE**

- DO-GTPase2.1+TM->GAP1-N2+GAP1-M+GAP1-C*->

■ **GCF__000010225.1; Corynebacterium; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCF_001912725.1; Corynebacterium glutamicum; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCF_001912755.2; Corynebacterium glutamicum; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCF_000828015.1; Corynebacterium glutamicum; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA_900102965.1; Paenibacillus jilunlii; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_002217275.1; Flavobacterium; counts= 1; multicellularity status: FALSE**

- GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->PNP_UDP_1+EAD1->

■ **GCA_900115275.1; Pseudomonas syringae; counts= 1; multicellularity status: FALSE**

- GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->

■ **GCA_900104815.1; Streptomyces misionensis; counts= 1; multicellularity status: TRUE**

- PP2C->Pkinase->?->?->?->HSP70_domain_2+low_complexity+domain_betaX->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->

■ **GCA_900111245.1; Streptomyces qinglanensis; counts= 1; multicellularity status: TRUE**

- PP2C->Pkinase->?->?->?->HSP70_domain_2+low_complexity+domain_betaX->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->

■ **GCA_001922145.1; Paenibacillus polymyxa; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_001929375.1; Actinomyces oris; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->?->??+DO-GTPase2.2->

■ **GCF_001936195.1; Corynebacterium glutamicum; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA_001937485.1; Actinomyces oris; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->?->??+DO-GTPase2.2->

■ **GCA_001937415.1; Actinomyces oris; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->?->??+DO-GTPase2.2->

■ **GCA_001937725.1; Actinomyces oris; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->?->??+DO-GTPase2.2->

■ **GCA_001937425.1; Actinomyces oris; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->||<-?||GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->?->??+DO-GTPase2.2->

■ **GCA__001632895.1; Mycobacterium kansasii; counts= 1; multicellularity status: FALSE**

- TM+DUF4190+TM->TM+DUF4190+TM->polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA__001632905.1; Mycobacterium kansasii; counts= 1; multicellularity status: FALSE**

- TM+DUF4190+TM->TM+DUF4190+TM->polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->TM+DUF4190+TM+PknH_C->

■ **GCA__001632975.1; Mycobacterium kansasii; counts= 1; multicellularity status: FALSE**

- TM+DUF4190+TM->TM+DUF4190+TM->polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA__001940785.1; Bacillus sp. MRMR6; counts= 1; multicellularity status: NA**

- SP+vWA+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__001941505.1; Corynebacterium sphenisci; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCF__001941445.1; Corynebacterium aquilae; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA__006539465.1; Corynebacterium flavescens; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->polar_leader+TM+TM+TM->

■ **GCA__001683055.1; Corynebacterium; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA__001942465.1; Actinomadura sp. CNU-125; counts= 1; multicellularity status: TRUE**

- GAP2->DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->

■ **GCA__001942625.1; Mycobacterium sp. 27335; counts= 1; multicellularity status: FALSE**

- HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->??+DO-GTPase2.2->

■ **GCA__001942045.1; Mycolicibacterium porcinum; counts= 1; multicellularity status: FALSE**

- HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->??+DO-GTPase2.2->

■ **GCA__001952675.1; Leptospira santarosai; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA__001431765.1; Streptomyces sp. FR-008; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__001955915.1; Paenibacillus sp. FSL R7-0333; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA__001953885.1; Streptomyces sp. IMTB 2501; counts= 1; multicellularity status: TRUE**

- GrpE->HSP70->TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+Jelly_roll+beta-sandwich->||<-STAND_NTPase+TM+TM+TM+TM+TM+TM+TM

■ **GCA_001954285.1; Paenibacillus odorifer; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_001954345.1; Paenibacillus odorifer; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_001954415.1; Paenibacillus borealis; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->?->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_001954425.1; Paenibacillus odorifer; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_001954575.1; Paenibacillus odorifer; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_003255855.1; Paenibacillus odorifer; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_001955765.1; Paenibacillus odorifer; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_001955785.1; Paenibacillus odorifer; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_001955865.1; Paenibacillus glucanolyticus; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_001955925.1; Paenibacillus sp. FSL R7-0337; counts= 1; multicellularity status: TRUE**

- TM+TM+TM+vWA+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C+polar_tail*->

■ **GCA_001953865.1; Amycolatopsis coloradensis; counts= 1; multicellularity status: TRUE**

- GrpE->HSP70->TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->PSE->?->HSP70->vWA(canonical)->||<-?<-?<-HSP70<-unknown+CASPASE

■ **GCA_001956115.1; Paenibacillus peoriae; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_001956185.1; Paenibacillus rhizosphaerae; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_001954455.1; Paenibacillus odorifer; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_001954515.1; Paenibacillus odorifer; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA__001954135.1; Mycobacterium sp. GA-1841; counts= 1; multicellularity status: FALSE**

- HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->??+DO-GTPase2.2->

■ **GCA__001954145.1; Mycolicibacterium fortuitum; counts= 1; multicellularity status: FALSE**

- HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->??+DO-GTPase2.2->

■ **GCA__001954595.1; Paenibacillus odorifer; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA__001955855.1; Paenibacillus sp. FSL R5-0765; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA__001954205.1; Mycolicibacterium conceptionense; counts= 1; multicellularity status: FALSE**

- HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->??+DO-GTPase2.2->

■ **GCA__001954655.1; Paenibacillus odorifer; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA__001955595.1; Paenibacillus odorifer; counts= 1; multicellularity status: TRUE**

- Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA__001955775.1; Paenibacillus odorifer; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA__001956045.1; Paenibacillus sp. FSL H7-0331; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+Cadherin-like*->

■ **GCA__001953975.1; Mycobacterium sp. NS-7484; counts= 1; multicellularity status: FALSE**

- HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->??+DO-GTPase2.2->

■ **GCA__001956105.1; Paenibacillus sp. FSL H8-0259; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA__001956175.1; Paenibacillus; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA__001956225.1; Paenibacillus peoriae; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA__001956295.1; Paenibacillus sp. FSL A5-0031; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA__001954335.1; Paenibacillus odorifer; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_001954535.1; Paenibacillus odorifer; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_001954675.1; Paenibacillus odorifer; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_001955555.1; Paenibacillus odorifer; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_001955545.1; Paenibacillus odorifer; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF_001955985.1; Paenibacillus pabuli; counts= 1; multicellularity status: TRUE**

- TM+TM+TM+vWA+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C+polar_tail*->

■ **GCA_001956155.1; Paenibacillus peoriae; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_001956235.1; Paenibacillus peoriae; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_001954375.1; Paenibacillus odorifer; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_001954445.1; Paenibacillus odorifer; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_001954495.1; Paenibacillus odorifer; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_001954505.1; Paenibacillus odorifer; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_001954585.1; Paenibacillus odorifer; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_001954665.1; Paenibacillus odorifer; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_001955495.1; Paenibacillus odorifer; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_001955835.1; Paenibacillus odorifer; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA__001955995.1; Paenibacillus amylolyticus; counts= 1; multicellularity status: TRUE**

- Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C+polar_tail*->

■ **GCA__001955975.1; Paenibacillus lautus; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->?->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA__001956055.1; Paenibacillus amylolyticus; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA__001956095.1; Paenibacillus sp. FSL H8-0548; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF__900156185.1; Pseudomonas putida; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA__001981425.1; Leptospira santarosai; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA__001975025.1; Streptomyces alfalfae; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->vWA(canonical)->PP2C->Pkinase+ZnR+beta-rich->

■ **GCF__900120345.1; Lachnoclostridium phocaeense; counts= 1; multicellularity status: FALSE**

- PP2C->?->DO-GTPase2.1->GAP1-N2+GAP1-M+TM+TM*->

■ **GCA__001983105.1; Frankia asymbiotica; counts= 1; multicellularity status: TRUE**

- GrpE->HSP70->TPR__containing__alpha__helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->

■ **GCA__001983215.1; Frankia sp. CcI49; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C+ZnR+DO-GTPase2*->

■ **GCA__001984175.1; Saccharothrix sp. ALI-22-I; counts= 1; multicellularity status: TRUE**

- vWA(canonical)+beta-rich+low_complexity->?->?->Tubulin+alpha_helical+??+??->??+TM+TM+TM+TM+??->Pkinase+TM->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C+TM+beta-rich*->

■ **GCA__001983935.1; Fuerstia marisgermanicae; counts= 1; multicellularity status: FALSE**

- ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+TM*->

■ **GCA__001984575.1; Streptomyces sp. MP131-18; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->vWA(canonical)->PP2C->Pkinase+ZnR+beta-rich->||<-TPR__containing__alpha__helical+Fibronectin-like__repeats

■ **GCA__900090055.1; Cuniculiplasma divulgatum; counts= 1; multicellularity status: TRUE**

- TM+TM+TM+TM+TM+TM+DO-GTPase2.1->GAP1-N2+GAP1-M+GAP1-C*->??->TM__region+DO-GTPase1->

■ **GCA__000742735.1; Corynebacterium glutamicum; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA__001997295.1; Tessaracoccus flavus; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->?->??+DO-GTPase2.2->

■ **GCA__001998865.1; Tessaracoccus flavescens; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->?->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->?->??+DO-GTPase2.2->

■ **GCA__001997345.1; Tessaracoccus aquimaris; counts= 1; multicellularity status: TRUE**

- ??+TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->?->?->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->?->??+DO-GTPase2.2->

■ **GCA__001998325.1; Nocardiopsis sinuspersici; counts= 1; multicellularity status: TRUE**

- TPR_containing_alpha_helical+Fibronectin-like_repeats+extended_insert+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__002553535.1; Mycolicibacterium boenickei; counts= 1; multicellularity status: FALSE**

- HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->??+DO-GTPase2.2->

■ **GCA__002006205.1; Clostridium beijerinckii; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA__002006875.1; Micromonospora sp. Rc5; counts= 1; multicellularity status: TRUE**

- GrpE->HSP70->TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->

■ **GCA__002007105.1; Hymenobacter sp. CRA2; counts= 1; multicellularity status: FALSE**

- GAP2->DO-GTPase2.1->DO-GTPase1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+PNP_UDP_1+EAD1*->

■ **GCA__002009175.1; Streptomyces niveus; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->vWA(canonical)->PP2C->Pkinase+ZnR+beta-rich->||<-TPR_containing_alpha_helical+Fibronectin-like_repeats

■ **GCF__002009845.1; Leptospira alexanderi; counts= 1; multicellularity status: FALSE**

- GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->PNP_UDP_1+EAD1->

■ **GCA__002021565.1; Paenibacillus selenitireducens; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF__000373405.1; Streptomyces sp. ScaeMP-e10; counts= 1; multicellularity status: TRUE**

- TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM->vWA(canonical)->PP2C->Pkinase+ZnR+beta-rich->||<-?<-?<-?||GAP1-N2+GAP1-M+GAP1-C*->

■ **GCF__002019645.1; Bacillus alkalitelluris; counts= 1; multicellularity status: FALSE**

- GrpE->HSP70->HSP70+vWA->DnaJ+DnaJ+ZnR+ZnR+coiled_coil+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->

■ **GCF__000702365.1; Streptomyces sp. CNS654; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCF__000717015.1; Streptomyces; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

- **GCF_000717105.1; Streptomyces anulatus; counts= 1; multicellularity status: TRUE**
  - GAP1-N2+GAP1-M+GAP1-C*->
- **GCF_000717665.1; Streptomyces floridae; counts= 1; multicellularity status: TRUE**
  - GAP1-N2+GAP1-M+GAP1-C*->
- **GCF_000716025.1; Streptomyces baarnensis; counts= 1; multicellularity status: TRUE**
  - GAP1-N2+GAP1-M+GAP1-C*->
- **GCF_000717215.1; Streptomyces vinaceus; counts= 1; multicellularity status: TRUE**
  - GAP1-N2+GAP1-M+GAP1-C*->
- **GCF_000377965.1; Streptomyces sp. CNB091; counts= 1; multicellularity status: TRUE**
  - GAP1-N2+GAP1-M+GAP1-C*->
- **GCF_000718915.1; Streptomyces; counts= 1; multicellularity status: TRUE**
  - GAP1-N2+GAP1-M+GAP1-C*->
- **GCF_000718455.1; Streptomyces globisporus; counts= 1; multicellularity status: TRUE**
  - GAP1-N2+GAP1-M+GAP1-C*->
- **GCF_000716945.1; Streptomyces albus; counts= 1; multicellularity status: TRUE**
  - GAP1-N2+GAP1-M+GAP1-C*->
- **GCF_002633395.1; Streptomyces; counts= 1; multicellularity status: TRUE**
  - GAP1-N2+GAP1-M+GAP1-C*->
- **GCA_900167605.1; Caloramator quimbayensis; counts= 1; multicellularity status: TRUE**
  - PNPase->?->GAP1-N2+GAP1-M+GAP1-C*->
- **GCA_002835505.1; Enterovibrio nigricans; counts= 1; multicellularity status: FALSE**
  - GAP1-N1+GAP1-M+GAP1-C*->
- **GCA_900167465.1; Geobacter thiogenes; counts= 1; multicellularity status: FALSE**
  - ??+PNP_UDP_1+EAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->
- **GCF_000720915.1; Streptomyces albus; counts= 1; multicellularity status: TRUE**
  - GAP1-N2+GAP1-M+GAP1-C*->
- **GCF_000719925.1; Streptomyces sp. NRRL F-2202; counts= 1; multicellularity status: TRUE**
  - GAP1-N2+GAP1-M+GAP1-C*->
- **GCF_000718695.1; Streptomyces griseus group; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

- **GCF_000721415.1; Streptomyces sp. NRRL F-5702; counts= 1; multicellularity status: TRUE**
  - GAP1-N2+GAP1-M+GAP1-C*->
- **GCF_000719585.1; Streptomyces sp. NRRL F-5681; counts= 1; multicellularity status: TRUE**
  - GAP1-N2+GAP1-M+GAP1-C*->
- **GCF_000720065.1; Streptomyces; counts= 1; multicellularity status: TRUE**
  - GAP1-N2+GAP1-M+GAP1-C*->
- **GCF_000719655.1; Streptomyces sp. NRRL B-1381; counts= 1; multicellularity status: TRUE**
  - GAP1-N2+GAP1-M+GAP1-C*->
- **GCF_000725705.1; Streptomyces sp. NRRL S-623; counts= 1; multicellularity status: TRUE**
  - GAP1-N2+GAP1-M+GAP1-C*->
- **GCF_001279425.1; Streptomyces sp. NRRL F-2295; counts= 1; multicellularity status: TRUE**
  - GAP1-N2+GAP1-M+GAP1-C*->
- **GCF_000718235.1; Streptomyces griseus; counts= 1; multicellularity status: TRUE**
  - GAP1-N2+GAP1-M+GAP1-C*->
- **GCA_003147545.1; Streptomyces griseus group; counts= 1; multicellularity status: TRUE**
  - GAP1-N2+GAP1-M+GAP1-C*->
- **GCF_001279735.1; Streptomyces sp. MMG1522; counts= 1; multicellularity status: TRUE**
  - GAP1-N2+GAP1-M+GAP1-C*->
- **GCF_001418625.1; Streptomyces luridiscabiei; counts= 1; multicellularity status: TRUE**
  - GAP1-N2+GAP1-M+GAP1-C*->
- **GCF_001746305.1; Streptomyces sp. EN23; counts= 1; multicellularity status: TRUE**
  - GAP1-N2+GAP1-M+GAP1-C*->
- **GCA_001687325.1; Streptomyces sp. PTY087I2; counts= 1; multicellularity status: TRUE**
  - GAP1-N2+GAP1-M+GAP1-C*->
- **GCF_001746315.1; Streptomyces sp. EN27; counts= 1; multicellularity status: TRUE**
  - GAP1-N2+GAP1-M+GAP1-C*->
- **GCF_001905595.1; Streptomyces sp. CB00316; counts= 1; multicellularity status: TRUE**
  - TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM->vWA(canonical)->PP2C->Pkinase+ZnR+beta-rich->||<-?<-?<-?||GAP1-N2+GAP1-M+GAP1-C*->
- **GCF_001931635.1; Streptomyces sp. Tue 6075; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCF_001905525.1; Streptomyces sp. TSRI0395; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCF_001905905.1; Streptomyces sp. CB02366; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_003367645.1; Streptomyces sp. IB2014 011-1; counts= 1; multicellularity status: TRUE**

- TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM->vWA(canonical)->PP2C->Pkinase+ZnR+beta-rich->||<-?<-?<-?||GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_001905485.1; Streptomyces sp. TSRI0261; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_002027255.1; Paenibacillus sp. VT-16-81; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->PSE->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_002326205.1; Pseudomonas; counts= 1; multicellularity status: FALSE**

- GAP2->DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->

■ **GCA_003814735.1; Streptomyces katrae; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_900168305.1; Paenibacillus; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF_002042965.1; Paenibacillus sp. 32352; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+Cadherin-like*->

■ **GCA_004271805.1; Salmonella enterica; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_003606245.1; Burkholderia pseudomallei; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_002071875.1; Burkholderia cenocepacia; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_002071905.1; Burkholderia cenocepacia; counts= 1; multicellularity status: FALSE**

- GAP2->DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->

■ **GCA_001293665.1; Pseudomonas syringae; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCF_001526225.1; Burkholderia ubonensis; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCF_000221965.1; Xanthomonas campestris; counts= 1; multicellularity status: FALSE**

- GAP2->DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->

■ **GCF_900169525.1; Corynebacterium sp. Marseille-P2417; counts= 1; multicellularity status: FALSE**

- TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->polar_leader+TM+TM+TM->

■ **GCA_900170035.1; Desulfamplus magnetovallimortis; counts= 1; multicellularity status: FALSE**

- GAP1-N2+GAP1-M+GAP1-C*->??->

■ **GCF_000834545.1; Pseudomonas fluorescens; counts= 1; multicellularity status: FALSE**

- GAP2->DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->

■ **GCF_001518935.2; Corynebacterium glutamicum; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCF_001718955.1; Burkholderia stagnalis; counts= 1; multicellularity status: FALSE**

- GAP2->||<-?||GAP1-N1+GAP1-M+GAP1-C+CASPASE*->

■ **GCA_003001535.1; Pseudomonas; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_002079265.1; Rhodococcus sp. BH4; counts= 1; multicellularity status: TRUE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCF_002003625.1; Mycobacterium kansasii; counts= 1; multicellularity status: FALSE**

- GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C->GAP1-M*->GAP1-N2+GAP1-M+GAP1-C->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCF_001643015.1; Corynebacterium crudilactis; counts= 1; multicellularity status: FALSE**

- TM+TM+TM->PSE->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->

■ **GCA_002086255.1; Mycolicibacterium insubricum; counts= 1; multicellularity status: FALSE**

- TM+DUF4190+TM->TM+DUF4190+TM->polar_leader+TM+TM+TM->PSE->Tubulin+alpha_helical+??+??->||<-PSE||PSE->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA_002086335.1; Mycobacterium mantenii; counts= 1; multicellularity status: FALSE**

- TM+DUF4190+TM->TM+DUF4190+TM->polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->TM+DUF4190+TM+PknH_C->TM+DUF4190+TM+PknH_C->TM+DUF4190+TM+PknH_C->TM+DUF4190+TM+PknH_C->

■ **GCA_002086675.1; Mycobacterium persicum; counts= 1; multicellularity status: FALSE**

- GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA_002086485.1; Mycobacterium aquaticum; counts= 1; multicellularity status: FALSE**

- TM+DUF4190+TM->polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->TM+DUF4190+TM+PknH_C->TM+DUF4190+TM+PknH_C->TM+DUF4190+TM+PknH_C->

■ **GCA_002082175.1; Streptomyces violaceoruber; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCF_001854655.1; Frankia sp. Cc1.17; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C+ZnR+DO-GTPase2*->

■ **GCA_900176515.1; Kibdelosporangium aridum; counts= 1; multicellularity status: TRUE**

- GrpE->HSP70->TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->?->HSP70->vWA(canonical)->unknown+CASPASE->HSP70->

■ **GCF_001651875.1; Sinorhizobium saheli; counts= 1; multicellularity status: TRUE**

- GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->

■ **GCA_002082585.1; Kitasatospora albolonga; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_003013675.1; Rhodococcus hoagii; counts= 1; multicellularity status: TRUE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA_002096055.1; Cnuibacter physcomitrellae; counts= 1; multicellularity status: FALSE**

- ??->PP2C->Pkinase+helical_region+TM_region->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+low_complexity+TM+TM*->

■ **GCA_900177515.1; Azospirillum oryzae; counts= 1; multicellularity status: FALSE**

- HSP70->HSP70+vWA(canonical)->?->DO-GTPase2.2(frag)->GAP1-N2+GAP1-M+GAP1-C*->?->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->

■ **GCA_002101995.1; Mycolicibacterium fallax; counts= 1; multicellularity status: FALSE**

- TM+DUF4190+TM->TM+DUF4190+TM->polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA_001052995.1; Mycolicibacterium conceptionense; counts= 1; multicellularity status: FALSE**

- HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->??+DO-GTPase2.2->

■ **GCA_002101965.1; Mycolicibacterium wolinskyi; counts= 1; multicellularity status: FALSE**

- HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->??+DO-GTPase2.2->

■ **GCA_002102105.1; Mycolicibacterium confluentis; counts= 1; multicellularity status: FALSE**

- Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->ZnR+ZnR+DO-GTPase2.2->

■ **GCA_002102115.1; Mycolicibacterium doricum; counts= 1; multicellularity status: FALSE**

- HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->??+DO-GTPase2.2->

■ **GCA_900155475.1; Methylomagnum ishizawai; counts= 1; multicellularity status: FALSE**

- PNP_UDP_1+EAD1->||<-?||GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->

■ **GCA_900177415.1; Rhizobium oryzae; counts= 1; multicellularity status: TRUE**

- Calcineurin+GAPEAD1->GAP2->DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_900177695.1; Rhodococcus rhodochrous; counts= 1; multicellularity status: TRUE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA_004196125.1; Streptomyces albidoflavus; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_900177815.1; Paenibacillus aquistagni; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_900177745.1; Corynebacterium pollutisoli; counts= 1; multicellularity status: FALSE**

- TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA_002119405.1; Pseudoruegeria sp. SK021; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->DO-GTPase2.1(fragment)->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_000172695.2; Rhizobium sp. Kim5; counts= 1; multicellularity status: TRUE**

- Calcineurin+GAPEAD1->GAP2->DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_002128305.1; Streptomyces sp. SCSIO 03032; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->PSE->PP2C->Pkinase+ZnR+beta-rich->?->?->||<-TPR_containing_alpha_helical+Fibronectin-like_repeats

■ **GCA_002143185.1; Acinetobacter baumannii; counts= 1; multicellularity status: FALSE**

- PNP_UDP_1+EAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->

■ **GCF_002150765.1; Lentzea kentuckyensis; counts= 1; multicellularity status: TRUE**

- vWA(canonical)+beta-rich+low_complexity->Tubulin+alpha_helical+??+??->??+TM+TM+TM+TM+??->Pkinase+TM->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+SLATT+SLATT*->TIR+??->?->?->STAND_NTPase+TPR_region->

■ **GCF_002154385.1; Streptomyces albovinaceus; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCF_002154345.1; Streptomyces fimicarius; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_006539165.1; Streptomyces cacaoi; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->PSE->?->||<-TPR_containing_alpha_helical+Fibronectin-like_repeats

■ **GCF_002155975.1; Amycolatopsis kentuckyensis; counts= 1; multicellularity status: TRUE**

- vWA(canonical)+beta-rich+low_complexity->?->?->Tubulin+alpha_helical+??+??->??+TM+TM+TM+TM+??->Pkinase+TM->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C+TM+beta-rich*->

■ **GCF_002154605.1; Streptomyces milbemycinicus; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_002156805.1; Corynebacterium striatum; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->polar_leader+TM+TM+TM->

■ **GCF_900163685.1; Corynebacterium glutamicum; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA_002157835.1; Mycobacterium dioxanotrophicus; counts= 1; multicellularity status: FALSE**

- TM+DUF4190+TM->polar_leader+TM+TM+TM->PSE->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->TM+DUF4190+TM+PknH_C->TM+DUF4190+TM+PknH_C->TM+DUF4190+TM+PknH_C->

■ **GCF_900143625.1; Nocardiopsis sp. JB363; counts= 1; multicellularity status: TRUE**

- TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->

■ **GCF_900155535.1; Corynebacterium urinapleomorphum; counts= 1; multicellularity status: FALSE**

- Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA_002160935.1; Drancourtella sp. An12; counts= 1; multicellularity status: FALSE**

- TM+vWA(canonical)+YtKA-like+IG-like+TM+??->Tubulin+coiled_coil+??->?->?->ZnR+insert+ZnR+DO-GTPase2.2+ZnR->GAP1-N2+GAP1-M+GAP1-C*->Pkinase->

■ **GCA_002160755.1; Lachnoclostridium sp. An14; counts= 1; multicellularity status: NA**

- Tubulin+coiled_coil+??->Tubulin+coiled_coil+??->?->??->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+TM+GAP1-C+TM+TM+TM*->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->

■ **GCA_002159835.1; Blautia sp. An249; counts= 1; multicellularity status: FALSE**

- Tubulin+coiled_coil+??->Tubulin+coiled_coil+??->?->?->ZnR+insert+ZnR+DO-GTPase2.2+??->GAP1-N2+GAP1-M+GAP1-C*->?->?->Pkinase->

■ **GCA_002160435.1; Pseudoflavonifractor sp. An176; counts= 1; multicellularity status: FALSE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_002161835.1; Brevibacillus brevis; counts= 1; multicellularity status: FALSE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF_002161865.1; Paenibacillus apiarius; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF_004001005.1; Paenibacillus thiaminolyticus; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_002165735.1; Rhodococcus sp. NCIMB 12038; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA_002188345.1; Streptomyces sp. CS057; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_002188355.1; Streptomyces sp. CS227; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_002189105.1; Saccharibacillus sp. O16; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->?->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->?->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_002192415.1; Paenibacillus donghaensis; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA__900177675.1; Bacillus sp. OV166; counts= 1; multicellularity status: NA**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF__900143175.1; Xanthomonas retroflexus; counts= 1; multicellularity status: FALSE**

- GAP2->DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->

■ **GCA__002198105.1; Mycolicibacterium peregrinum; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->TM+DUF4190+TM+PknH_C->TM+DUF4190+TM+PknH_C->

■ **GCA__002205895.1; Saccharibacillus sp. O23; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->?->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF__900188525.1; Paenibacillus sp. St-s; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA__900187925.1; Streptomyces sp. PgraA7; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCF__900188505.1; Paenibacillus elgii; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->?->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+Cadherin-like*->

■ **GCA__002215235.1; Rhodococcus sp. BUPNP1; counts= 1; multicellularity status: TRUE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA__002215075.1; Brevibacillus formosus; counts= 1; multicellularity status: FALSE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA__002091955.1; Rhodococcus sp. 1168; counts= 1; multicellularity status: TRUE**

- GrpE->HSP70->TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->??->HSP70->

■ **GCA__900091445.1; Micromonospora echinofusca; counts= 1; multicellularity status: TRUE**

- TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->

■ **GCF__002217715.1; Streptomyces sp. SS07; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__900188005.1; Actinoplanes regularis; counts= 1; multicellularity status: TRUE**

- HSP70->TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->TPR_region+CASPASE->?->||<-CASPASE+low_complexity

■ **GCF__900188375.1; Geodermatophilus pulveris; counts= 1; multicellularity status: TRUE**

- Pkinase+TM->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->Pkinase+low_complexity->

■ **GCA__900188105.1; Actinomadura mexicana; counts= 1; multicellularity status: TRUE**

- GrpE->HSP70->TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM->

■ **GCA__900188445.1; Actinomadura meyerae; counts= 1; multicellularity status: TRUE**

- GrpE->HSP70->TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM->

■ **GCA__002224835.1; Paenibacillus sp. SSG-1; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA__900107795.1; Chitinophaga terrae Kim and Jung 2007; counts= 1; multicellularity status: TRUE**

- TIR+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA__900067065.1; Eubacteriaceae bacterium CHKCI005; counts= 1; multicellularity status: NA**

- TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->?->HSP70->HSP70+vWA(canonical)->DnaJ+DnaJ+ZnR+ZnR+coiled_coil+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__900109175.1; Pseudomonas linyingensis; counts= 1; multicellularity status: FALSE**

- GAP2->DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->

■ **GCA__900110825.1; Mycobacterium; counts= 1; multicellularity status: FALSE**

- HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->??+DO-GTPase2.2->

■ **GCA__001245615.1; Mycolicibacterium neworleansense; counts= 1; multicellularity status: FALSE**

- HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->??+DO-GTPase2.2->

■ **GCA__900100345.1; Paenibacillus tianmuensis; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->?->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+Cadherin-like*->

■ **GCA__900099765.1; Paenibacillus typhae; counts= 1; multicellularity status: TRUE**

- ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA__900103525.1; Bacillus sp. OK048; counts= 1; multicellularity status: NA**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA__900107875.1; Paenibacillus sp. 276b; counts= 1; multicellularity status: TRUE**

- TM+TM+TM+vWA+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C+polar_tail*->

■ **GCA__900110315.1; Paenibacillus sophorae; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA__900109125.1; Paenibacillus sp. 181mfcol5.1; counts= 1; multicellularity status: TRUE**

- Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C+polar_tail*->

■ **GCF__900110055.1; Paenibacillus sp. OK076; counts= 1; multicellularity status: TRUE**

- TM+TM+TM+vWA+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C+polar_tail*->

■ **GCA__900109305.1; Paenibacillus sp. cl141a; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA__900102085.1; Paenibacillus polysaccharolyticus; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA__900114615.1; Pelosinus propionicus; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA__900101205.1; Paenibacillus sp. OK060; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA__900113065.1; Aureimonas phyllosphaerae; counts= 1; multicellularity status: FALSE**

- GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->

■ **GCF__900109515.1; Paenibacillus sp. OK003; counts= 1; multicellularity status: TRUE**

- TM+TM+TM+vWA+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C+polar_tail*->

■ **GCF__900095775.1; Paenibacillus amylolyticus; counts= 1; multicellularity status: TRUE**

- Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C+polar_tail*->

■ **GCF__900101225.1; Paenibacillus sp. CF095; counts= 1; multicellularity status: TRUE**

- Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C+polar_tail*->

■ **GCA__900114475.1; Paenibacillus sp. 1__12; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+Cadherin-like*->

■ **GCA__900102215.1; Fontibacillus panacisegetis; counts= 1; multicellularity status: FALSE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA__001536285.1; Frankia sp. G2; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C+ZnR+DO-GTPase2*->

■ **GCA__900091595.1; Micromonospora haikouensis; counts= 1; multicellularity status: TRUE**

- GrpE->HSP70->TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->

■ **GCF__900114385.1; Geodermatophilus ruber; counts= 1; multicellularity status: TRUE**

- Pkinase+TM->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->

■ **GCF__900104025.1; Geodermatophilus sp. DSM 45219; counts= 1; multicellularity status: TRUE**

- Pkinase+TM->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->||<-?<-?||?->Pkinase+low_complexity->

■ **GCA__900101685.1; Alloactinosynnema iranicum; counts= 1; multicellularity status: TRUE**

- GrpE->HSP70->TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->?->||<-?<-?<-HSP70

■ **GCF__900111115.1; Giesbergeria anulus; counts= 1; multicellularity status: FALSE**

- GAP2->DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->

■ **GCA__900105385.1; Microlunatus soli; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->HSP70_domain_1->

■ **GCA__900116615.1; Algoriphagus locisalis; counts= 1; multicellularity status: FALSE**

- GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->EAD1+Trypsin->?->??+EAD1->

■ **GCA__900103445.1; Methylobacterium phyllostachyos; counts= 1; multicellularity status: TRUE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA__900113225.1; Mitsuaria sp. PDC51; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA__900113665.1; Planctomicrobium piriforme; counts= 1; multicellularity status: TRUE**

- ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+TM+GAP1-C*->??+TM+??+beta-rich??->?->GYF+GYF+ZnR+TM+TM+TM->

■ **GCF__900101405.1; Bradyrhizobium sp. R5; counts= 1; multicellularity status: TRUE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA__900114075.1; Brevibacillus sp. OK042; counts= 1; multicellularity status: FALSE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA__900111995.1; Collimonas sp. OK607; counts= 1; multicellularity status: FALSE**

- GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->

■ **GCA__900108985.1; Achromobacter sp. NFACC18-2; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA__900092135.1; Raineyella antarctica; counts= 1; multicellularity status: TRUE**

- ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+low_complexity*->

■ **GCA__900114325.1; Rhodanobacter glycinis; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCF__900111175.1; Actinokineospora terrae; counts= 1; multicellularity status: TRUE**

- CASPASE+TPR_region->?->GAP1-N2+GAP1-M*->

■ **GCA__900099715.1; Ruminococcaceae bacterium YRB3002; counts= 1; multicellularity status: NA**

- HSP70->HSP70+??->DnaJ+DnaJ+ZnR+ZnR+coiled_coil+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->

■ **GCF__900101545.1; Variovorax sp. CF079; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA__003635025.1; Saccharopolyspora antimicrobica; counts= 1; multicellularity status: TRUE**

- GrpE->HSP70->TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->PSE->?->?->||<-?<-?<-HSP70<-unknown+CASPASE

■ **GCA__900106995.1; Saccharopolyspora shandongensis; counts= 1; multicellularity status: TRUE**

- GrpE->HSP70->TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->HSP70->vWA(canonical)->

■ **GCA__003053965.1; Saccharopolyspora; counts= 1; multicellularity status: TRUE**

- GrpE->HSP70->TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->PSE->?->?->||<-?<-?<-HSP70<-unknown+CASPASE

■ **GCF__900101695.1; Pseudomonas sp. UC 17F4; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA__900115295.1; Sphingomonas sp. OK281; counts= 1; multicellularity status: FALSE**

- GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA__900092005.1; Streptomyces sp. Cmuel-A718b; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__002797835.1; Streptomyces; counts= 1; multicellularity status: TRUE**

- TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->PSE->vWA(canonical)->PP2C->Pkinase+ZnR+beta-rich->

■ **GCA__900091765.1; Streptomyces; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__900091725.1; Streptomyces sp. DvalAA-43; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__900091905.1; Streptomyces sp. OspMP-M43; counts= 1; multicellularity status: TRUE**

- HSP70_domain_2+low_complexity+domain_betaX->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__900091995.1; Streptomyces sp. MnatMP-M17; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__900090065.1; Streptomyces sp. OspMP-M45; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__900090075.1; Streptomyces sp. MnatMP-M77; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__900091775.1; Streptomyces sp. ScaeMP-e83; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__900105515.1; Streptomyces sp. 2131.1; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__900101975.1; Streptomyces sp. 136MFCol5.1; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_900090085.1; Streptomyces sp. Ncost-T6T-1; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_900091845.1; Streptomyces sp. SolWspMP-5a-2; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->vWA(canonical)->PP2C->Pkinase+ZnR+beta-rich->

■ **GCA_900091885.1; Streptomyces sp. ScaeMP-6W; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_900091955.1; Streptomyces sp. Ncost-T10-10d; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_900090135.1; Streptomyces sp. LaPpAH-199; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_900103585.1; Streptomyces sp. cf386; counts= 1; multicellularity status: TRUE**

- TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM->vWA(canonical)->PP2C->Pkinase+ZnR+beta-rich->

■ **GCA_900116325.1; Streptomyces sp. ok210; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_002234615.1; Paenibacillus rigui; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+Cadherin-like*->

■ **GCA_002240055.1; Leptotrichia sp. oral taxon 498; counts= 1; multicellularity status: TRUE**

- TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->?->HSP70->HSP70+vWA(canonical)->DnaJ+DnaJ+ZnR+ZnR+coiled_coil+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_002240415.1; Paenibacillus kribbensis; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF_002242735.1; Streptomyces sp. 2R; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_002245895.1; Rhodococcus sp. OK302; counts= 1; multicellularity status: TRUE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA_002250525.1; Propionibacteriaceae bacterium NML 150272; counts= 1; multicellularity status: NA**

- GrpE->HSP70->TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->??->?->?->?->?->HSP70->

■ **GCA_002250625.1; Propionibacteriaceae bacterium NML 130396; counts= 1; multicellularity status: NA**

- TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA_002251155.1; Streptomyces sp. FBKL.4005; counts= 1; multicellularity status: TRUE**

- TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM->vWA(canonical)->PSE->||<-PSE||Pkinase+ZnR+beta-rich->

■ **GCA_002250475.1; Propionibacteriaceae bacterium NML 160184; counts= 1; multicellularity status: NA**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA_002250565.1; Propionibacteriaceae bacterium NML 150081; counts= 1; multicellularity status: NA**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA_002257645.1; Paenibacillus sp. XY044; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->?->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_002259035.1; Rhodococcus; counts= 1; multicellularity status: TRUE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA_002259605.1; Pseudoscardovia radai; counts= 1; multicellularity status: FALSE**

- TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->GrpE->HSP70->DnaJ+DnaJ+ZnR+ZnR+coiled_coil+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_002259645.1; Bifidobacterium tissieri; counts= 1; multicellularity status: FALSE**

- TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->GrpE->HSP70->HSP70+vWA(canonical)->DnaJ+DnaJ+ZnR+ZnR+coiled_coil+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->

■ **GCF_002259955.1; Brevibacillus laterosporus; counts= 1; multicellularity status: FALSE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_002260685.1; Nocardiopsis dassonvillei; counts= 1; multicellularity status: TRUE**

- TPR_containing_alpha_helical+Fibronectin-like_repeats+extended_insert+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->

■ **GCA_002264385.1; Paenibacillus sp. VTT E-133280; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_002264395.1; Paenibacillus sp. VTT E-133291; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_002264345.1; Paenibacillus odorifer; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_002262935.1; Bacillus sp. SA5d-4; counts= 1; multicellularity status: NA**

- PIN+WG_repeats+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->

■ **GCF_002264305.1; Paenibacillus taichungensis; counts= 1; multicellularity status: TRUE**

- ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_002271635.1; Bacillus circulans; counts= 1; multicellularity status: FALSE**

- GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_002272715.1; Paenibacillus sp. 7516; counts= 1; multicellularity status: TRUE**

- Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C+polar_tail*->

■ **GCA__002271985.1; Bacillus circulans; counts= 1; multicellularity status: FALSE**

- GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA__002276415.1; Paenibacillus sp. 7523-1; counts= 1; multicellularity status: TRUE**

- Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C+polar_tail*->

■ **GCA__002277955.1; Thermogutta terrifontis; counts= 1; multicellularity status: TRUE**

- ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->??+TM+??+beta-rich??->GYF+GYF+TM+TM+TM->

■ **GCF__002286935.1; Bifidobacterium criceti; counts= 1; multicellularity status: FALSE**

- TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->GrpE->HSP70->HSP70+vWA(canonical)->DnaJ+DnaJ+ZnR+ZnR+coiled_coil+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__002286725.1; Pseudomonas indica; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA__002288075.1; Streptomyces sp. CLI2509; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__002289305.1; Streptomyces albidoflavus; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__002292625.1; Mycobacterium chimaera; counts= 1; multicellularity status: FALSE**

- TM+DUF4190+TM->TM+DUF4190+TM->polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP__unknown1+TM+TM+GAP__unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C(frag)*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA__002303875.1; Rhodococcus erythropolis; counts= 1; multicellularity status: TRUE**

- GrpE->HSP70->TPR__containing__alpha__helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->??->HSP70->vWA(canonical)->

■ **GCA__002317035.1; Streptomyces albidoflavus; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__002317005.1; Streptomyces albidoflavus; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__002318995.1; Shewanella algae; counts= 1; multicellularity status: FALSE**

- GAP1-N1+GAP1-M+GAP1-C+EAD1*->SLATT->

■ **GCA__002332445.1; Brevibacterium linens; counts= 1; multicellularity status: FALSE**

- TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP__unknown1+TM+TM+GAP__unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA__002332325.1; Brevibacterium; counts= 1; multicellularity status: FALSE**

- GrpE->HSP70->TPR__containing__alpha__helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->

■ **GCA__900221035.1; Streptomyces sp. 2323.1; counts= 1; multicellularity status: TRUE**

- TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->PSE->vWA(canonical)->PP2C->Pkinase+ZnR+beta-rich->

■ **GCA__002351405.1; Corynebacterium accolens; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->polar_leader+TM+TM+TM->

■ **GCA__002356095.1; Pseudomonas putida; counts= 1; multicellularity status: FALSE**

- GAP2->DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->

■ **GCF__002355155.1; Corynebacterium glutamicum; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA__002382885.1; Streptomyces sp. WZ.A104; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__002407025.1; Paenibacillus lautus; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA__002412145.1; Brevibacillus laterosporus; counts= 1; multicellularity status: FALSE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA__900230175.1; Salinibacterium xinjiangense; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCF__900221045.1; Paenibacillus sp. RU26A; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA__900215145.1; Geodermatophilus sabuli; counts= 1; multicellularity status: TRUE**

- Pkinase+TM->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->?->||<-?<-?||?->Pkinase+low_complexity->

■ **GCA__003268965.1; Streptomyces microflavus; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__002531555.1; Sinorhizobium sp. BJ1; counts= 1; multicellularity status: TRUE**

- Calcineurin+GAPEAD1->GAP2->DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA__002531955.1; Rhizobium sp. M10; counts= 1; multicellularity status: TRUE**

- Calcineurin+GAPEAD1->GAP2->DO-GTPase2.1->PSE->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA__002529455.1; Glycomyces fuscus; counts= 1; multicellularity status: TRUE**

- TPR_containing_alpha_helical+Fibronectin-like_repeats+extended_insert+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+ZnR+ZnR+DO-GTPase2.2->

■ **GCF__002551245.1; Streptomyces sp. rh34; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCF__002551335.1; Streptomyces sp. ms184; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

- **GCF_002551135.1; Streptomyces sp. st140; counts= 1; multicellularity status: TRUE**
  - GAP1-N2+GAP1-M+GAP1-C*->
- **GCF_002551105.1; Streptomyces sp. st170; counts= 1; multicellularity status: TRUE**
  - GAP1-N2+GAP1-M+GAP1-C*->
- **GCF_002551045.1; Streptomyces sp. wa1063; counts= 1; multicellularity status: TRUE**
  - TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM->vWA(canonical)->PP2C->Pkinase+ZnR+beta-rich->
- **GCF_002551215.1; Streptomyces sp. rh207; counts= 1; multicellularity status: TRUE**
  - GAP1-N2+GAP1-M+GAP1-C*->
- **GCF_002551345.1; Streptomyces sp. ms115; counts= 1; multicellularity status: TRUE**
  - GAP1-N2+GAP1-M+GAP1-C*->
- **GCF_002551015.1; Streptomyces; counts= 1; multicellularity status: TRUE**
  - ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM->vWA(canonical)->PP2C->Pkinase+ZnR+beta-rich->
- **GCF_002551305.1; Streptomyces sp. or20; counts= 1; multicellularity status: TRUE**
  - GAP1-N2+GAP1-M+GAP1-C*->
- **GCF_002551375.1; Streptomyces sp. gb14; counts= 1; multicellularity status: TRUE**
  - GAP1-N2+GAP1-M+GAP1-C*->
- **GCF_002551435.1; Streptomyces sp. f150; counts= 1; multicellularity status: TRUE**
  - GAP1-N2+GAP1-M+GAP1-C*->
- **GCF_002551415.1; Streptomyces sp. f51; counts= 1; multicellularity status: TRUE**
  - GAP1-N2+GAP1-M+GAP1-C*->
- **GCF_002551185.1; Streptomyces sp. sk226; counts= 1; multicellularity status: TRUE**
  - GAP1-N2+GAP1-M+GAP1-C*->
- **GCF_002551235.1; Streptomyces sp. rh195; counts= 1; multicellularity status: TRUE**
  - GAP1-N2+GAP1-M+GAP1-C*->
- **GCF_002551475.1; Streptomyces sp. b62; counts= 1; multicellularity status: TRUE**
  - GAP1-N2+GAP1-M+GAP1-C*->
- **GCF_002551145.1; Streptomyces sp. st115; counts= 1; multicellularity status: TRUE**
  - GAP1-N2+GAP1-M+GAP1-C*->
- **GCA_002556545.1; Streptomyces formicae; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->vWA(canonical)->PP2C->Pkinase+ZnR+beta-rich->||<-TPR_containing_alpha_helical+Fibronectin-like_repeats

■ **GCA_002565135.1; Bacillus sp. AFS076308; counts= 1; multicellularity status: NA**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C*->

■ **GCF_002573715.1; Paenibacillus sp. EZ-K15; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->?->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF_002551295.1; Streptomyces sp. or3; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCF_002551065.1; Streptomyces sp. t99; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCF_002551175.1; Streptomyces sp. st77; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_002584635.1; Bacillus sp. AFS031507; counts= 1; multicellularity status: NA**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_002585305.1; Bacillus sp. AFS037270; counts= 1; multicellularity status: NA**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_900090175.1; Streptomyces sp. LamerLS-316; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_002727115.1; Streptomyces cinnamoneus; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCF_002688625.1; Xanthomonas citri; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->GAP2->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_900090185.1; Streptomyces sp. AmelKG-D3; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_002223215.2; Burkholderia sp. AU18528; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->DO-GTPase2.1(fragment)->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCF_002705925.1; Mycobacterium kansasii; counts= 1; multicellularity status: FALSE**

- TM+DUF4190+TM->polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCF_900232885.1; Anaeromassilibacillus sp. Marseille-P4683; counts= 1; multicellularity status: FALSE**

- TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->?->HSP70->HSP70+vWA(canonical)->DnaJ+DnaJ+ZnR+ZnR+coiled_coil+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->

■ **GCF_002735705.1; Janthinobacterium sp. BJB426; counts= 1; multicellularity status: FALSE**

- GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->

■ **GCF_002735695.1; Chitinimonas sp. BJB300; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_002736145.1; Collinsella aerofaciens; counts= 1; multicellularity status: FALSE**

- TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->GrpE->HSP70->HSP70+vWA(canonical)->DnaJ+DnaJ+ZnR+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_002741035.1; Paenibacillus sp. BIHB4019; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_002754245.1; Chryseobacterium sp. 52; counts= 1; multicellularity status: FALSE**

- GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->??+EAD1->EAD1+Trypsin->

■ **GCF_002750415.1; Paenibacillus polymyxa; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_002775065.1; Corynebacterium striatum; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->polar_leader+TM+TM+TM->

■ **GCA_002794355.1; Pseudorhodobacter sp. MZDSW-24AT; counts= 1; multicellularity status: FALSE**

- AB_hydrolase+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_002795805.1; Mariprofundus aestuarium; counts= 1; multicellularity status: TRUE**

- GAP2->ZnR(fragment)+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->PNP_UDP_1+EAD1->

■ **GCA_002797655.1; Streptomyces sp. CNZ306; counts= 1; multicellularity status: TRUE**

- PP2C->Pkinase->?->?->?->HSP70_domain_2+low_complexity+domain_betaX->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->

■ **GCA_002802945.1; Streptomyces sp. TSRI0384-2; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA_002798385.1; Mycolicibacterium goodii; counts= 1; multicellularity status: FALSE**

- HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->??+DO-GTPase2.2->

■ **GCA_002803315.1; Paenibacillus sp. GM1FR; counts= 1; multicellularity status: TRUE**

- Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C+polar_tail*->

■ **GCA_002803325.1; Paenibacillus sp. GM2FR; counts= 1; multicellularity status: TRUE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA_002256345.1; Bradyrhizobium sp. UASWS1016; counts= 1; multicellularity status: TRUE**

- DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_002803175.1; Streptomyces sp. CB02613; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__002804085.1; Corynebacterium striatum; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->polar_leader+TM+TM+TM->

■ **GCF__002813225.1; Streptomyces sp. Ag109_G2-1; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__002844215.1; Streptomyces sp. EAG2; counts= 1; multicellularity status: TRUE**

- GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__002846895.1; Bifidobacterium asteroides; counts= 1; multicellularity status: FALSE**

- TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->?->HSP70->HSP70+vWA(canonical)->DnaJ+DnaJ+ZnR+ZnR+coiled_coil+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__003335365.1; Brevibacterium aurantiacum; counts= 1; multicellularity status: FALSE**

- TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->

■ **GCA__900169375.1; Brevibacterium sp. Mu109; counts= 1; multicellularity status: FALSE**

- GrpE->HSP70->TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->

■ **GCF__002860365.1; Bifidobacterium parmae; counts= 1; multicellularity status: FALSE**

- TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->GrpE->HSP70->HSP70+vWA(canonical)->DnaJ+DnaJ+ZnR+ZnR+coiled_coil+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__002860255.1; Bacillus cucumis; counts= 1; multicellularity status: FALSE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C*->

■ **GCA__002865525.1; Brevibacillus laterosporus; counts= 1; multicellularity status: FALSE**

- TM+vWA(canonical)+YtKA-like+TM+??->Tubulin+coiled_coil+??->Tubulin+coiled_coil+HTH?+??->TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail->Fibronectin-like_repeats+??->ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR->GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCF__900199695.1; Clostridiales bacterium mt7; counts= 1; multicellularity status: FALSE**

- GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->

■ **GCA__002861325.1; Corynebacterium riegelii; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->?->??+DO-GTPase2.2->?->||<-?<-?<-HSP70

■ **GCA__002861385.1; Corynebacterium aurimucosum; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->polar_leader+TM+TM+TM->

■ **GCA__001742065.1; Psychrobacter sp. Choline-02u-9; counts= 1; multicellularity status: FALSE**

- PNP_UDP_1+EAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->

■ **GCA__002871735.1; Corynebacterium aurimucosum; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->beta-rich+vWA(canonical)->??+DO-GTPase2.2->polar_leader+TM+TM+TM->

■ **GCA__002871875.1; Brevibacterium paucivorans; counts= 1; multicellularity status: FALSE**

- polar_leader+TM+TM+TM->TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail->Tubulin+alpha_helical+??+??->GAP_unknown1+TM+TM+GAP_unknown2->HRDC-like?+Fibronectin-like_repeats->GAP1-N2+GAP1-M+GAP1-C*->?->??+DO-GTPase2.2->?->||<-?<-?<-TM+TM+vWA(canonical)+TM<-TM+TM+vWA(canonical)+TM

■ **GCA_002871975.1; Actinomyces graevenitzii; counts= 1; multicellularity status: TRUE**

- GrpE->HSP70->TPR_containing_alpha_helical+Fibronectin-like_repeats->ZnR+ZnR+DO-GTPase2.2->GAP1-N2+GAP1-M+GAP1-C*->TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->

■ **GCA_002890895.1; Pseudomonas stutzeri; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_002892225.1; Phaeobacter inhibens; counts= 1; multicellularity status: FALSE**

- AB_hydrolase+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_002892085.1; Phaeobacter inhibens; counts= 1; multicellularity status: FALSE**

- AB_hydrolase+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCF_002893865.1; Vibrio campbellii; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_002904025.1; Pectobacterium carotovorum; counts= 1; multicellularity status: FALSE**

- GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_002925765.1; Aeromonas jandaei; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_002943465.1; Rhodoferax sp. TS-BS-61-7; counts= 1; multicellularity status: FALSE**

- GAP2->DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->

■ **GCA_002981255.1; Burkholderia multivorans; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCF_003002825.1; Spirosoma oryzae; counts= 1; multicellularity status: TRUE**

- GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->PNP_UDP_1+EAD1->

■ **GCA_003008595.1; Simplicispira sp. SC1-8; counts= 1; multicellularity status: NA**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->PSE->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCF_001008325.2; Leptospira santarosai; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->PSE->PSE->ZnR+DO-GTPase2.1->DO-GTPase1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_003049865.1; Vibrio splendidus; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCA_003063455.1; Limnohabitans parvus; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->PSE->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCF_003057255.1; Klebsiella aerogenes; counts= 1; multicellularity status: FALSE**

- Calcineurin+GAPEAD1->GAP2->ZnR+DO-GTPase2.1->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C*->

■ **GCF_002168275.1; Herrania umbratica; counts= 1; multicellularity status: NA**

- GAP1-N2+GAP1-M+GAP1-C(frag)*->

NucA systems

- **GCF_000503075.1; Mesorhizobium sp. LSHC422A00; counts= 2; multicellularity status: TRUE**
  - EAD1+Trypsin+TM+NPLC_P60*->
  - EAD1+Trypsin+TM+TM+disordered*->
- **GCF_000503035.1; Mesorhizobium sp. LSHC412B00; counts= 2; multicellularity status: TRUE**
  - EAD1+Trypsin+TM+NPLC_P60*->
  - Trypsin+NucA->EAD1+Trypsin*->EADunk+helical_domain->low_complexity+TM+NucA(inactive)+iSvmX2->
- **GCF_000344805.1; Bradyrhizobium oligotrophicum; counts= 2; multicellularity status: TRUE**
  - calcineurin(low_complexity_insert)->Trypsin+EAD1+coiled_coil*->wHTH+TM+PPRs+TPRs->
  - EAD1+Trypsin->*EAD7+helical_domain*->STAND+TM+TPRs->
- **GCF_900113985.1; Phyllobacterium sp. CL33Tsu; counts= 2; multicellularity status: TRUE**
  - EAD1+Trypsin*->||<-?<-?<-Ploop_NTPase+TM+??
  - IG-like+EAD1*->
- **GCF_000686005.1; Phyllobacterium sp. UNC302MFCol5.2; counts= 2; multicellularity status: TRUE**
  - EAD1+Trypsin*->||<-?<-?<-Ploop_NTPase+TM+??
  - IG-like+EAD1*->
- **GCF_000970465.2; Devosia insulae; counts= 2; multicellularity status: FALSE**
  - EAD1+Trypsin*->
  - Trypsin->EAD1+lysozyme->EAD1+Trypsin->*EAD1+helical_domain*->low_complexity+TM+NucA(inactive)+iSvmX2->Trypsin+NucA->
- **GCF_000502815.1; Mesorhizobium sp. LSJC269B00; counts= 2; multicellularity status: TRUE**
  - EAD1+Trypsin*->?->STAND+wHTH+TPRs->
  - Trypsin+NucA->EAD1+Trypsin*->EADunk+helical_domain->low_complexity+TM+NucA(inactive)+iSvmX2->
- **GCF_001043915.1; Methylobacterium aquaticum; counts= 1; multicellularity status: TRUE**
  - EAD1+Trypsin+EAD1+STAND*->low_complexity+TM+NucA(inactive)+iSvmX2->||<-?<-CASPASE+??||Trypsin->
- **GCA_000503035.1; Mesorhizobium sp. LSHC412B00; counts= 1; multicellularity status: TRUE**
  - EAD1+Trypsin+TM+NPLC_P60*->
- **GCF_900112185.1; Bosea sp. DSM 18164; counts= 1; multicellularity status: TRUE**
  - <-Trypsin_2+NucA+Calcineurin<-?<-?||EAD1+Trypsin*->?->??+TM+??+??+iSvmX2->

- **GCF_000022085.1; Methylobacterium nodulans; counts= 1; multicellularity status: TRUE**
  - lysozyme+peptidase_MD->||<-Trypsin+NucA||EAD1+Trypsin*->?->??+TM+SH3+iSvmX2->
- **GCF_000015165.1; Bradyrhizobium sp. BTAi1; counts= 1; multicellularity status: TRUE**
  - EAD1+Trypsin*->?->Ploop_NTPase+TM+??->
- **GCF_001296055.1; Novosphingobium sp. AAP93; counts= 1; multicellularity status: FALSE**
  - EAD1+Trypsin*->?->AAA_ATPase(inactive)+TM+SH3+iSvmX2->||<-PSE||?->Trypsin+NucA->
- **GCF_900117425.1; Novosphingobium sp. NDB2Meth1; counts= 1; multicellularity status: FALSE**
  - EAD1+Trypsin*->?->AAA_ATPase(inactive)+TM+SH3+iSvmX2->||<-PSE||?->Trypsin+NucA->
- **GCF_000985995.1; Neorhizobium galegae; counts= 1; multicellularity status: FALSE**
  - <-Trypsin+NucA||lysozyme+PGBD->EAD1+Trypsin*->EADunk+helical_domain->low_complexity+TM+NucA(inactive)+iSvmX2->GDSL->
- **GCF_001426195.1; Sphingomonas sp. Leaf339; counts= 1; multicellularity status: FALSE**
  - Trypsin+NucA->EAD1+Trypsin*->?->STAND+TM+iSvmX2->
- **GCF_001676615.1; Labrys sp. WJW; counts= 1; multicellularity status: NA**
  - EAD1+Trypsin*->EADunk+helical_domain->??+TM+??->
- **GCA_002858925.1; Caulobacter zeae; counts= 1; multicellularity status: FALSE**
  - EAD1+Trypsin*->?->||<-?<-?||Trypsin->
- **GCF_001624695.1; Labrenzia sp. OB1; counts= 1; multicellularity status: FALSE**
  - Trypsin_2+NucA+Subtilisin->Trypsin->bDLD2+Trypsin+STAND->STAND+wHTH+TPRs->EAD1+Trypsin*->?->low_complexity+Pentapeptide_repeats+TPRs->
- **GCF_000178815.2; Methylosinus; counts= 1; multicellularity status: TRUE**
  - subtilase->EAD1+Trypsin*->STAND+TM+TPRs->||<-PLD+PLD
- **GCF_002407205.1; Rhodobacter sp. CZR27; counts= 1; multicellularity status: FALSE**
  - <-GDSL<-lysozyme+PGBD||??+Trypsin->EAD1+Trypsin*->EADunk+helical_domain->low_complexity+TM+NucA(inactive)+iSvmX2->
- **GCF_002844445.1; Rhodobacter azotoformans; counts= 1; multicellularity status: FALSE**
  - <-GDSL<-lysozyme+PGBD||??+Trypsin->EAD1+Trypsin*->EADunk+helical_domain->low_complexity+TM+NucA(inactive)+iSvmX2->
- **GCF_000016405.1; Rhodobacter sphaeroides; counts= 1; multicellularity status: FALSE**
  - <-GDSL<-lysozyme+PGBD||??+Trypsin->EAD1+Trypsin*->EADunk+helical_domain->low_complexity+TM+NucA(inactive)+iSvmX2->
- **GCF_900104165.1; Phyllobacterium sp. YR620; counts= 1; multicellularity status: TRUE**
  - EAD1+Trypsin*->||<-?<-?<-Ploop_NTPase+TM+??
- **GCF_000376105.1; Asticcacaulis benevestitus; counts= 1; multicellularity status: FALSE**
  - Trypsin+NucA->?->EAD1+Trypsin->*EAD1+Trypsin*->?->AAA_ATPase(inactive)+TM+SH3+iSvmX2->

- **GCA_900106665.1; Paracoccus sanguinis; counts= 1; multicellularity status: NA**
  - <-Trypsin+NucA||EAD1+Trypsin*->?->??+TM+SH3+iSvmX2->GDSL->
- **GCF_001672445.1; Mesorhizobium sp. WSM3873; counts= 1; multicellularity status: TRUE**
  - <-Trypsin<-subtilase<-?<-?<-??+GDSL<-PSE||EAD1+Trypsin*->?->STAND+wHTH+TPRs->
- **GCF_000763825.1; Paracoccus sanguinis; counts= 1; multicellularity status: NA**
  - <-Trypsin+NucA||EAD1+Trypsin*->
- **GCF_002091475.1; Sphingomonas azotifigens; counts= 1; multicellularity status: FALSE**
  - Trypsin+NucA->?->?->AAA_ATPase(inactive)+TM+SH3+iSvmX2->?->EAD1+Trypsin*->
- **GCA_000239775.2; Bradyrhizobium sp. ORS 375; counts= 1; multicellularity status: TRUE**
  - EAD1+Trypsin->*EAD1+??+Ploop_NTPase+??->*
- **GCF_000261805.1; Bradyrhizobium yuanmingense; counts= 1; multicellularity status: TRUE**
  - EAD1+Trypsin*->||<-EAD5+Trypsin<-STAND+wHTH+TPRs<-?<-PLD+PLD<-Trypsin
- **GCF_000233995.1; Mesorhizobium amorphae; counts= 1; multicellularity status: TRUE**
  - Trypsin+NucA->EAD1+Trypsin*->EADunk+helical_domain->
- **GCF_000502255.1; Mesorhizobium sp. L103C120A0; counts= 1; multicellularity status: TRUE**
  - Trypsin+NucA->EAD1+Trypsin*->EADunk+helical_domain->low_complexity+TM+NucA(inactive)+iSvmX2->
- **GCF_000502295.1; Mesorhizobium sp. L103C565B0; counts= 1; multicellularity status: TRUE**
  - Trypsin+NucA->EAD1+Trypsin*->PSE->EADunk+helical_domain->low_complexity+TM+NucA(inactive)+iSvmX2->
- **GCF_000502615.1; Mesorhizobium sp. LNJC405B00; counts= 1; multicellularity status: TRUE**
  - Trypsin+NucA->EAD1+Trypsin*->EADunk+helical_domain->low_complexity+TM+NucA(inactive)+iSvmX2->
- **GCF_000502755.1; Mesorhizobium sp. LSJC264A00; counts= 1; multicellularity status: TRUE**
  - Trypsin+NucA->EAD1+Trypsin*->EADunk+helical_domain->low_complexity+TM+NucA(inactive)+iSvmX2->
- **GCF_000502775.1; Mesorhizobium sp. LSJC265A00; counts= 1; multicellularity status: TRUE**
  - Trypsin+NucA->EAD1+Trypsin*->EADunk+helical_domain->low_complexity+TM+NucA(inactive)+iSvmX2->
- **GCF_000427585.1; Sinorhizobium meliloti; counts= 1; multicellularity status: TRUE**
  - GDSL+CASPASE->subtilase->?->EAD1+Trypsin*->
- **GCF_000502475.1; unclassified Mesorhizobium; counts= 1; multicellularity status: NA**
  - Trypsin+NucA->EAD1+Trypsin*->EADunk+helical_domain->low_complexity+TM+NucA(inactive)+iSvmX2->
- **GCF_000502555.1; unclassified Mesorhizobium; counts= 1; multicellularity status: NA**
  - Trypsin+NucA->EAD1+Trypsin*->EADunk+helical_domain->low_complexity+TM+NucA(inactive)+iSvmX2->

- **GCF_000502695.1; unclassified Mesorhizobium; counts= 1; multicellularity status: NA**
  - Trypsin+NucA->EAD1+Trypsin*->EADunk+helical_domain->low_complexity+TM+NucA(inactive)+iSvmX2->
- **GCF_000502795.1; unclassified Mesorhizobium; counts= 1; multicellularity status: NA**
  - NucA->EAD1+Trypsin*->EADunk+helical_domain->low_complexity+TM+NucA(inactive)+iSvmX2->
- **GCF_000502995.1; unclassified Mesorhizobium; counts= 1; multicellularity status: NA**
  - Trypsin+NucA->EAD1+Trypsin*->EADunk+helical_domain->low_complexity+TM+NucA(inactive)+iSvmX2->
- **GCF_000503155.1; unclassified Mesorhizobium; counts= 1; multicellularity status: NA**
  - Trypsin+NucA->EAD1+Trypsin*->EADunk+helical_domain->low_complexity+TM+NucA(inactive)+iSvmX2->
- **GCF_000502235.1; Mesorhizobium sp. L103C119B0; counts= 1; multicellularity status: TRUE**
  - Trypsin+NucA->EAD1+Trypsin*->EADunk+helical_domain->low_complexity+TM+NucA(inactive)+iSvmX2->
- **GCF_000284375.1; Bradyrhizobium japonicum; counts= 1; multicellularity status: TRUE**
  - calcineurin(low_complexity_insert)->Trypsin+EAD1+coiled_coil*->wHTH+TM+PPRs+TPRs->
- **GCF_000472985.1; Bradyrhizobium japonicum; counts= 1; multicellularity status: TRUE**
  - calcineurin(low_complexity_insert)->Trypsin+EAD1+coiled_coil*->wHTH+TM+PPRs+TPRs->
- **GCF_000773865.1; Bradyrhizobium japonicum; counts= 1; multicellularity status: TRUE**
  - calcineurin(low_complexity_insert)->Trypsin+EAD1+coiled_coil*->wHTH+TM+PPRs+TPRs->
- **GCF_001693485.1; Bradyrhizobium sp. LMTR 3; counts= 1; multicellularity status: TRUE**
  - calcineurin(low_complexity_insert)->Trypsin+EAD1+coiled_coil*->wHTH+TM+PPRs+TPRs->
- **GCF_001641335.1; Bradyrhizobium stylosanthis; counts= 1; multicellularity status: TRUE**
  - calcineurin(low_complexity_insert)->Trypsin+EAD1+coiled_coil*->wHTH+TM+PPRs+TPRs->
- **GCA_000344805.1; Bradyrhizobium oligotrophicum S58; counts= 1; multicellularity status: TRUE**
  - EAD1+Trypsin->EAD7+Lysozyme*->STAND+TM+TPRs->
- **GCF_000011365.1; Bradyrhizobium; counts= 1; multicellularity status: TRUE**
  - HNH+PNPase+EAD7*->
- **GCA_002200945.1; Mesorhizobium amorphae CCBAU 01583; counts= 1; multicellularity status: TRUE**
  - Trypsin->Trypsin->NucA->EAD1*->Trypsin->EAD1->EADunk+helical_domain->??+TM+??->NucA->
- **GCF_900188295.1; Paracoccus sediminis; counts= 1; multicellularity status: NA**
  - Trypsin->||<-?||EAD1+Trypsin-*>EAD1+STAND*->STAND+wHTH+TPRs->

EACC1 systems

- **GCF_000373585.1; Streptomyces sp. MspMP-M5; counts= 5; multicellularity status: TRUE**
  - ??->EACC1*->CASPASE+TPRs->
  - EACC1*->CASPASE+??+TM+TM->
  - EACC1*->CASPASE+TM+??->
  - EACC1*->CASPASE+TM+Beta_rich->
  - EACC1*->CASPASE+TM+BetaPropeller->
- **GCF_000504285.1; Actinospica robiniae; counts= 5; multicellularity status: TRUE**
  - EACC1*->
  - EACC1*->CASPASE+??->
  - EACC1*->CASPASE+Pkinase+TM?+??->
  - EACC1*->CASPASE+TPRs->
  - polar_lead?+TM+TM+TM+polar_tail?+low-complexity->??->EACC1*->CASPASE+TPRs->
- **GCA_001729485.1; Streptomyces lydicus; counts= 4; multicellularity status: TRUE**
  - EACC1*->CASPASE+??->
  - EACC1*->CASPASE+FGS_fold-domain->??->??->TM+TM+BaxI_1->?->NUDIX->
  - Glyoxalase->EACC1*->CASPASE+DnaJ_ZnR+DnaJ_ZnR+DnaJ_C->
  - polar_lead?+TM+TM+TM+polar_tail?+low-complexity->??->EACC1*->CASPASE+TPRs->
- **GCA_000698495.1; Streptomyces sp. NTK 937; counts= 4; multicellularity status: TRUE**
  - EACC1*->CASPASE+STAND+PBPB->
  - EACC1*->CASPASE+STAND+PBPB->
  - EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->
  - EACC1*->CASPASE+TPRs->
- **GCA_002846295.1; Streptomyces sp. 59; counts= 4; multicellularity status: TRUE**
  - EACC1*->?->CASPASE+STAND+polar_region+TM+BetaPropeller->TM+Acid_phosphat_B->
  - EACC1*->CASPASE+??+TM+TM+TM+TPRs->
  - EACC1*->CASPASE+BetaPropeller->
  - Pkinase+??->?->?->||<-?<-?||HATPase_c_2->EACC1*->CASPASE+??+SF1-helicase+Vsr(PDDEXK)?->
- **GCA_900107045.1; Amycolatopsis xylanica; counts= 4; multicellularity status: TRUE**
  - ??+TM+TM+??+TM->PBPB->EACC1*->CASPASE+TPRs->PknG_rubred+Pkinase+PknG_TPR->ZnR+PP2C->vWA+alpha-helical->
  - EACC1*->CASPASE+DnaJ_ZnR+DnaJ_ZnR+DnaJ_C->

- EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->
- GATase->ABC-ATPase+DUF4162->cNMP_cyclase+TM+TM+TM+TM+TM+TM->EACC1*->

■ **GCA_000349325.1; Streptomyces davaonensis; counts= 4; multicellularity status: TRUE**

- EACC1*->
- EACC1*->CASPASE+TM?+DUF3558+DUF3558->
- EACC1*->CASPASE+TM+TM+bPH_domain+TM+TM+bPH_domain+TM+TM->
- EAD2+VMAP-M0+CASPASE->EACC1*->

■ **GCF_000720135.1; Streptomyces sp. NRRL S-1022; counts= 4; multicellularity status: TRUE**

- EACC1*->
- EACC1*->CASPASE+low-complexity+BetaPropeller->
- EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->
- EACC1*->CASPASE+TM+TM+bPH_domain?->

■ **GCF_001613485.1; Nocardia rhamnosiphila; counts= 4; multicellularity status: TRUE**

- EACC1*->CASPASE+??+SF1-helicase+Vsr(PDDEXK)?->
- EACC1*->CASPASE+TPRs->
- EACC1*->CASPASE+TPRs->
- EACC1*->CASPASE+TPRs->

■ **GCF_000746395.1; Streptomyces mirabilis; counts= 4; multicellularity status: TRUE**

- ??->EACC1*->CASPASE+TM+TM+PBPB+vWA->
- EACC1*->CASPASE+Cpn60_TCP1->
- EACC1*->CASPASE+STAND+TPRs->
- polar_lead?+TM+TM+TM+polar_tail?+low-complexity->??->EACC1*->CASPASE+TPRs->

■ **GCA_001514065.1; Streptomyces antibioticus; counts= 4; multicellularity status: TRUE**

- EACC1*->CASPASE+STAND+BetaPropeller->
- EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->
- EACC1*->CASPASE+TM+TM+TM+TM+TM+TM->
- EACC1*->CASPASE+TPRs->

■ **GCF_002155975.1; Amycolatopsis kentuckyensis; counts= 4; multicellularity status: TRUE**

- EACC1*->
- EACC1*->CASPASE+TPRs->
- GATase->ABC-ATPase+DUF4162->cNMP_cyclase+TM+TM+TM+TM+TM+TM->EACC1*->
- PBPB->?->?->Aminotran_5+PAS_6+HTH_22->EACC1*->

■ **GCA_003173275.1; Streptomyces; counts= 4; multicellularity status: TRUE**

- EACC1*->
- EACC1*->CASPASE+??+SF1-helicase+Vsr(PDDEXK)?->
- EACC1*->CASPASE+Beta_rich_repeat->

- EACC1*->CASPASE+FGS_fold-domain->??->??->TM+TM+BaxI_1->?->NUDIX->

■ **GCA_002573955.1; Streptomyces sp. Ru87; counts= 4; multicellularity status: TRUE**

- EACC1*->
- EACC1*->CASPASE+TM?+Phytase-like->||<-DUF664
- low-complexity+HD+Tox-RelA+TGS+ACT->Pkinase+TPRs->EACC1*->CASPASE+TPRs->
- polar_lead?+TM+TM+TM+polar_tail?+low-complexity->??->EACC1*->CASPASE+TPRs->

■ **GCA_000494755.1; Actinoplanes friuliensis DSM 7358; counts= 3; multicellularity status: TRUE**

- EACC1*->
- EACC1*->CASPASE+??->
- EACC1*->CASPASE+DUF179->SIR2+??->??->

■ **GCA_002591335.1; Streptomyces malaysiensis; counts= 3; multicellularity status: TRUE**

- EACC1*->CASPASE+HisKA+HATPase_c->
- EACC1*->CASPASE+TM+??->
- TetR_N+TetR_C_6->EACC1*->CASPASE+low-complexity+TM+PBPB->

■ **GCA_000938975.1; Streptomyces iranensis; counts= 3; multicellularity status: TRUE**

- EACC1*->
- EACC1*->CASPASE+low-complexity+TM+PBPB->
- EACC1*->CASPASE+TM+??->

■ **GCA_001511815.1; Streptomyces reticuli; counts= 3; multicellularity status: TRUE**

- ??->??->EACC1*->CASPASE+??->
- AMP-binding+AMP-binding_C->AMP-binding+AMP-binding_C->EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->
- EACC1*->CASPASE+TM?+DUF3558+DUF3558->

■ **GCA_000388135.1; Amycolatopsis vancoresmycina DSM 44592; counts= 3; multicellularity status: TRUE**

- EACC1*->CASPASE+Cpn60_TCP1->
- GATase->ABC-ATPase+DUF4162->cNMP_cyclase+TM+TM+TM+TM+TM+TM->EACC1*->
- PBPB->?->?->Aminotran_5+PAS_6+HTH_22->EACC1*->CASPASE+??+TM+TM->||<-Glyco_trans_4_4+UDPGT

■ **GCA_000611795.1; Streptomyces sp. Tu 6176; counts= 3; multicellularity status: TRUE**

- EACC1*->
- EACC1*->
- TPRs->EACC1*->CASPASE+TPRs->

■ **GCA_001507455.1; Streptomyces albus subsp. albus; counts= 3; multicellularity status: TRUE**

- EACC1*->CASPASE+??->
- EACC1*->CASPASE+PBPB+vWA->
- EACC1*->CASPASE+TPRs->

■ **GCA_001866665.1; Streptomyces sp. MUSC 1; counts= 3; multicellularity status: TRUE**

- EACC1*->
- EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->
- Pkinase+TPRs->EACC1*->CASPASE+TPRs->

■ **GCA_001905885.1; Streptomyces sp. CB03234; counts= 3; multicellularity status: TRUE**

- EACC1*->
- EACC1*->
- FAD_binding_4+??+BBE->EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->

■ **GCA_002007125.1; Streptomyces tsukubensis; counts= 3; multicellularity status: TRUE**

- EACC1*->CASPASE+??+SF1-helicase+Vsr(PDDEXK)?->
- EACC1*->CASPASE+TPRs->Pkinase+??->
- low-complexity+HD+Tox-RelA+TGS+ACT->Pkinase+TPRs->EACC1*->CASPASE+TPRs->

■ **GCA_002754555.1; Streptomyces sp. 94; counts= 3; multicellularity status: TRUE**

- EACC1*->CASPASE+TM+??->
- EACC1*->CASPASE+TM+PBPI->
- EACC1*->CASPASE+TPRs+LysM+PG-binding->

■ **GCA_002846355.1; Streptomyces sp. GP55; counts= 3; multicellularity status: TRUE**

- EACC1*->CASPASE+??+STAND+??->
- EACC1*->CASPASE+DnaJ_ZnR+DnaJ_C+DnaJ_C+TM+TM->
- polar_lead?+TM+TM+TM+polar_tail?+low-complexity->??->EACC1*->CASPASE+TPRs->

■ **GCA_002846415.1; Streptomyces sp. TLI_146; counts= 3; multicellularity status: TRUE**

- EACC1*->
- EACC1*->CASPASE+low-complexity+BetaPropeller->
- low-complexity+HD+Tox-RelA+TGS+ACT->Pkinase+TPRs->EACC1*->CASPASE+TPRs->

■ **GCA_002934265.1; Actinokineospora auranticolor; counts= 3; multicellularity status: TRUE**

- EACC1*->CASPASE+TM+TM->TM+PBPB->
- EACC1*->CASPASE+TPRs->
- EACC1+CASPASE*->?->Phytase-like->

■ **GCA_900090095.1; Streptomyces sp. SceaMP-e96; counts= 3; multicellularity status: TRUE**

- EACC1*->CASPASE+Beta_rich_repeat->
- EACC1*->CASPASE+FGS_fold-domain->??->??->TM+TM+BaxI_1->?->NUDIX->
- EACC1*->TM+TM->

■ **GCA_900105945.1; Amycolatopsis tolypomycina; counts= 3; multicellularity status: TRUE**

- EACC1*->
- GATase->ABC-ATPase+DUF4162->cNMP_cyclase+TM+TM+TM+TM+TM+TM->EACC1*->
- PBPB->?->?->?->EACC1*->CASPASE+TM+TM->

- **GCA_900119165.1; Amycolatopsis australiensis; counts= 3; multicellularity status: TRUE**
  - EACC1*->CASPASE+TPRs->
  - MFS_1->||<-?||GATase->ABC-ATPase+DUF4162->cNMP_cyclase+TM+TM+TM+TM+TM+TM->EACC1->CASPASE+TM+TM+TM+TM->EACC1*->
  - MFS_1->||<-?||GATase->ABC-ATPase+DUF4162->cNMP_cyclase+TM+TM+TM+TM+TM+TM->EACC1*->
- **GCA_900142595.1; Streptomyces yunnanensis; counts= 3; multicellularity status: TRUE**
  - EACC1*->CASPASE+TM+MFS_1+TM+TM+TM+TM+TM+TM+TM+TM->
  - low-complexity+HD+Tox-RelA+TGS+ACT->Pkinase+TPRs->EACC1*->CASPASE+TPRs->
  - polar_lead?+TM+TM+TM+polar_tail?+low-complexity->??->EACC1*->CASPASE+TPRs->
- **GCA_900188105.1; Actinomadura mexicana; counts= 3; multicellularity status: TRUE**
  - ??+EACC1*->
  - EACC1*->CASPASE+??+TM+TM+TM->
  - EACC1*->CASPASE+TM+TM->
- **GCA_900230195.1; Streptomyces zhaozhouensis; counts= 3; multicellularity status: TRUE**
  - EACC1*->CASPASE+JAB->
  - EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->
  - Pkinase+TPRs->EACC1*->CASPASE+TPRs->
- **GCA_900230245.1; Burkholderia sp. OK806; counts= 3; multicellularity status: FALSE**
  - EACC1->Tnp_DNA_bind+DDE_Tnp_1+Dimer_Tnp_Tn5->CASPASE+TPRs->EACC1->CASPASE(fragment)->EACC1*->CASPASE+CASPASE+TM+TPRs->CASPASE(fragment)->
  - EACC1->Tnp_DNA_bind+DDE_Tnp_1+Dimer_Tnp_Tn5->CASPASE+TPRs->EACC1*->CASPASE(fragment)->EACC1->CASPASE+CASPASE+TM+TPRs->CASPASE(fragment)->
  - EACC1*->Tnp_DNA_bind+DDE_Tnp_1+Dimer_Tnp_Tn5->CASPASE+TPRs->
- **GCA_000196835.1; Amycolatopsis mediterranei; counts= 3; multicellularity status: TRUE**
  - EACC1*->CASPASE+??->
  - GATase->ABC-ATPase+DUF4162->cNMP_cyclase+TM+TM+TM+TM+TM+TM->EACC1*->
  - PBPB->?->?->Aminotran_5+PAS_6+HTH_22->EACC1*->||<-Glyco_trans_4_4+UDPGT
- **GCA_000240165.1; Streptomyces cattleya; counts= 3; multicellularity status: TRUE**
  - EACC1*->CASPASE+??+SF1-helicase+Vsr(PDDEXK)?->
  - EACC1-*->CASPASE+low-complexity+BetaPropeller___*_##->*
  - EACC1*->CASPASE+PBPB+vWA->
- **GCF_000375625.1; Streptomyces sp. FxanaC1; counts= 3; multicellularity status: TRUE**
  - EACC1*->CASPASE+Beta_rich_repeat->
  - EACC1*->CASPASE+DnaJ_ZnR+DnaJ_ZnR+DnaJ_C->
  - EACC1*->CASPASE+FGS_fold-domain->??->??->TM+TM+BaxI_1->?->NUDIX->
- **GCF_000381925.1; Nocardia sp. BMG111209; counts= 3; multicellularity status: TRUE**
  - EACC1*->
  - EACC1*->CASPASE+TM+Phytase-like->CASPASE+TM+TM+Phytase-like->CASPASE+TM+Phytase-like->

- EACC1*->CASPASE+TPRs->

■ **GCF_000514995.1; Streptomyces sp. CNT371; counts= 3; multicellularity status: TRUE**

- EACC1*->CASPASE->
- EACC1*->CASPASE+Beta_rich_repeat->
- EACC1*->CASPASE+TPRs->

■ **GCF_000717745.1; Streptomyces violens; counts= 3; multicellularity status: TRUE**

- EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->
- EACC1*->CASPASE+TM?+Phytase-like->
- EACC1*->CASPASE+TPRs->

■ **GCF_000719865.1; Streptomyces albus; counts= 3; multicellularity status: TRUE**

- EACC1*->CASPASE+PBPB+vWA->
- EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->
- EACC1*->CASPASE+TPRs->??->??->

■ **GCF_000719605.1; Streptomyces sp. NRRL S-1813; counts= 3; multicellularity status: TRUE**

- EACC1*->CASPASE+DnaJ_ZnR+DnaJ_ZnR+DnaJ_C->
- EACC1*->CASPASE+FGS_fold-domain->??->??->
- EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->

■ **GCF_000721935.1; Streptomyces sp. NRRL WC-3549; counts= 3; multicellularity status: TRUE**

- EACC1*->
- EACC1*->
- EACC1*->CASPASE+TPRs->TPRs->

■ **GCF_000725465.1; Streptomyces bicolor; counts= 3; multicellularity status: TRUE**

- EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->
- EACC1*->CASPASE+TM?+Phytase-like->MDMPI_N+MDMPI_C->
- EACC1*->CASPASE+TM+PBPI->

■ **GCF_000518265.1; Actinomadura oligospora; counts= 3; multicellularity status: TRUE**

- EACC1*->CASPASE+BetaPropeller->
- EACC1*->CASPASE+low-complexity+BetaPropeller->
- EACC1*->CASPASE+SAD+HNH->?->||<-METHYLASE

■ **GCF_000308835.1; Nocardia vinacea; counts= 3; multicellularity status: TRUE**

- EACC1*->CASPASE+??->
- EACC1*->CASPASE+EAL->
- EACC1*->CASPASE+TM+Phytase-like->

■ **GCF_000725485.1; Nonomuraea candida; counts= 3; multicellularity status: TRUE**

- EACC1*->CASPASE+low-complexity+BetaPropeller->

- EACC1*->CASPASE+SAD+HNH->
- EACC1*->CASPASE+TM+TM+??->

■ **GCF_000721075.1; Streptosporangium amethystogenes; counts= 3; multicellularity status: TRUE**

- EACC1*->BetaPropeller(fragment)->
- EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->
- EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->

■ **GCA_900105465.1; Streptomyces sp. PAN_FS17; counts= 3; multicellularity status: TRUE**

- EACC1*->
- EACC1*->CASPASE+??->
- EACC1*->CASPASE+TPRs->

■ **GCF_001417735.1; Streptomyces sp. NBRC 110028; counts= 3; multicellularity status: TRUE**

- EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->
- EACC1*->CASPASE+TPRs->Clp_N+Clp_N+Clp_N+Clp_N+ClpABN-AAA->
- HATPase_c_2->EACC1*->

■ **GCA_001424875.1; Kitasatospora sp. Root107; counts= 3; multicellularity status: TRUE**

- EACC1*->CASPASE+TPRs->
- EACC1*->CASPASE+TPRs->
- polar_lead?+TM+TM+TM+polar_tail?+low-complexity->??->EACC1*->CASPASE+TPRs->

■ **GCA_001514055.1; Streptomyces corchorusii; counts= 3; multicellularity status: TRUE**

- EACC1*->CASPASE+low-complexity+TM+PBPB->
- EACC1*->CASPASE+TM?+Phytase-like->MDMPI_N+MDMPI_C->META->
- EACC1*->CASPASE+TPRs->

■ **GCF_001613225.1; Nocardia pseudovaccinii; counts= 3; multicellularity status: TRUE**

- EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->
- EACC1*->CASPASE+TPRs->
- EACC1*->CASPASE+TPRs->

■ **GCA_001542625.2; Streptomyces griseochromogenes; counts= 3; multicellularity status: TRUE**

- EACC1*->CASPASE+low-complexity+BetaPropeller->
- EACC1*->CASPASE+wHTH+BetaPropeller->
- low-complexity+HD+Tox-RelA+TGS+ACT->Pkinase+TPRs->EACC1*->CASPASE+TPRs->

■ **GCA_900104815.1; Streptomyces; counts= 3; multicellularity status: TRUE**

- EACC1*->CASPASE+??+ZnR+ZnR->
- EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->
- EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->

■ **GCA_001905485.1; Streptomyces sp. TSRI0261; counts= 3; multicellularity status: TRUE**

- Beta_rich?->EACC1*->CASPASE+TPRs->??->??->
- EACC1*->CASPASE+??+SF1-helicase+Vsr(PDDEXK)?->
- EACC1*->CASPASE+Beta_rich_repeat->??+SUKH->

■ **GCF_002154375.1; Streptomyces glaucescens; counts= 3; multicellularity status: TRUE**

- EACC1*->CASPASE+??+BsuPI->
- EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->
- EACC1*->PSE->AB_hydrolase->

■ **GCA_002188345.1; Streptomyces sp. CS057; counts= 3; multicellularity status: TRUE**

- EACC1*->
- EACC1*->CASPASE+Beta_rich_repeat->
- EACC1*->CASPASE+STAND+??+TPRs+??->

■ **GCA_002234595.1; Amycolatopsis sp. H5; counts= 3; multicellularity status: TRUE**

- GATase->ABC-ATPase+DUF4162->cNMP_cyclase+TM+TM+TM+TM+TM+TM->EACC1->CASPASE+EAD2+TM+TM+TM+TM->EACC1*->
- GATase->ABC-ATPase+DUF4162->cNMP_cyclase+TM+TM+TM+TM+TM+TM->EACC1*->CASPASE+EAD2+TM+TM+TM+TM->EACC1->
- PBPB->?->?->Aminotran_5+PAS_6+HTH_22->EACC1*->CASPASE+??+TM+TM->

■ **GCF_002904335.1; Amycolatopsis sp. CA-126428; counts= 3; multicellularity status: TRUE**

- EACC1*->CASPASE+HSP70->
- GATase->ABC-ATPase+DUF4162->cNMP_cyclase+TM+TM+TM+TM+TM+TM->EACC1*->
- PBPB->?->?->Aminotran_5+PAS_6+HTH_22->EACC1*->||<-Glyco_trans_4_4+UDPGT

■ **GCA_000147815.3; Streptomyces violaceusniger Tu 4113; counts= 2; multicellularity status: TRUE**

- EACC1*->CASPASE+TM+TM->
- TetR_N+TetR_C_6->EACC1*->CASPASE+low-complexity+TM+PBPB->

■ **GCA_000418455.1; Streptomyces rapamycinicus NRRL 5491; counts= 2; multicellularity status: TRUE**

- EACC1*->
- EACC1*->CASPASE+low-complexity+TM+PBPB->

■ **GCA_000523235.1; Nocardia nova SH22a; counts= 2; multicellularity status: TRUE**

- DUF2510(W3)+BicD+DUF4041+T5orf172->EACC1*->CASPASE+TPRs->
- EACC1*->TM+TM->

■ **GCA_000695235.1; Streptomyces albulus; counts= 2; multicellularity status: TRUE**

- EACC1*->
- EACC1*->CASPASE+TM+TM+bPH_domain?->

■ **GCA_000827005.1; Streptomyces albus; counts= 2; multicellularity status: TRUE**

- EACC1*->CASPASE+HisKA+HATPase_c->
- low-complexity+HD+Tox-RelA+TGS+ACT->Pkinase+TPRs->EACC1*->CASPASE+TPRs->

- **GCA_000931445.1; Streptomyces cyaneogriseus subsp. noncyanogenus; counts= 2; multicellularity status: TRUE**
  - EACC1*->
  - EACC1*->CASPASE+TPRs->Clp_N+Clp_N+ClpABN-AAA->
- **GCA_000952035.2; Streptomyces lydicus; counts= 2; multicellularity status: TRUE**
  - EACC1*->
  - EACC1*->CASPASE+low-complexity+TM+PBPB->
- **GCA_000993785.2; Streptomyces xiamenensis; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+TPRs->
  - TM+TM+TM+PP2C->EACC1*->CASPASE+PBPB+vWA->
- **GCA_001040905.1; Streptomyces sp. PBH53; counts= 2; multicellularity status: TRUE**
  - ??->??->EACC1*->CASPASE+??->
  - EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->
- **GCA_001735805.1; Streptomyces puniciscabiei; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+Pkinase+TM?+??->
  - EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->
- **GCA_001886715.1; Nocardia sp. Y48; counts= 2; multicellularity status: TRUE**
  - EACC1*->
  - EACC1*->CASPASE+TPRs->
- **GCA_002021875.1; Streptomyces hygroscopicus; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->
  - TetR_N+TetR_C_6->EACC1*->CASPASE+low-complexity+TM+PBPB->
- **GCA_003595545.1; Streptomyces sp. 11-1-2; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->
  - Pkinase+TPRs->EACC1*->CASPASE+TPRs->
- **GCA_002812405.1; Streptomyces sp. M56; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+TM+??->
  - TetR_N+TetR_C_6->EACC1*->CASPASE+low-complexity+TM+PBPB->
- **GCA_002943525.1; Kitasatospora sp. MMS16-BH015; counts= 2; multicellularity status: TRUE**
  - EACC1*->
  - EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->
- **GCA_002849735.1; Amycolatopsis sp. BJA-103; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->
  - EACC1*->TM+ZU5+??->

- **GCA_000284295.1; Actinoplanes missouriensis 431; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+TPRs->
  - EACC1*->Clp_N+Clp_N+ClpABN-AAA+CASPASE->
- **GCA_000158915.1; Streptomyces himastatinicus ATCC 53653; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+TPRs->Clp_N+Clp_N+Clp_N+Clp_N+ClpABN-AAA->
  - HATPase_c_2->EACC1*->
- **GCA_000414115.1; Streptomyces aurantiacus JA 4570; counts= 2; multicellularity status: TRUE**
  - EACC1*->
  - EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->
- **GCA_000497425.1; Streptomyces niveus NCIMB 11891; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+??+SF1-helicase+Vsr(PDDEXK)?->
  - EACC1*->CASPASE+Beta_rich_repeat->
- **GCA_001653075.1; Planomonospora sphaerica; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+SAD+HNH->
  - EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->
- **GCA_001653115.1; Streptomyces sp. F-3; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+??->
  - EACC1*->CASPASE+TM+TM+PBPB+vWA->
- **GCA_000696115.1; Streptomyces olindensis; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->
  - EACC1*->CASPASE+TM?+Phytase-like->
- **GCA_001047335.1; Streptomyces regensis; counts= 2; multicellularity status: TRUE**
  - EACC1*->
  - EACC1*->CASPASE+TM?+Phytase-like->MDMPI_N+MDMPI_C->META->
- **GCA_001189015.1; Streptomyces acidiscabies; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+low-complexity+BetaPropeller->
  - EACC1*->CASPASE+TM+TM+PBPB+vWA->
- **GCA_001189025.1; Streptomyces europaeiscabiei; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+Beta_rich_repeat->??+SUKH->
  - EACC1*->CASPASE+STAND+??+TPRs+??->
- **GCA_001279985.1; Streptomyces sp. AS58; counts= 2; multicellularity status: TRUE**
  - EACC1*->
  - EACC1*->CASPASE+TM+TM+bPH_domain+TM+TM+bPH_domain+TM+TM->

- **GCA_001279545.1; Streptomyces sp. NRRL B-3648; counts= 2; multicellularity status: TRUE**
  - EACC1*->
  - EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->
- **GCA_001298565.1; Actinobacteria bacterium OK006; counts= 2; multicellularity status: NA**
  - EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->
  - EACC1*->CASPASE+TPRs->
- **GCA_001298575.1; Actinobacteria bacterium OK074; counts= 2; multicellularity status: NA**
  - EACC1*->CASPASE+low-complexity+BetaPropeller->
  - EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->
- **GCA_001509475.1; Streptomyces regalis; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->
  - TPRs->EACC1*->CASPASE+TPRs->
- **GCA_001513965.1; Streptomyces cellostaticus; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+low-complexity+BetaPropeller->
  - EACC1*->CASPASE+PBPB->
- **GCA_001613935.1; Amycolatopsis regifaucium; counts= 2; multicellularity status: TRUE**
  - EACC1*->
  - EACC1*->
- **GCA_001687325.1; Streptomyces sp. PTY087I2; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+??+SF1-helicase+Vsr(PDDEXK)?->??->
  - EACC1*->CASPASE+TPRs->
- **GCA_000974985.2; Streptomyces mangrovisoli; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+alpha-helical+TM+TM+??+TM+TM->
  - Pkinase+TPRs->EACC1*->CASPASE+TPRs->
- **GCA_001917385.1; Actinobacteria bacterium 13_2_20CM_2_71_6; counts= 2; multicellularity status: NA**
  - EACC1*->
  - EACC1*->CASPASE+FTSK+FTSK+FTSK+FTSK->
- **GCA_001920275.1; Actinobacteria bacterium 13_1_20CM_3_71_11; counts= 2; multicellularity status: NA**
  - EACC1*->CASPASE+DUF179->SIR2+??->
  - EACC1+CASPASE+TPR_repeats+low_complexity+TM_region*->
- **GCA_001984575.1; Streptomyces sp. MP131-18; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+JAB->?->MFS_1->
  - EACC1*->CASPASE+TPRs->

- **GCA_000968685.2; Streptomyces antioxidans; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+Peripla_BP_5->
  - EACC1*->CASPASE+TM+??->
- **GCA_002119195.1; Streptomyces platensis; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE->TPRs->
  - EACC1*->CASPASE+Beta_rich_repeat->
- **GCA_002224125.1; Streptomyces sp. NBS 14/10; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+TM+TM+??+TM+TM+??+TM+TM+??->
  - low-complexity+HD+Tox-RelA+TGS+ACT->Pkinase+TPRs->EACC1*->CASPASE+TPRs->
- **GCA_002242805.1; Streptomyces diastatochromogenes; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+low-complexity+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+BetaPropeller->
  - EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->TM+Acid_phosphat_B->
- **GCA_002300485.1; Streptomyces sp. Ag82_O1-15; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+BetaPropeller->
  - EACC1*->CASPASE+TM+PBPI->
- **GCA_002754415.1; Micromonospora sp. CNZ299; counts= 2; multicellularity status: TRUE**
  - EACC1*->
  - TM+TM+TM+Peptidase_M48+TM+DUF4864+??->EACC1*->
- **GCA_002813405.1; Streptomyces sp. 69; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+STAND->TM+BetaPropeller->TM+Acid_phosphat_B->
  - EACC1*->CASPASE+STAND+TPRs->
- **GCA_002907485.1; Streptomyces sp. ZL-24; counts= 2; multicellularity status: TRUE**
  - Beta_rich?->EACC1*->CASPASE+TPRs->??->??->
  - Pkinase+TPRs->EACC1*->CASPASE+TPRs->
- **GCA_002941025.1; Streptomyces sp. QL37; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->
  - low-complexity+HD+Tox-RelA+TGS+ACT->Pkinase+TPRs->EACC1*->CASPASE+TPRs->
- **GCA_003001815.1; Actinoplanes italicus; counts= 2; multicellularity status: TRUE**
  - EACC1+CASPASE+TPR_repeats+low_complexity+TM_region*->STAND+TPRs->
  - Glyco_trans_4_4+UDPGT->EACC1*->CASPASE+PBPB+vWA->TM+PBPB->
- **GCA_003041235.1; Streptomyces sp. A244; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+??->
  - EACC1*->CASPASE+TM+TM+PBPB+vWA->

- **GCA_003148685.1; Actinoplanes xinjiangensis; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+PBPB+vWA->TM+PBPB->
  - EACC1*->CASPASE+TM+PASTA+PASTA+PASTA->
- **GCA_003182135.1; Nocardia neocaledoniensis; counts= 2; multicellularity status: TRUE**
  - DUF742->EACC1*->CASPASE+??->
  - EACC1*->CASPASE+TPRs->
- **GCA_900091855.1; Streptomyces sp. DvalAA-14; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+??->
  - EACC1*->CASPASE+TPRs->
- **GCA_900091535.1; Micromonospora carbonacea; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->
  - TM+TM+TM+Peptidase_M48+TM+DUF4864+??->EACC1*->
- **GCA_900091505.1; Micromonospora chokoriensis; counts= 2; multicellularity status: TRUE**
  - EACC1*->
  - TM+TM+TM+Peptidase_M48+TM+DUF4864+??->EACC1*->
- **GCA_900091955.1; Streptomyces sp. Ncost-T10-10d; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+??->
  - EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->
- **GCA_900101585.1; Streptomyces prasinopilosus; counts= 2; multicellularity status: TRUE**
  - ??+CASPASE->EACC1*->
  - <-CASPASE<-?<-?||HATPase_c_2->EACC1+CASPASE(frag)*->
- **GCA_900105395.1; Streptomyces sp. TLI_053; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+HSP70->
  - FAD_binding_4+FAD-oxidase_C->DAGK_cat+DAGK_acc->EACC1*->CASPASE+TPRs->Clp_N+Clp_N+ClpABN-AAA->
- **GCA_900105695.1; Streptomyces melanosporofaciens; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->
  - TetR_N+TetR_C_6->EACC1*->CASPASE+low-complexity+TM+PBPB->
- **GCA_900108335.1; Nonomuraea solani; counts= 2; multicellularity status: TRUE**
  - ARSR-HTH+RHOD-CDC25->??->??->EACC1*->
  - EACC1*->CASPASE+BetaPropeller->
- **GCA_900111175.1; Actinokineospora terrae; counts= 2; multicellularity status: TRUE**
  - EACC1*->
  - EACC1*->CASPASE+??+TM+TM+TM+TM+TM+TM+TM+TM+TM->CASPASE+??+TM+TM+TM+TM+TM+TM+TM+TM->

- **GCA_900111685.1; Nonomuraea wenchangensis; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->
  - TM+TM+vWA+TM->TM+TM+vWA+TM->EACC1*->CASPASE+TPRs->
- **GCA_900112845.1; Streptomyces alni; counts= 2; multicellularity status: TRUE**
  - EACC1*->
  - EACC1*->CASPASE+low-complexity+BetaPropeller->
- **GCA_900187925.1; Streptomyces sp. PgraA7; counts= 2; multicellularity status: TRUE**
  - EACC1*->
  - EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->
- **GCA_900188005.1; Actinoplanes regularis; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+BetaPropeller->
  - EACC1*->CASPASE+TPRs->
- **GCA_900188345.1; Streptosporangium subroseum; counts= 2; multicellularity status: TRUE**
  - EACC1*->
  - EACC1*->CASPASE+??->
- **GCA_000177175.2; Streptomyces sp. ACT-1; counts= 2; multicellularity status: TRUE**
  - Beta_rich?->EACC1*->CASPASE+TPRs->??->??->
  - EACC1*->CASPASE+TPRs->
- **GCA_000340415.1; Amycolatopsis azurea; counts= 2; multicellularity status: TRUE**
  - CASPASE+TPRs->?->EACC1*->
  - EACC1*->CASPASE+TPRs->
- **GCA_002846475.1; Saccharopolyspora spinosa; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+??+SF1-helicase+Vsr(PDDEXK)?->
  - EACC1*->CASPASE+BetaPropeller->
- **GCA_000024545.1; Stackebrandtia nassauensis; counts= 2; multicellularity status: TRUE**
  - Clp_N+ClpABN-AAA+CASPASE->EACC1*->
  - EACC1*->
- **GCA_000245355.1; Streptomyces hygroscopicus; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+low-complexity+TM+PBPB->
  - EACC1*->CASPASE+TM?+Phytase-like->MDMPI_N+MDMPI_C->META->
- **GCA_000328705.1; Saccharothrix espanaensis; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+TM+TM->TM+PBPB->
  - TM+TM+TM->CASPASE+STAND+polar_region+TM+BetaPropeller->EACC1*->

- **GCA_000400635.2; Amycolatopsis orientalis; counts= 2; multicellularity status: TRUE**
  - EACC1*->
  - EACC1*->CASPASE+DnaJ_ZnR+DnaJ_ZnR+DnaJ_C->
- **GCA_000411315.1; Streptomyces sp. HGB0020; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+??+TM+??->
  - EACC1*->CASPASE+TPRs->
- **GCF_000373685.1; Streptomyces sp. PsTaAH-124; counts= 2; multicellularity status: TRUE**
  - EACC1*->
  - TPRs->EACC1*->CASPASE+TPRs->
- **GCF_000259895.1; Streptomyces sp. TOR3209; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+TPRs->
  - Trypsin+HDxxH+VMAP-M0+CASPASE->EACC1*->
- **GCA_002234385.1; Amycolatopsis alba; counts= 2; multicellularity status: TRUE**
  - EACC1*->
  - EACC1*->CASPASE+TPRs->
- **GCA_003947255.1; Amycolatopsis balhimycina; counts= 2; multicellularity status: TRUE**
  - GATase->ABC-ATPase+DUF4162->cNMP_cyclase+TM+TM+TM+TM+TM+TM->EACC1*->
  - PBPB->?->?->Aminotran_5+PAS_6+HTH_22->EACC1*->
- **GCA_001270575.1; Streptomyces decoyicus; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+DnaJ_ZnR+DnaJ_ZnR+DnaJ_C->
  - EACC1*->CASPASE+FGS_fold-domain->??->??->TM+TM+BaxI_1->?->NUDIX->
- **GCF_000718515.1; Micromonospora parva; counts= 2; multicellularity status: TRUE**
  - EACC1*->
  - TM+TM+TM+Peptidase_M48+TM+DUF4864+??->EACC1*->
- **GCF_000718025.1; Kitasatospora purpeofusca; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+HSP70->
  - FAD_binding_4+FAD-oxidase_C->DAGK_cat+DAGK_acc->EACC1*->CASPASE+TPRs->Clp_N+Clp_N+ClpABN-AAA->
- **GCF_000719365.1; Streptomyces sp. NRRL S-1448; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+TM+Beta_rich->
  - EACC1*->CASPASE+TM+PBPB+vWA->
- **GCF_000718555.1; Micromonospora chokoriensis; counts= 2; multicellularity status: TRUE**
  - EACC1*->
  - TM+TM+TM+Peptidase_M48+TM+DUF4864+??->EACC1*->

- **GCF_000718675.1; Streptomyces rimosus; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+??+SF1-helicase+Vsr(PDDEXK)?->??->
  - EACC1*->CASPASE+TM?+Phytase-like->
- **GCF_000718625.1; Streptomyces lavenduligriseus; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+??+SF1-helicase+Vsr(PDDEXK)?->
  - EACC1*->CASPASE+TM?+BetaPropeller->
- **GCF_000720175.1; Streptomyces sp. NRRL S-337; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+TM?+BetaPropeller->
  - EACC1*->CASPASE+TM+Beta_rich->
- **GCF_000721625.1; Streptomyces sp. NRRL S-384; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+alpha-helical+TM+TM+??+TM+TM->
  - polar_lead?+TM+TM+TM+polar_tail?+low-complexity->??->EACC1*->CASPASE+TPRs->
- **GCF_000719555.1; Streptomyces sp. NRRL F-5727; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+STAND+??+TPRs+??->
  - HATPase_c_2->EACC1*->CASPASE+??+SF1-helicase+Vsr(PDDEXK)?->
- **GCF_000725475.1; Streptomyces durhamensis; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+??+SF1-helicase+Vsr(PDDEXK)?->
  - EACC1*->CASPASE+TM+TM+bPH_domain?->
- **GCF_000717335.1; Amycolatopsis jejuensis; counts= 2; multicellularity status: TRUE**
  - EACC1->CASPASE+TPRs->?->EACC1*->
  - EACC1*->CASPASE+TPRs->?->EACC1->
- **GCF_000716885.1; Kitasatospora aureofaciens; counts= 2; multicellularity status: TRUE**
  - EACC1*->
  - EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->
- **GCF_000720255.1; Streptomyces griseus; counts= 2; multicellularity status: TRUE**
  - ??->EACC1*->CASPASE+TM+TM+PBPB+vWA->
  - EACC1*->CASPASE+Trypsin+STAND+??+TM->
- **GCA_000590515.1; Streptomyces sp. PRh5; counts= 2; multicellularity status: TRUE**
  - EACC1*->
  - EACC1*->CASPASE+STAND+TPRs->
- **GCA_000732925.1; Amycolatopsis japonica; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+??->
  - EACC1*->CASPASE+TPRs->

- **GCF_000494755.1; Actinoplanes friuliensis; counts= 2; multicellularity status: TRUE**
  - EACC1*->
  - EACC1*->CASPASE+DUF179->SIR2+??->??->
- **GCA_000829715.2; Streptomyces sp. NBRC 110027; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE->TPRs->
  - EACC1*->CASPASE+Beta_rich_repeat->
- **GCF_000308415.1; Nocardia asiatica; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+STAND->BetaPropeller->
  - EACC1*->CASPASE+STAND+BetaPropeller+BetaPropeller->
- **GCA_000695625.1; Amycolatopsis rifamycinica; counts= 2; multicellularity status: TRUE**
  - GATase->ABC-ATPase+DUF4162->cNMP_cyclase+TM+TM+TM+TM+TM+TM->EACC1*->
  - PBPB->?->?->Aminotran_5+PAS_6+HTH_22->EACC1*->
- **GCA_900103775.1; Allokutzneria albata; counts= 2; multicellularity status: TRUE**
  - EACC1*->
  - EACC1*->CASPASE+DnaJ_ZnR+DnaJ_ZnR+DnaJ_C->
- **GCF_000331005.1; Streptomyces; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+TM+TM+bPH_domain+TM+TM+bPH_domain+TM+TM->
  - HTH+CASPASE->EACC1*->
- **GCF_000962825.1; Actinoplanes rectilineatus; counts= 2; multicellularity status: TRUE**
  - EACC1*->||<-CASPASE+STAND+TM+polar_region+TM+BetaPropeller
  - EACC1*->CASPASE+TPRs->
- **GCA_000982955.1; Micromonospora sp. HK10; counts= 2; multicellularity status: TRUE**
  - EACC1*->
  - TM+TM+TM+Peptidase_M48+TM+DUF4864+??->EACC1*->
- **GCF_001083785.1; Nonomuraea sp. SBT364; counts= 2; multicellularity status: TRUE**
  - EACC1*->
  - EACC1*->CASPASE+low-complexity+BetaPropeller->
- **GCA_001187435.1; Streptomyces caatingaensis; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->
  - EACC1*->CASPASE+TPRs->
- **GCF_001650215.1; Streptomyces himastatinicus; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+low-complexity+TM+PBPB->
  - EACC1*->CASPASE+TPRs->Clp_N+Clp_N+Clp_N+Clp_N+ClpABN-AAA->

- **GCF_000620785.1; Pseudonocardia acaciae; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->
  - EACC1*->CASPASE+TM+TM+TM+TM->
- **GCF_000719415.1; Streptomyces sp. NRRL B-5680; counts= 2; multicellularity status: TRUE**
  - EACC1*->
  - EACC1*->CASPASE+??->
- **GCF_000935125.1; Streptomyces natalensis; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+low-complexity+BetaPropeller->
  - PAS+GAF+PP2C+HATPase_c_2->EACC1*->CASPASE+TM+Beta_rich->
- **GCF_000744785.1; Kitasatospora azatica; counts= 2; multicellularity status: TRUE**
  - cNMP_cyclase+EACC1*->CASPASE+TPRs->
  - EACC1*->CASPASE+DnaJ_ZnR+DnaJ_C+DnaJ_C+TM+TM->
- **GCA_000816025.1; Streptomyces sp. 769; counts= 2; multicellularity status: TRUE**
  - low-complexity+HD+Tox-RelA+TGS+ACT->Pkinase+TPRs->EACC1*->CASPASE+TPRs->
  - polar_lead?+TM+TM+TM+polar_tail?+low-complexity->??->EACC1*->CASPASE+TPRs->
- **GCF_000721495.1; Streptomyces sp. NRRL F-5123; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+BetaPropeller->
  - EACC1*->CASPASE+STAND+TPRs->
- **GCF_000935185.3; Streptomyces albulus; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+PBPB->
  - EACC1*->CASPASE+TM+TM+bPH_domain?->
- **GCA_001280065.1; Streptomyces sp. NRRL B-1140; counts= 2; multicellularity status: TRUE**
  - ??->EACC1*->CASPASE+TM+TM+PBPB+vWA->
  - EACC1*->CASPASE->TPRs->
- **GCA_001279655.1; Streptomyces sp. WM6372; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+??->
  - low-complexity+HD+Tox-RelA+TGS+ACT->Pkinase+TPRs->EACC1*->CASPASE+TPRs->
- **GCF_001279545.1; Streptomyces sp. NRRL B-3648; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+low-complexity+BetaPropeller->
  - EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->
- **GCA_001294335.1; Streptomyces chattanoogensis; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+TM?+BetaPropeller->
  - TPRs->EACC1*->CASPASE+TPRs->

- **GCF_001298575.1; Actinobacteria bacterium OK074; counts= 2; multicellularity status: NA**
  - EACC1*->
  - EACC1*->CASPASE+low-complexity+BetaPropeller->
- **GCF_001418475.1; Streptomyces ossamyceticus; counts= 2; multicellularity status: TRUE**
  - EACC1*->
  - EACC1*->CASPASE->TPRs->
- **GCF_001419705.1; Streptomyces prasinus; counts= 2; multicellularity status: TRUE**
  - ??->EACC1*->CASPASE+TPRs->
  - EACC1*->CASPASE+??->
- **GCA_001447075.1; Streptomyces hygroscopicus; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+low-complexity+TM+PBPB->
  - EACC1*->CASPASE+TM?+Phytase-like->MDMPI_N+MDMPI_C->META->
- **GCA_001509775.1; Streptomyces; counts= 2; multicellularity status: TRUE**
  - EACC1*->
  - TetR_N+TetR_C_6->EACC1*->
- **GCA_002251155.1; Streptomyces; counts= 2; multicellularity status: TRUE**
  - ??->??->EACC1*->CASPASE+??->
  - AMP-binding+AMP-binding_C->AMP-binding+AMP-binding_C->EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->
- **GCA_001611795.1; Streptomyces sp. S10(2016); counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+RE_Eco29kI+??->
  - TM+TM+TM+PP2C->??->EACC1*->CASPASE+TM+TM+PBPB+vWA->
- **GCA_001590865.1; Streptomyces sp. NBRC 110611; counts= 2; multicellularity status: TRUE**
  - *
  - EACC1*->CASPASE+TPRs->
- **GCF_001700515.1; Streptomyces lushanensis; counts= 2; multicellularity status: TRUE**
  - EACC1*->
  - Pkinase+TPRs->EACC1*->CASPASE+TPRs->
- **GCA_001653515.1; Streptomyces sp. ERV7; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+BetaPropeller->||<-DUF664
  - low-complexity+HD+Tox-RelA+TGS+ACT->Pkinase+TPRs->EACC1*->CASPASE+TPRs->
- **GCA_001542325.1; Micromonospora rifamycinica; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+TM+TM->PBPB->
  - TM+TM+TM+Peptidase_M48+TM+DUF4864+??->EACC1*->

- **GCF_001613065.1; Nocardia miyunensis; counts= 2; multicellularity status: TRUE**
  - EACC1*->
  - EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->
- **GCF_001613145.1; Nocardia jejuensis; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+STAND+BetaPropeller->
  - EACC1*->CASPASE+TPRs->
- **GCF_001612785.1; Nocardia beijingensis; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->
  - Pkinase+TM+LppX_LprAFG->CASPASE+TPRs->EACC1*->
- **GCF_001653075.1; Planomonospora sphaerica; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+SAD+HNH->
  - EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->
- **GCF_001696485.1; Planobispora rosea; counts= 2; multicellularity status: TRUE**
  - EACC1*->
  - EACC1*->CASPASE+TM+TM+TM+TM+TM+TM+BetaPropeller->
- **GCF_001746285.1; Streptomyces sp. EN16; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+Beta_rich_repeat->??+SUKH->
  - EACC1*->CASPASE+STAND+??+TPRs+??->
- **GCF_001746365.1; Streptomyces sp. LUP30; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+??+SF1-helicase+Vsr(PDDEXK)?->
  - EACC1*->CASPASE+TPRs->
- **GCA_900079405.3; Streptomyces sp. F-1; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->
  - EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->
- **GCF_900142575.1; Streptomyces paucisporeus; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+HSP70->
  - EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->
- **GCA_001905505.1; Streptomyces sp. CB02058; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+??->
  - EACC1*->CASPASE+STAND+??+TPRs->
- **GCA_001905445.1; Streptomyces sp. CB00455; counts= 2; multicellularity status: TRUE**
  - HATPase_c_2->EACC1*->CASPASE+??+SF1-helicase+Vsr(PDDEXK)?->
  - low-complexity+HD+Tox-RelA+TGS+ACT->Pkinase+TPRs->EACC1*->CASPASE+TPRs->

- **GCF_001906585.1; Streptomyces kebangsaanensis; counts= 2; multicellularity status: TRUE**
  - ??->EACC1*->CASPASE+TM+TM+PBPB+vWA->
  - <-CASPASE+HATPase_c_4+STAND+TPRs||EACC1*->
- **GCA_001921215.1; Actinophytocola xinjiangensis; counts= 2; multicellularity status: TRUE**
  - Beta_rich?->EACC1*->CASPASE+TPRs->??->??->
  - EACC1*->CASPASE+TM+TM->TM+PBPB->
- **GCF_001941275.1; Streptomyces acidiscabies; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+TM+TM+PBPB+vWA->
  - EACC1*->CASPASE+TPRs->
- **GCA_001984155.1; Actinosynnema sp. ALI-1.44; counts= 2; multicellularity status: TRUE**
  - EACC1*->
  - PALP->Trp_syntA->TM+LGT->EACC1*->
- **GCF_001866665.1; Streptomyces sp. MUSC 1; counts= 2; multicellularity status: TRUE**
  - EACC1*->
  - EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->
- **GCA_001983975.1; Streptomyces autolyticus; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+TM+??->
  - TetR_N+TetR_C_6->EACC1*->CASPASE+low-complexity+TM+PBPB->
- **GCF_001298565.1; Actinobacteria bacterium OK006; counts= 2; multicellularity status: NA**
  - EACC1*->CASPASE+TPRs->
  - low_complexity+EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->
- **GCA_002082195.1; Streptomyces gilvosporeus; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+low-complexity+TM+PBPB->
  - PAS+GAF+PP2C+HATPase_c_2->EACC1*->CASPASE+TM+Beta_rich->
- **GCA_002090335.1; Streptomyces sp. MOE7; counts= 2; multicellularity status: TRUE**
  - Glyoxalase->EACC1*->CASPASE+DnaJ_ZnR+DnaJ_ZnR+DnaJ_C->
  - polar_lead?+TM+TM+TM+polar_tail?+low-complexity->??->EACC1*->CASPASE+TPRs->
- **GCA_002114215.1; Streptomyces sp. 13-12-16; counts= 2; multicellularity status: TRUE**
  - ??->EACC1*->CASPASE+TPRs->
  - EACC1*->CASPASE+TPRs->
- **GCA_002128465.1; Streptomyces pharetrae; counts= 2; multicellularity status: TRUE**
  - EACC1*->?->AB_hydrolase->
  - EACC1*->CASPASE(fragment)->CASPASE+STAND+polar_region+TM+BetaPropeller->

- **GCF_002155905.1; Streptomyces tricolor; counts= 2; multicellularity status: TRUE**
  - ??->??->EACC1*->CASPASE+??->
  - AMP-binding+AMP-binding_C->AMP-binding+AMP-binding_C->EACC1*->
- **GCF_002154505.1; Streptomyces carpinensis; counts= 2; multicellularity status: TRUE**
  - ??->EACC1*->
  - EACC1*->CASPASE+TM+TM+bPH_domain?->
- **GCF_002155965.1; Allokutzneria sp. NRRL B-24872; counts= 2; multicellularity status: TRUE**
  - EACC1*->
  - EACC1*->CASPASE+TPRs->
- **GCA_002210435.1; Micromonospora wenchangensis; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+STAND+TPRs->||<-TM+TM+TM
  - TM+TM+TM+Peptidase_M48+TM+DUF4864+??->EACC1*->
- **GCA_002300315.1; Streptomyces; counts= 2; multicellularity status: TRUE**
  - EACC1*->
  - EACC1*->CASPASE+TM+PBPB+vWA->
- **GCA_900090275.1; Micromonospora zamorensis; counts= 2; multicellularity status: TRUE**
  - EACC1*->
  - TM+TM+TM+Peptidase_M48+TM+DUF4864+??->EACC1*->
- **GCA_900111005.1; Lentzea albida; counts= 2; multicellularity status: TRUE**
  - polar_lead?+TM+TM+TM+polar_tail?+low-complexity->??->EACC1*->CASPASE+TPRs->
  - TM+TM+BPD_transp_1->OppC_N+TM+TM+BPD_transp_1->ABC-ATPase+ABC-ATPase->PBPB->TM+Beta_rich+TM+Beta_rich+TM+TM->EACC1+CASPASE+TPR_repeats+low_complexity+TM_region*->
- **GCA_900107455.1; Asanoa ishikariensis; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+PRTase->
  - TPRs+CASPASE->?->?->EACC1*->?->CASPASE+TPRs->
- **GCF_900111685.1; Nonomuraea wenchangensis; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->
  - TM+TM+vWA+TM->TM+TM+vWA+TM->EACC1*->CASPASE+TPRs->
- **GCA_900091525.1; Micromonospora matsumotoense; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+STAND+TPRs->||<-?<-?<-?<-TM+TM+TM
  - TM+TM+TM+Peptidase_M48+TM+DUF4864+??->EACC1*->
- **GCA_900091575.1; Micromonospora saelicesensis; counts= 2; multicellularity status: TRUE**
  - EACC1*->
  - TM+TM+TM+Peptidase_M48+TM+DUF4864+??->EACC1*->

- **GCA_900101685.1; Alloactinosynnema iranicum; counts= 2; multicellularity status: TRUE**
  - EACC1*->
  - EACC1*->CASPASE+TPRs->
- **GCA_003053965.1; Saccharopolyspora; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+BetaPropeller->
  - EACC1*->CASPASE+FTSK+FTSK+FTSK+FTSK->
- **GCA_900115955.1; Lentzea waywayandensis; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->
  - TM+TM+BPD_transp_1->OppC_N+TM+TM+BPD_transp_1->ABC-ATPase+ABC-ATPase->PBPB->TM+Beta_rich+TM+Beta_rich+TM+TM->EACC1+CASPASE+TPR_repeats+low_complexity+TM_region*->
- **GCA_900091995.1; Streptomyces sp. MnatMP-M17; counts= 2; multicellularity status: TRUE**
  - EACC1*->
  - EACC1*->CASPASE+TM+TM+bPH_domain?->
- **GCF_900090095.1; Streptomyces sp. SceaMP-e96; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+Beta_rich_repeat->
  - Phage_int_SAM_3+Phage_integrase->EACC1*->CASPASE+TPRs->
- **GCF_002242805.1; Streptomyces diastatochromogenes; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+low-complexity+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+BetaPropeller->
  - EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->TM+Acid_phosphat_B->
- **GCA_900215205.1; Actinoplanes atraurantiacus; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+Pentapeptide_repeats->
  - EACC1*->CASPASE+TPRs->
- **GCA_003173635.1; Streptomyces; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+??+SF1-helicase+Vsr(PDDEXK)?->
  - EACC1*->CASPASE+TPRs??+GHKL_ATPase+TPRs??->
- **GCA_002754435.1; Streptomyces sp. 76; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+??->
  - Glyoxalase->EACC1*->CASPASE+DnaJ_ZnR+DnaJ_ZnR+DnaJ_C->
- **GCF_002754535.1; Streptomyces sp. 61; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+GAF+PAS+GGDEF->
  - low-complexity+HD+Tox-RelA+TGS+ACT->Pkinase+TPRs->EACC1*->CASPASE+TPRs->
- **GCA_002754615.1; Streptomyces sp. 1; counts= 2; multicellularity status: TRUE**
  - Pkinase+TPRs->EACC1*->CASPASE+TPRs->
  - polar_lead?+TM+TM+TM+polar_tail?+low-complexity->??->EACC1*->CASPASE+TPRs->

- **GCF_002754555.1; Streptomyces sp. 94; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+TM+??->
  - EACC1*->CASPASE+TPRs+LysM+PG-binding->
- **GCA_002803155.1; Streptomyces sp. CB02959; counts= 2; multicellularity status: TRUE**
  - low-complexity+HD+Tox-RelA+TGS+ACT->Pkinase+TPRs->EACC1*->CASPASE+TPRs->
  - low_complexity+EACC1*->CASPASE+TM+TM+bPH_domain?->
- **GCF_002910875.1; Streptomyces sp. SM13; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+??+SF1-helicase+Vsr(PDDEXK)?->
  - EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->
- **GCF_002954775.1; Streptomyces geranii; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+STAND+??+TPRs->
  - TPR_region+EACC1*->
- **GCA_003002065.1; Pseudosporangium ferrugineum; counts= 2; multicellularity status: TRUE**
  - EACC1*->CASPASE+DUF179->SIR2+??->??->
  - EACC1*->CASPASE+TPRs->
- **GCF_003001815.1; Actinoplanes italicus; counts= 2; multicellularity status: TRUE**
  - EACC1+CASPASE+TPR_repeats+low_complexity+TM_region*->STAND+TPRs->
  - Glyco_trans_4_4+UDPGT->EACC1*->CASPASE+PBPB+vWA->TM+PBPB->
- **GCA_003172955.1; Micromonospora sp. 5R2A7; counts= 2; multicellularity status: TRUE**
  - EACC1*->
  - TM+TM+TM+Peptidase_M48+TM+DUF4864+??->EACC1*->
- **GCA_000237145.1; Actinoplanes sp. SE50/110; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+JAB->
- **GCA_000525635.1; Kutzneria albida DSM 43870; counts= 1; multicellularity status: TRUE**
  - polar_lead?+TM+TM+TM+polar_tail?+low-complexity->??->EACC1*->CASPASE+TPRs->?->CASPASE+??+TPRs?->
- **GCA_001027185.1; Streptomyces incarnatus; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+TPRs->
- **GCA_001747425.1; Actinoalloteichus hymeniacidonis; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+??+SF1-helicase+Vsr(PDDEXK)?->
- **GCA_001865855.1; Nocardia seriolae; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+STAND+TPRs->
- **GCA_001941845.1; Streptomyces sp. TN58; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+RE_Eco29kI+??->

- **GCA_002009175.1; Streptomyces niveus; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+??->
- **GCA_000058485.1; Frankia alni ACN14a; counts= 1; multicellularity status: TRUE**
  - FHA+??+low-complexity+FHA+ABC-ATPase+TM->||<-?||EACC1+EAD1*->||<-CASPASE+STAND+polar_region+TM+BetaPropeller
- **GCA_000284035.1; Nocardia cyriacigeorgica GUH-2; counts= 1; multicellularity status: TRUE**
  - RNR_N+Ribonuc_red_lgN+Ribonuc_red_lgC->EACC1*->CASPASE+FTSK+FTSK+FTSK+FTSK->
- **GCA_000826545.1; Kibdelosporangium sp. MJ126-NF4; counts= 1; multicellularity status: TRUE**
  - PALP->Trp_syntA->TM+LGT->EACC1*->
- **GCA_000170715.1; Beggiatoa sp. PS; counts= 1; multicellularity status: TRUE**
  - EACC1*->
- **GCA_000154945.1; Streptomyces pristinaespiralis ATCC 25486; counts= 1; multicellularity status: TRUE**
  - low-complexity+HD+Tox-RelA+TGS+ACT->Pkinase+TPRs->EACC1*->CASPASE+TPRs->
- **GCA_000158815.1; Micromonospora sp. ATCC 39149; counts= 1; multicellularity status: TRUE**
  - TM+TM+TM+Peptidase_M48+TM+DUF4864+??->EACC1*->
- **GCA_000156455.1; Streptomyces roseosporus NRRL 15998; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+Beta_rich_repeat->
- **GCA_000162775.1; Streptomyces sp. e14; counts= 1; multicellularity status: TRUE**
  - TPRs->EACC1*->CASPASE+TPRs->
- **GCA_000158975.1; Streptomyces griseoflavus Tu4000; counts= 1; multicellularity status: TRUE**
  - MglB->?->sGTP-MglA->?->Beta_rich?->EACC1*->CASPASE+TPRs->??->??->
- **GCA_000239075.2; Streptomyces sp. W007; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+PBPB->
- **GCA_000244955.1; Saccharomonospora marina XMU15; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+TM+TM+TM+TM->
- **GCA_000340335.2; Streptomyces bottropensis ATCC 25435; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+TPRs->
- **GCA_000497445.1; Streptomyces roseochromogenus subsp. oscitans DS 12.976; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+BetaPropeller->||<-?<-?||HATPase_c_2->
- **GCA_000498935.1; Streptomyces sp. HCCB10043; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+Beta_rich_repeat->

- **GCA_000564855.1; Actinokineospora spheciospongiae; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+??+ART->
- **GCA_000707925.1; Streptomyces rimosus R6-500; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+??+SF1-helicase+Vsr(PDDEXK)?->REase+STAND->
- **GCA_000811985.1; Nocardia vulneris; counts= 1; multicellularity status: TRUE**
  - DUF2510(W3)+BicD+DUF4041+T5orf172->EACC1*->
- **GCA_000817655.1; Streptomyces sp. RSD-27; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+STAND(fragment)->AAA(fragment-helical-region)+wHTH+TM+BetaPropeller->
- **GCA_000932205.1; Streptomyces sp. MBRL 601; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+STAND+TM+polar_region+TM+BetaPropeller->
- **GCA_000966955.1; Streptomyces sp. NRRL S-495; counts= 1; multicellularity status: TRUE**
  - FAD_binding_4+FAD-oxidase_C->DAGK_cat+DAGK_acc->EACC1*->
- **GCA_000967025.1; Streptomyces sp. NRRL B-1568; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->
- **GCA_001279885.1; Streptomyces sp. XY593; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+??+SF1-helicase+Vsr(PDDEXK)?->
- **GCA_001279805.1; Streptomyces sp. XY431; counts= 1; multicellularity status: TRUE**
  - EACC1*->
- **GCA_001280005.1; Streptomyces sp. NRRL WC-3618; counts= 1; multicellularity status: TRUE**
  - EACC1*->
- **GCA_001426245.1; Phycicoccus sp. Root101; counts= 1; multicellularity status: NA**
  - EACC1*->CASPASE+??+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM->
- **GCA_001426405.1; Streptomyces sp. Root1304; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->||<-MFS_1
- **GCA_001456965.1; Rhodococcus enclensis; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+??->
- **GCA_001482415.1; Streptomyces silvensis; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+Type_III_YscG+VHL->
- **GCA_001509495.1; Actinoplanes awajinensis subsp. mycoplanecinus; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+??->

■ **GCA_001541145.1; Streptomyces albus subsp. albus; counts= 1; multicellularity status: TRUE**

- EACC1*->

■ **GCA_001666935.1; Mycobacterium sp. E188; counts= 1; multicellularity status: FALSE**

- EACC1*->TM+TM->

■ **GCA_001746415.1; Streptomyces agglomeratus; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+BetaPropeller->

■ **GCA_001188955.3; Kitasatospora aureofaciens; counts= 1; multicellularity status: TRUE**

- EACC1*->

■ **GCA_001866675.1; Streptomyces sp. MUSC 14; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->

■ **GCA_001905645.1; Streptomyces sp. CB02115; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+Beta_rich_repeat->??+SUKH->

■ **GCA_001905845.1; Streptomyces sp. TSRI0107; counts= 1; multicellularity status: TRUE**

- EACC1*->

■ **GCA_001905365.1; Streptomyces sp. CB02488; counts= 1; multicellularity status: TRUE**

- MglB->DUF742->sGTP-MglA->?->?->EACC1*->

■ **GCA_001920315.1; Catenulispora sp. 13_1_20CM_3_70_7; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+PBPB->

■ **GCA_001942255.1; Nocardiopsis sp. CNR-923; counts= 1; multicellularity status: TRUE**

- EACC1*->

■ **GCA_002027195.1; Streptomyces sp. GKU 895; counts= 1; multicellularity status: TRUE**

- EACC1*->

■ **GCA_002104855.1; Streptomyces sp. 4F; counts= 1; multicellularity status: TRUE**

- low-complexity+HD+Tox-RelA+TGS+ACT->Pkinase+TPRs->EACC1*->CASPASE+TPRs->

■ **GCA_002276245.1; Streptomyces sp. alain-838; counts= 1; multicellularity status: TRUE**

- low-complexity+HD+Tox-RelA+TGS+ACT->Pkinase+TPRs->EACC1*->CASPASE+TPRs->

■ **GCA_002564045.1; Amycolatopsis sulphurea; counts= 1; multicellularity status: TRUE**

- GATase->ABC-ATPase+DUF4162->cNMP_cyclase+TM+TM+TM+TM+TM+TM->EACC1*->

■ **GCA_002754455.1; Streptomyces sp. 2233.5; counts= 1; multicellularity status: TRUE**

- Phage_int_SAM_3+Phage_integrase->EACC1*->CASPASE+TPRs->

■ **GCA_002754595.1; Streptomyces sp. 93; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->

■ **GCA_002754535.1; Streptomyces sp. 61; counts= 1; multicellularity status: TRUE**

- low-complexity+HD+Tox-RelA+TGS+ACT->Pkinase+TPRs->EACC1*->CASPASE+TPRs->

■ **GCA_002784125.1; Flexibacter sp. CG_4_10_14_3_um_filter_32_15; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+??->

■ **GCA_001896795.2; Thermomonospora sp. CIF 1; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+??+NUDIX->

■ **GCA_002911015.1; Streptomyces populi; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE(fragment)->

■ **GCA_002846315.1; Streptomyces sp. 73; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->

■ **GCA_002846625.1; Streptomyces sp. OK885; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+TPRs->Pkinase+??->

■ **GCA_002855875.1; Klebsiella pneumoniae; counts= 1; multicellularity status: FALSE**

- EACC1*->

■ **GCA_002920575.1; Streptomyces sp. Ru73; counts= 1; multicellularity status: TRUE**

- EACC1*->

■ **GCA_002920535.1; Streptomyces sp. Ru71; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+TPRs->Clp_N+Clp_N+ClpABN-AAA->

■ **GCA_003001935.1; Nonomuraea fuscirosea; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+PBPB->

■ **GCA_003002955.1; Glycomyces artemisiae; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+TPRs->

■ **GCA_900067225.1; Candidatus Frankia californiensis; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+SF1-helicase->

■ **GCA_900091795.1; Streptomyces sp. Termitarium-T10T-6; counts= 1; multicellularity status: TRUE**

- low_complexity+EACC1*->CASPASE+GAF+PAS->

■ **GCA_900091835.1; Streptomyces sp. PpalLS-921; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+STAND+PBPB->

■ **GCA_900091965.1; Streptomyces sp. Ncost-T6T-2b; counts= 1; multicellularity status: TRUE**

- EACC1*->

■ **GCA_900092015.1; Streptomyces sp. MnatMP-M27; counts= 1; multicellularity status: TRUE**

- TetR_N+TetR_C_6->EACC1*->CASPASE+TPRs->

■ **GCA_900090165.1; Streptomyces sp. AmelKG-E11A; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+TPRs->

■ **GCA_900101745.1; Glycomyces harbinensis; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+TPRs->

■ **GCA_900100325.1; Frankineae bacterium MT45; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+low-complexity+DUF4190(has2TM)->

■ **GCA_900103585.1; Streptomyces sp. cf386; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+TPRs->

■ **GCA_900099985.1; Thermostaphylospora chromogena; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+Astro_capsid_N->

■ **GCA_900106995.1; Saccharopolyspora shandongensis; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->

■ **GCA_900108315.1; Saccharopolyspora hirsuta; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+BetaPropeller->BetaPropeller(fragment)->

■ **GCA_900107965.1; Streptomyces yanglinensis; counts= 1; multicellularity status: TRUE**

- low-complexity+HD+Tox-RelA+TGS+ACT->Pkinase+TPRs->EACC1*->CASPASE+TPRs->

■ **GCA_900109115.1; Xiangella phaseoli; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+Pkinase->

■ **GCA_900115345.1; Amycolatopsis rubida; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+??+SF1-helicase+Vsr(PDDEXK)?->vWA->

■ **GCA_900115095.1; Actinomadura madurae; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+??+TM+TM+TM->

■ **GCA_900119365.1; Streptomyces atratus; counts= 1; multicellularity status: TRUE**

- EACC1*->

■ **GCA_900142575.1; Streptomyces paucisporeus; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->

■ **GCA_900143515.1; Micromonospora cremea; counts= 1; multicellularity status: TRUE**

- EACC1*->

■ **GCA_900188025.1; Blastococcus sp. DSM 44272; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+TM+TM+TM+TM+TM+TM+TM+TM->Aminotran_5->

■ **GCA_900188205.1; Geodermatophilus saharensis; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+??+TM+TM->

■ **GCA_900230215.1; Jatrophihabitans sp. GAS493; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+low-complexity+DUF4190(has2TM)->?->Glyoxalase->

■ **GCA_900215565.1; Streptomyces sp. Ag109_G2-15; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->TM+Acid_phosphat_B->

■ **GCA_900230275.1; Streptomyces sp. OV198; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+TM+PBPI->

■ **GCA_900236475.1; Streptomyces chartreusis NRRL 3882; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->

■ **GCA_001693675.1; Streptomyces clavuligerus; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+??+SF1-helicase+Vsr(PDDEXK)?->

■ **GCA_000331185.1; Streptomycetaceae; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+TM?+Phytase-like->

■ **GCA_000342125.1; Streptomyces mobaraensis; counts= 1; multicellularity status: TRUE**

- EACC1*->

■ **GCA_000342345.1; Streptomyces; counts= 1; multicellularity status: TRUE**

- TM+TM+TM+PP2C->??->EACC1*->CASPASE+TM+TM+PBPB+vWA->

■ **GCA_000331005.1; Streptomyces turgidiscabies; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+TM+TM+bPH_domain+TM+TM+bPH_domain+TM+TM->

■ **GCF_000231035.2; Saccharomonospora paurometabolica; counts= 1; multicellularity status: TRUE**

- CASPASE+??->EACC1*->

■ **GCA_000342005.1; Amycolatopsis decaplanina; counts= 1; multicellularity status: TRUE**

- MFS_1->?->||<-?||EACC1*->

■ **GCA_000154965.1; Streptomyces sviceus; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+??+SF1-helicase+Vsr(PDDEXK)?->

■ **GCA_000297395.2; Micromonospora lupini; counts= 1; multicellularity status: TRUE**

- EACC1*->

■ **GCA_000225525.2; Streptomyces zinciresistens; counts= 1; multicellularity status: TRUE**

- HATPase_c_2->EACC1*->CASPASE+??+SF1-helicase+Vsr(PDDEXK)?->

■ **GCA_000178855.1; Ktedonobacter racemifer; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+STAND+??->

■ **GCA_000154885.1; Streptomyces sp. Mg1; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->

■ **GCA_002796545.1; Actinobacteria; counts= 1; multicellularity status: TRUE**

- EACC1*->

■ **GCA_000448385.1; Saccharopolyspora erythraea; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+??+SF1-helicase+Vsr(PDDEXK)?->

■ **GCF_000226455.1; Streptomyces chartreusis; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->

■ **GCA_001485105.1; Streptomyces acidiscabies; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+TM+TM+PBPB+vWA->

■ **GCF_000203835.1; Streptomyces coelicolor; counts= 1; multicellularity status: TRUE**

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■ **GCA_000010605.1; Streptomyces griseus; counts= 1; multicellularity status: TRUE**

- Beta_rich?->EACC1*->CASPASE+TPRs->??->??->

■ **GCA_000024865.1; Streptosporangium roseum; counts= 1; multicellularity status: TRUE**

- EACC1+??*->

■ **GCA_000092985.1; Nocardiopsis dassonvillei; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+TM?+Phytase-like->

■ **GCA_000166135.1; Frankia inefficax; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+TIR->

■ **GCA_000092385.1; Streptomyces; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+TM+TM+??+TM+TM+??+TM+TM+??->

■ **GCA_000265505.1; Bernardetia litoralis; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+??->

- **GCA_000311765.1; Gluconobacter oxydans; counts= 1; multicellularity status: FALSE**
  - EACC1*->CASPASE+GAPEAD1->
- **GCA_000024025.1; Catenulispora acidiphila; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+low-complexity+BetaPropeller->CASPASE+low-complexity+BetaPropeller->
- **GCA_000023245.1; Actinosynnema mirum; counts= 1; multicellularity status: TRUE**
  - EACC1*->
- **GCA_000963515.1; Streptomyces albulus; counts= 1; multicellularity status: TRUE**
  - EACC1*->
- **GCF_000309385.1; Nodosilinea nodulosa; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+DUF4062+??+HATPase_c_4+STAND->
- **GCF_000341105.1; Nocardiopsis potens; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+TM?+Phytase-like->
- **GCF_000341025.1; Nocardiopsis salina; counts= 1; multicellularity status: TRUE**
  - EACC1*->
- **GCA_000739085.1; Amycolatopsis methanolica; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->
- **GCF_000379825.1; Longispora albida; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->
- **GCA_001445835.1; Streptomyces vitaminophilus; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+TPRs->
- **GCF_000373305.1; Streptomyces sp. CcalMP-8W; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+TPRs??+GHKL_ATPase+TPRs??->
- **GCF_000373665.1; Streptomyces sp. BoleA5; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+PBPB+vWA->
- **GCF_000374305.1; Actinomadura flavalba; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+SAD+HNH->
- **GCF_000374445.1; Actinokineospora enzanensis; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+TPRs->
- **GCF_000377165.1; Streptomyces sp. CNY243; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+??->

- **GCF_000377545.1; Streptomyces sp. CNY228; counts= 1; multicellularity status: TRUE**
  - TM+REase->EACC1*->CASPASE+??+SF1-helicase+Vsr(PDDEXK)?->
- **GCF_000377965.1; Streptomyces sp. CNB091; counts= 1; multicellularity status: TRUE**
  - Beta_rich?->EACC1*->CASPASE+TPRs->??->??->
- **GCF_000367365.1; Streptomyces prunicolor; counts= 1; multicellularity status: TRUE**
  - polar_lead?+TM+TM+TM+polar_tail?+low-complexity->??->EACC1*->CASPASE+TPRs->
- **GCF_000376565.1; Streptomyces hokutonensis; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+STAND+BetaPropeller->
- **GCA_002260685.1; Nocardiopsis; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+TM?+Phytase-like->
- **GCF_000469645.1; Rhodococcus; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+??->
- **GCF_000384175.1; Streptomyces purpureus; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->
- **GCF_000383935.1; Streptomyces sp. Amel2xE9; counts= 1; multicellularity status: TRUE**
  - TPRs->EACC1*->CASPASE+TPRs->
- **GCF_000340335.1; Streptomyces bottropensis; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+TPRs->
- **GCF_000383615.1; Streptomyces canus; counts= 1; multicellularity status: TRUE**
  - low-complexity+HD+Tox-RelA+TGS+ACT->Pkinase+TPRs->EACC1*->CASPASE+TPRs->
- **GCF_000383655.1; Streptomyces sp. 351MFTsu5.1; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+TPRs->
- **GCF_000383675.1; Terracoccus sp. 273MFTsu3.1; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+??+TM+TM+TM+TM+TM+TM+TM+TM->
- **GCF_000231075.2; Amycolatopsis sp. ATCC 39116; counts= 1; multicellularity status: TRUE**
  - Pkinase+TM+TM+DUF3298+PSBP->EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->||<-?||?->||<-PSE<-?<-?<-FAD_binding_4+??+BBE
- **GCA_000018005.1; Frankia sp. EAN1pec; counts= 1; multicellularity status: TRUE**
  - ??+TM+BetaPropeller->TIR+EACC1+EAD1*->
- **GCF_000379645.1; Actinoplanes globisporus; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->

■ **GCF_000383915.1; Amycolatopsis benzoatilytica; counts= 1; multicellularity status: TRUE**

- GATase->ABC-ATPase+DUF4162->cNMP_cyclase+TM+TM+TM+TM+TM+TM->EACC1*->

■ **GCF_000384315.1; Amycolatopsis nigrescens; counts= 1; multicellularity status: TRUE**

- ??+TM+TM+??+TM->PBPB->EACC1*->CASPASE+TPRs->PknG_rubred+Pkinase+PknG_TPR->ZnR+PP2C->vWA+alpha-helical->

■ **GCF_000526215.1; Nocardia sp. BMG51109; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+??->

■ **GCF_000468475.2; Actinomadura madurae; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+??+TM+TM+TM->

■ **GCF_000512185.1; Aeromonas hydrophila; counts= 1; multicellularity status: FALSE**

- EACC1*->

■ **GCF_000525635.1; Kutzneria albida; counts= 1; multicellularity status: TRUE**

- polar_lead?+TM+TM+TM+polar_tail?+low-complexity->??->EACC1*->CASPASE+TPRs->?->CASPASE+??+TPRs?->

■ **GCA_900116145.1; Streptomyces; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+??+SF1-helicase+Vsr(PDDEXK)?->

■ **GCF_000620185.1; Geodermatophilaceae bacterium URHB0062; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+TM+TM+TM+TM+TM+TM+TM+TM->

■ **GCF_000427885.1; Glycomyces tenuis; counts= 1; multicellularity status: TRUE**

- EACC1*->

■ **GCF_000422585.1; Hugenholtzia roseola; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+??->

■ **GCF_000482585.1; Streptomyces sp. CNQ329; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+STAND+TPRs->

■ **GCF_000473265.1; Amycolatopsis thermoflava; counts= 1; multicellularity status: TRUE**

- Pkinase+TM+TM+DUF3298+PSBP->EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->

■ **GCF_000647875.1; Streptomyces sp. SolWspMP-sol2th; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+TPRs??+GHKL_ATPase+TPRs??->

■ **GCF_000426165.1; Streptomyces sp. TAA486; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+TPRs->

■ **GCF_000422825.1; Nocardioides insulae; counts= 1; multicellularity status: TRUE**

- EACC1*->

- **GCA_000710755.1; Saccharopolyspora rectivirgula; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+??+SF1-helicase+Vsr(PDDEXK)?->
- **GCF_000717015.1; Streptomyces; counts= 1; multicellularity status: TRUE**
  - low-complexity+HD+Tox-RelA+TGS+ACT->Pkinase+TPRs->EACC1*->CASPASE+TPRs->
- **GCF_000717245.1; [Kitasatospora] papulosa; counts= 1; multicellularity status: TRUE**
  - EACC1*->
- **GCF_000717915.1; Streptomyces sp. NRRL S-244; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+??+SF1-helicase+Vsr(PDDEXK)?->
- **GCA_004364985.1; Glycomyces sp. NRRL B-16210; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+TPRs->
- **GCF_000718945.1; Streptomyces sp. NRRL S-813; counts= 1; multicellularity status: TRUE**
  - ??->EACC1*->
- **GCA_900090135.1; Streptomyces; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+Concanavalin?->
- **GCF_000719335.1; Streptomyces sp. NRRL S-87; counts= 1; multicellularity status: TRUE**
  - low-complexity+HD+Tox-RelA+TGS+ACT->Pkinase+TPRs->EACC1*->CASPASE+TPRs->
- **GCA_002082175.1; Streptomyces; counts= 1; multicellularity status: TRUE**
  - low-complexity+HD+Tox-RelA+TGS+ACT->Pkinase+TPRs->EACC1*->CASPASE+TPRs->
- **GCF_000718785.1; Streptomyces sp. NRRL WC-3626; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->HTH+N6_Mtase+Methylase_S->
- **GCF_000717875.1; Streptomyces; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+STAND+??+TPRs+??->
- **GCA_001279425.1; Streptomyces; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+Concanavalin?->
- **GCA_000707945.1; Streptomycetaceae; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+??+SF1-helicase+Vsr(PDDEXK)?->REase+STAND->
- **GCF_000717665.1; Streptomyces floridae; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+Concanavalin?->
- **GCF_000719065.1; Herbidospora cretacea; counts= 1; multicellularity status: TRUE**

- EACC1*->

- **GCF_000720835.1; Streptomyces achromogenes; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+??+SF1-helicase+Vsr(PDDEXK)?->
- **GCA_900090065.1; Streptomyces; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+??+SF1-helicase+Vsr(PDDEXK)?->
- **GCF_000720405.1; Streptomyces sp. NRRL B-24051; counts= 1; multicellularity status: TRUE**
  - EACC1*->
- **GCF_000721105.1; Streptomyces cellulosae; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+TPRs->
- **GCA_900090075.1; Streptomyces; counts= 1; multicellularity status: TRUE**
  - Beta_rich?->EACC1*->CASPASE+TPRs->??->??->
- **GCF_000720115.1; Streptomyces sp. NRRL F-2580; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+??+SF1-helicase+Vsr(PDDEXK)?->
- **GCF_000719915.1; Streptomyces sp. NRRL F-2890; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+TPRs->??->??->
- **GCF_000718235.1; Streptomyces griseus; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+TPRs->
- **GCA_000966965.1; Streptomyces; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+??+SF1-helicase+Vsr(PDDEXK)?->
- **GCA_001279005.1; Streptomyces; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+STAND+??+TPRs->
- **GCF_000719855.1; Streptomyces sp. NRRL F-4474; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+TPRs->
- **GCA_001270595.1; Streptomyces varsoviensis; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+Pkinase+TM?+??->
- **GCF_000721305.1; Streptomyces sp. NRRL S-1868; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+TPRs->
- **GCF_000721445.1; Streptomyces sp. NRRL F-5053; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+TPRs->
- **GCF_000721715.1; Streptomyces sp. NRRL B-24720; counts= 1; multicellularity status: TRUE**

- EACC1*->

- **GCF_000719575.1; Streptomyces sp. NRRL S-1824; counts= 1; multicellularity status: TRUE**
  - DUF262+DUF1524+DNA_binding_1+??->?->polar_lead?+TM+TM+TM+polar_tail?+low-complexity->??->EACC1*->
- **GCF_000725555.1; Streptomyces erythrochromogenes; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+??+SF1-helicase+Vsr(PDDEXK)?->
- **GCA_004219385.1; Enterobacteriaceae; counts= 1; multicellularity status: FALSE**
  - EACC1*->
- **GCF_000156455.1; Streptomyces filamentosus; counts= 1; multicellularity status: TRUE**
  - EACC1*->
- **GCA_003947585.1; Streptomyces rimosus; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+??+SF1-helicase+Vsr(PDDEXK)?->??->
- **GCA_000583715.2; Nocardia seriolae; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+STAND+TPRs->
- **GCF_000388135.1; Amycolatopsis vancoresmycina; counts= 1; multicellularity status: TRUE**
  - PBPB->?->?->Aminotran_5+PAS_6+HTH_22->EACC1*->CASPASE+??+TM+TM->||<-Glyco_trans_4_4+UDPGT
- **GCA_002189675.1; Streptomyces; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+TPRs->
- **GCF_001984445.1; Streptomyces lydicus; counts= 1; multicellularity status: TRUE**
  - Glyoxalase->EACC1*->CASPASE+DnaJ_ZnR+DnaJ_ZnR+DnaJ_C->
- **GCF_000717055.1; Streptomyces iakyrus; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+TM+TM+PBPB+vWA->
- **GCF_000797385.1; Streptomyces sp. CNQ431; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+??->
- **GCF_000787755.1; Streptacidiphilus albus; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+TPRs->Pkinase+??->
- **GCA_003182415.1; Actinokineospora spheciospongiae; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+??+ART->
- **GCF_000482865.1; Actinokineospora inagensis; counts= 1; multicellularity status: TRUE**
  - EACC1*->
- **GCF_000158815.1; Micromonospora sp. ATCC 39149; counts= 1; multicellularity status: TRUE**

- TM+TM+TM+Peptidase_M48+TM+DUF4864+??->EACC1*->

■ **GCA_005863225.1; Nocardia cyriacigeorgica; counts= 1; multicellularity status: TRUE**

- RNR_N+Ribonuc_red_lgN+Ribonuc_red_lgC->EACC1*->

■ **GCF_000478275.1; Amycolatopsis orientalis; counts= 1; multicellularity status: TRUE**

- EACC1*->

■ **GCA_000754115.1; Amycolatopsis sp. MJM2582; counts= 1; multicellularity status: TRUE**

- EACC1*->

■ **GCF_000411975.1; Amycolatopsis orientalis; counts= 1; multicellularity status: TRUE**

- EACC1*->

■ **GCF_000744815.1; Streptacidiphilus oryzae; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+TPRs->

■ **GCF_000373645.1; Streptomyces sp. ATexAB-D23; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+STAND+PBPB->

■ **GCA_003073355.1; Streptomyces scopuliridis; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->

■ **GCF_000424805.1; Streptomyces sp. CNQ865; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+Beta_rich_repeat->

■ **GCA_004217635.1; Streptomyces sp. CNQ-525; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+TPRs->

■ **GCF_000701285.1; Streptomyces sp. CNQ-525; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+Beta_rich_repeat->

■ **GCF_000426325.1; Streptomyces sp. CNS606; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+??->

■ **GCF_000720075.1; Streptomyces sp. NRRL F-3213; counts= 1; multicellularity status: TRUE**

- GATase->ABC-ATPase+DUF4162->cNMP_cyclase+TM+TM+TM+TM+TM+TM->EACC1*->

■ **GCF_000698495.1; Streptomyces sp. NTK 937; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+STAND+PBPB->

■ **GCA_000802245.2; Streptomyces; counts= 1; multicellularity status: TRUE**

- HATPase_c_2->EACC1*->CASPASE+??+SF1-helicase+Vsr(PDDEXK)?->

■ **GCF_000308435.1; Nocardia araoensis; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+TM+TM->

- **GCF_000308695.1; Nocardia takedensis; counts= 1; multicellularity status: TRUE**
  - EACC1*->
- **GCF_000308875.1; Nocardia transvalensis; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+TPRs->
- **GCF_000308815.1; Nocardia concava; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+BetaPropeller->
- **GCF_000308615.1; Nocardia jiangxiensis; counts= 1; multicellularity status: TRUE**
  - DUF262+DUF1524+DNA_binding_1+??->?->EACC1*->CASPASE+STAND+TPRs+OMPdecase->
- **GCF_000242715.1; Streptomyces acidiscabies; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+TM+TM+PBPB+vWA->
- **GCF_000308655.1; Nocardia niigatensis; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+STAND+TPRs->
- **GCA_000308475.2; Nocardia brasiliensis; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+??->
- **GCF_000162775.1; Streptomyces sp. e14; counts= 1; multicellularity status: TRUE**
  - TPRs->EACC1*->CASPASE+TPRs->
- **GCA_000819545.1; Streptomyces nodosus; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->
- **GCF_000718165.1; Streptomyces fulvoviolaceus; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+TPRs->
- **GCA_001190165.1; Streptomyces; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+PBPB+vWA->
- **GCF_000716435.1; Streptomyces xylophagus; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+TPRs->
- **GCF_000411995.1; Amycolatopsis orientalis; counts= 1; multicellularity status: TRUE**
  - GATase->ABC-ATPase+DUF4162->cNMP_cyclase+TM+TM+TM+TM+TM+TM->EACC1*->
- **GCA_000876225.1; Micromonospora carbonacea; counts= 1; multicellularity status: TRUE**
  - ??+TM+TM+TM+Peptidase_M48+TM+DUF4864+??->EACC1*->
- **GCF_000931445.1; Streptomyces cyaneogriseus; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+Pkinase->

- **GCA_000943515.2; Amycolatopsis orientalis; counts= 1; multicellularity status: TRUE**
  - EACC1*->
- **GCA_000955955.1; Lechevalieria aerocolonigenes; counts= 1; multicellularity status: TRUE**
  - EACC1*->
- **GCF_000958545.1; Streptomyces sp. FxanaA7; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+TM+TM+bPH_domain+TM+TM+bPH_domain+TM+TM->
- **GCA_003687835.1; Enterobacteriaceae; counts= 1; multicellularity status: FALSE**
  - EACC1*->
- **GCF_000718635.1; Streptomyces varsoviensis; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+Pkinase+TM?+??->
- **GCA_001280045.1; Streptomyces; counts= 1; multicellularity status: TRUE**
  - EACC1*->PSE->MDMPI_N+MDMPI_C->META->
- **GCF_900092705.1; Escherichia coli; counts= 1; multicellularity status: FALSE**
  - EACC1*->
- **GCF_000719175.1; Kitasatospora aureofaciens; counts= 1; multicellularity status: TRUE**
  - EACC1*->
- **GCF_001189015.1; Streptomyces acidiscabies; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+TM+TM+PBPB+vWA->
- **GCF_000715845.1; Streptomyces monomycini; counts= 1; multicellularity status: TRUE**
  - EACC1*->
- **GCF_000716515.1; Streptomyces rimosus; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+TM?+Phytase-like->
- **GCF_000514555.1; Salinispora arenicola; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->
- **GCF_000158975.1; Streptomyces griseoflavus; counts= 1; multicellularity status: TRUE**
  - MglB->DUF742->sGTP-MglA->?->Beta_rich?->EACC1*->CASPASE+TPRs->??->??->
- **GCF_000154945.1; Streptomyces pristinaespiralis; counts= 1; multicellularity status: TRUE**
  - low-complexity+HD+Tox-RelA+TGS+ACT->Pkinase+TPRs->EACC1*->CASPASE+TPRs->
- **GCF_000058485.1; Frankia alni; counts= 1; multicellularity status: TRUE**

- FHA+??+low-complexity+FHA+ABC-ATPase+TM->EACC1+EAD1*->||<-CASPASE+STAND+polar_region+TM+BetaPropeller

- **GCF_000308755.1; Nocardia pneumoniae; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->
- **GCF_000284295.1; Actinoplanes missouriensis; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+TPRs->
- **GCF_000316095.1; Streptomyces viridosporus; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+TPRs->??->??->
- **GCF_000308515.1; Nocardia carnea; counts= 1; multicellularity status: TRUE**
  - EACC1*->
- **GCF_000308455.1; Nocardia abscessus; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->
- **GCF_000308575.1; Nocardia exalbida; counts= 1; multicellularity status: TRUE**
  - Pkinase+TM+LppX_LprAFG->CASPASE+TPRs->EACC1*->
- **GCF_000426185.1; Cellulomonas sp. URHD0024; counts= 1; multicellularity status: FALSE**
  - EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->
- **GCF_000429085.1; Streptomyces flavidovirens; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+TM?+Phytase-like->
- **GCA_003752125.1; Amycolatopsis thermoflava; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+TM+TM+TM+TM->
- **GCF_000428945.1; Hamadaea tsunoensis; counts= 1; multicellularity status: TRUE**
  - PBPB->?->?->?->?->?->EACC1*->
- **GCA_000696185.1; Kitasatospora cheerisanensis; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+??+ZnR+ZnR->
- **GCF_000695235.1; Streptomyces albulus; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+TM+TM+bPH_domain?->
- **GCF_000701325.1; Streptomyces sp. URHA0041; counts= 1; multicellularity status: TRUE**
  - Pkinase+TPRs->EACC1*->CASPASE+TPRs->
- **GCA_001294325.1; Streptomyces sp. NRRL F-5917; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+TPRs->
- **GCF_000719095.1; Streptacidiphilus jeojiense; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+TPRs->Pkinase+??->

■ **GCF_000719495.1; Streptomyces griseus; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+??->

■ **GCF_000717175.1; Pseudonocardia autotrophica; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->

■ **GCF_000710405.2; Kitasatospora sp. MBT66; counts= 1; multicellularity status: TRUE**

- FAD_binding_4+FAD-oxidase_C->DAGK_cat+DAGK_acc->EACC1*->CASPASE+TPRs->?->Clp_N+Clp_N+ClpABN-AAA->

■ **GCA_900176525.1; Lentzea albidocapillata; counts= 1; multicellularity status: TRUE**

- TM+TM+BPD_transp_1->OppC_N+TM+TM+BPD_transp_1->ABC-ATPase+ABC-ATPase->PBPB->TM+Beta_rich+TM+Beta_rich+TM+TM->EACC1+CASPASE+TPR_repeats+low_complexity+TM_region*->

■ **GCF_000719695.1; Streptomyces sp. NRRL F-6131; counts= 1; multicellularity status: TRUE**

- FAD_binding_4+FAD-oxidase_C->DAGK_cat+DAGK_acc->EACC1*->CASPASE+TPRs->Clp_N+Clp_N+ClpABN-AAA->

■ **GCF_000717135.1; Catenuloplanes japonicus; counts= 1; multicellularity status: TRUE**

- METHYLASE->EACC1*->CASPASE+TM+TM+TM+TM->

■ **GCF_000721345.1; Kitasatospora sp. NRRL B-11411; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+alpha-helical+TM+TM+??+TM+TM->

■ **GCF_000717945.1; Streptomyces sp. NRRL S-920; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+GAF+PAS+GGDEF->

■ **GCF_000717595.1; Streptomyces flavochromogenes; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+TPRs+LysM+PG-binding->

■ **GCF_000720805.1; Streptomyces violaceoruber; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+TM+TM+bPH_domain?->

■ **GCA_001513955.1; Streptomyces; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+GAF+PAS->

■ **GCF_000720765.1; Streptomyces sp. NRRL S-646; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+??+TM+??->

■ **GCF_000717655.1; Streptomyces katrae; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+??->

■ **GCF_000720635.1; Streptomyces sp. NRRL WC-3742; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+??+TPRs->

■ **GCF_000725705.1; Streptomyces sp. NRRL S-623; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+TPRs->

- **GCF_000718375.1; Streptomyces; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->
- **GCF_000718315.1; Streptomyces griseofuscus; counts= 1; multicellularity status: TRUE**
  - EACC1*->
- **GCA_003933295.1; Streptomyces griseofuscus; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+GAF+PAS->
- **GCF_000720475.1; Streptomyces aureocirculatus; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+PBPB->
- **GCA_003846255.1; Streptomyces anulatus; counts= 1; multicellularity status: TRUE**
  - Beta_rich?->EACC1*->CASPASE+TPRs->??->??->
- **GCF_000725545.1; Streptomyces exfoliatus; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+TPRs->DUF664->
- **GCF_000745345.1; Streptomyces yeochonensis; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+TPRs->
- **GCF_000744705.1; Streptacidiphilus albus; counts= 1; multicellularity status: TRUE**
  - EACC1*->||<-?<-?||Pkinase+??->
- **GCF_000785985.1; Actinoplanes utahensis; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+??->
- **GCF_001613425.1; Nocardia vulneris; counts= 1; multicellularity status: TRUE**
  - DUF2510(W3)+BicD+DUF4041+T5orf172->EACC1*->CASPASE+TPRs->
- **GCF_000519205.1; Amycolatopsis taiwanensis; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+CLP_protease->
- **GCF_000739045.1; Streptomyces luteus; counts= 1; multicellularity status: TRUE**
  - low-complexity+HD+Tox-RelA+TGS+ACT->Pkinase+TPRs->EACC1*->CASPASE+TPRs->
- **GCA_000761215.1; Streptomyces glaucescens; counts= 1; multicellularity status: TRUE**
  - EACC1*->AB_hydrolase->
- **GCF_000826545.1; Kibdelosporangium sp. MJ126-NF4; counts= 1; multicellularity status: TRUE**
  - PALP->Trp_syntA->TM+LGT->EACC1*->
- **GCF_000938975.1; Streptomyces iranensis; counts= 1; multicellularity status: TRUE**

- EACC1*->

- **GCF_000967025.1; Streptomyces sp. NRRL B-1568; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->
- **GCF_000966955.1; Streptomyces sp. NRRL S-495; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+TPRs->Clp_N+Clp_N+ClpABN-AAA->
- **GCF_000720235.1; Streptomyces; counts= 1; multicellularity status: TRUE**
  - EACC1*->
- **GCA_005490965.1; Streptomyces sp. MBT28; counts= 1; multicellularity status: TRUE**
  - low-complexity+HD+Tox-RelA+TGS+ACT->Pkinase+TPRs->EACC1*->CASPASE+TPRs->
- **GCF_000974985.2; Streptomyces mangrovisoli; counts= 1; multicellularity status: TRUE**
  - Pkinase+TPRs->EACC1*->CASPASE+TPRs->
- **GCF_001011035.1; Streptomyces sp. CNQ-509; counts= 1; multicellularity status: TRUE**
  - EACC1+CASPASE+Phytase-like*->Phytase-like->
- **GCF_000718775.1; Streptomyces sp. NRRL S-31; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+TM+??->
- **GCF_001044425.1; Streptomyces roseus; counts= 1; multicellularity status: TRUE**
  - low-complexity+HD+Tox-RelA+TGS+ACT->Pkinase+TPRs->EACC1*->CASPASE+TPRs->
- **GCA_002249075.1; Enterobacteriaceae; counts= 1; multicellularity status: FALSE**
  - EACC1*->
- **GCA_001279445.1; Streptomyces; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+TPRs->
- **GCA_001279855.1; Streptomyces; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+TPRs->
- **GCF_001279805.1; Streptomyces sp. XY431; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+TPRs->Clp_N+Clp_N+ClpABN-AAA->
- **GCA_001279555.1; Micromonospora sp. NRRL B-16802; counts= 1; multicellularity status: TRUE**
  - EACC1*->
- **GCF_001279725.1; Streptomyces sp. WM4235; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+??+SF1-helicase+Vsr(PDDEXK)?->
- **GCA_001279725.1; Streptomyces sp. WM4235; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+TM?+BetaPropeller->

- **GCF_001279885.1; Streptomyces sp. XY593; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+??+SF1-helicase+Vsr(PDDEXK)?->
- **GCF_001279655.1; Streptomyces sp. WM6372; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+??->
- **GCA_001279525.1; Nocardia sp. NRRL S-836; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+Cpn60_TCP1->
- **GCA_001279775.1; Streptomyces sp. MMG1533; counts= 1; multicellularity status: TRUE**
  - EACC1*->
- **GCF_001279775.1; Streptomyces sp. MMG1533; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+STAND+TPRs->
- **GCF_001280885.1; Streptomyces sp. XY332; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+??->
- **GCF_001279345.1; Streptomyces rimosus; counts= 1; multicellularity status: TRUE**
  - EACC1*->
- **GCF_001282115.1; Streptomyces sp. NRRL B-24085; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+BetaPropeller->
- **GCF_001294335.1; Streptomyces chattanoogensis; counts= 1; multicellularity status: TRUE**
  - PAS+GAF+PP2C+HATPase_c_2->EACC1*->
- **GCA_001292625.1; Shimia sp. SK013; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+TM+??->
- **GCA_900070365.1; Alloactinosynnema sp. L-07; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+STAND+TPRs->
- **GCA_002056725.1; Comamonas kerstersii; counts= 1; multicellularity status: FALSE**
  - EACC1*->
- **GCA_001302585.1; Kibdelosporangium phytohabitans; counts= 1; multicellularity status: TRUE**
  - PALP->Trp_syntA->TM+LGT->EACC1*->
- **GCF_001618405.1; Nocardia arizonensis; counts= 1; multicellularity status: TRUE**
  - EACC1*->
- **GCA_001414035.1; Frankia sp. ACN1ag; counts= 1; multicellularity status: TRUE**

- <-CASPASE+STAND+polar_region+TM+BetaPropeller||EACC1+EAD1*->

- **GCA_002005225.1; Streptomyces pactum; counts= 1; multicellularity status: TRUE**
  - polar_lead?+TM+TM+TM+polar_tail?+low-complexity->??->EACC1*->CASPASE+TPRs->
- **GCF_001418495.1; Streptomyces pathocidini; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+Peripla_BP_5->
- **GCF_001418565.1; Streptomyces graminilatus; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+PBPB->
- **GCF_001418325.1; Streptomyces atriruber; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+TPRs->
- **GCF_001418575.1; Streptomyces griseoplanus; counts= 1; multicellularity status: TRUE**
  - ??->EACC1*->CASPASE+TPRs->
- **GCF_001418415.1; Streptomyces hirsutus; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->
- **GCF_001418165.1; Streptomyces prasinus; counts= 1; multicellularity status: TRUE**
  - TIR+CASPASE->EACC1*->
- **GCF_001418175.1; Streptomyces hirsutus; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+TPRs->
- **GCF_001419695.1; Streptomyces prasinopilosus; counts= 1; multicellularity status: TRUE**
  - ??+CASPASE->EACC1*->
- **GCF_001748305.1; Streptomyces; counts= 1; multicellularity status: TRUE**
  - low-complexity+HD+Tox-RelA+TGS+ACT->Pkinase+TPRs->EACC1*->CASPASE+TPRs->
- **GCA_003129505.1; Streptomyces; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+TM+TM+PBPB+vWA->
- **GCF_001420875.1; Frankia sp. AvcI1; counts= 1; multicellularity status: TRUE**
  - FHA+??+low-complexity+FHA+ABC-ATPase+TM->EACC1+EAD1*->||<-CASPASE+STAND+polar_region+TM+BetaPropeller
- **GCA_001426325.1; Streptomyces; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+STAND+??+TPRs+??->
- **GCA_001429655.1; Terrabacter sp. Soil811; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+??+TM+TM+TM+TM+TM+TM+TM+TM->
- **GCA_001426615.1; Streptomyces; counts= 1; multicellularity status: TRUE**

- ??+CASPASE->EACC1*->

- **GCA_001427245.1; Streptomyces sp. Root55; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->
- **GCA_001429185.1; Terrabacter sp. Root85; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+??+TM+TM+TM+TM+TM+TM+TM+TM->
- **GCA_900094765.1; Rhodococcus enclensis; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+??->
- **GCA_002903025.1; Klebsiella pneumoniae; counts= 1; multicellularity status: FALSE**
  - EACC1*->
- **GCA_900114955.1; Streptomyces; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+TM+TM+bPH_domain+TM+TM+bPH_domain+TM+TM->
- **GCF_001550235.1; Streptomyces scabiei; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+TPRs->
- **GCA_000772045.1; Streptomyces sp. CCM_MD2014; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+TPRs->
- **GCA_001595515.1; Streptomyces sp. CC71; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE(fragment)->
- **GCF_000974485.1; Streptomyces sp. NBRC 109706; counts= 1; multicellularity status: TRUE**
  - TM+TM+TM+PP2C->EACC1*->CASPASE+PBPB+vWA->
- **GCF_001570525.1; Herbidospora sakaeratensis; counts= 1; multicellularity status: TRUE**
  - EACC1*->
- **GCA_001514235.1; Streptomyces caeruleatus; counts= 1; multicellularity status: TRUE**
  - *
- **GCA_002943895.1; Streptomyces; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->
- **GCF_001613385.1; Nocardia flavorosea; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+TPRs->
- **GCF_001612725.1; Nocardia anaemiae; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+TPRs->
- **GCF_001612865.1; Nocardia cummidelens; counts= 1; multicellularity status: TRUE**

- DUF2510(W3)+BicD+DUF4041+T5orf172->EACC1->CASPASE+TPRs->EACC1*->CASPASE+EAL->

- **GCF_001613445.1; Nocardia grenadensis; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+TPRs->
- **GCF_001613205.1; Nocardia sienata; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+??+SF1-helicase+Vsr(PDDEXK)?->
- **GCA_001632865.1; Streptomyces ambofaciens; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+GTP_EFTU+GTP_EFTU_D2+GTP_EFTU_D3->
- **GCF_001418335.1; Streptomyces aurantiacus; counts= 1; multicellularity status: TRUE**
  - EACC1*->
- **GCA_001646665.1; Streptomyces albulus; counts= 1; multicellularity status: TRUE**
  - HATPase_c_2->EACC1*->CASPASE+??+SF1-helicase+Vsr(PDDEXK)?->
- **GCA_001654495.1; Streptomyces sp. SAT1; counts= 1; multicellularity status: TRUE**
  - ??->EACC1*->CASPASE+TM+TM+PBPB+vWA->
- **GCA_001672315.1; Streptomyces sp. H-KF8; counts= 1; multicellularity status: TRUE**
  - ??->EACC1*->CASPASE+TPRs->
- **GCF_001687325.1; Streptomyces sp. PTY087I2; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+TPRs->
- **GCA_002844785.1; Enterobacteriaceae; counts= 1; multicellularity status: FALSE**
  - EACC1*->
- **GCF_001570545.1; Herbidospora mongoliensis; counts= 1; multicellularity status: TRUE**
  - EACC1*->
- **GCA_001509485.1; Streptomyces sp. NRRL F-4489; counts= 1; multicellularity status: TRUE**
  - low-complexity+HD+Tox-RelA+TGS+ACT->Pkinase+TPRs->EACC1*->CASPASE+TPRs->
- **GCA_001514035.1; Streptomyces yokosukanensis; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+TPRs->
- **GCA_001514125.1; Streptomyces longwoodensis; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+STAND+??->
- **GCA_001514285.1; Streptomyces sp. DSM 15324; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+low-complexity+BetaPropeller->
- **GCA_001704275.1; Streptomyces noursei; counts= 1; multicellularity status: TRUE**

- low-complexity+HD+Tox-RelA+TGS+ACT->Pkinase+TPRs->EACC1*->CASPASE+TPRs->

- **GCF_001612745.1; Nocardia amamiensis; counts= 1; multicellularity status: TRUE**
  - low_complexity+EACC1*->
- **GCA_004362495.1; Nocardia ignorata; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+EAL->
- **GCF_001553785.1; Actinoplanes sp. TFC3; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+SF1-helicase->
- **GCF_001613345.1; Nocardia uniformis; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+??->
- **GCA_001651785.1; Amycolatopsis; counts= 1; multicellularity status: TRUE**
  - GATase->ABC-ATPase+DUF4162->cNMP_cyclase+TM+TM+TM+TM+TM+TM->EACC1*->
- **GCF_001612615.1; Nocardia amikacinitolerans; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+TPRs->
- **GCF_001612945.1; Nocardia inohanensis; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+??->
- **GCF_001552235.1; Actinomadura; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+??+NUDIX->
- **GCF_001612825.1; Nocardia caishijiensis; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+TM+TM+TM+TM+TM+TM+TM+TM->
- **GCF_001613165.1; Nocardia mexicana; counts= 1; multicellularity status: TRUE**
  - EACC1*->
- **GCA_004563805.1; Streptomyces niveus; counts= 1; multicellularity status: TRUE**
  - EACC1*->?->PALP->
- **GCA_003353555.1; Streptomyces sp. EN27; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+TPRs->
- **GCA_001751255.1; Streptomyces nanshensis; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+STAND+??+TPRs->
- **GCA_001751305.1; Streptomyces; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+TPRs->
- **GCA_001858135.1; Enterobacter cloacae complex 'Hoffmann cluster IV'; counts= 1; multicellularity status: FALSE**

- EACC1*->

■ **GCA_001866645.1; Streptomyces sp. MUSC 93; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+??+TM+TM+??->

■ **GCA_001879105.1; Streptomyces gilvigriseus; counts= 1; multicellularity status: TRUE**

- DUF742->?->?->||<-?<-?||EACC1*->?->CASPASE+PBPB+vWA->?->||<-?||MFS_1->

■ **GCA_001884705.1; Couchioplanes caeruleus; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+DUF179->SIR2+??->??->

■ **GCF_001885705.1; Streptomyces cinnamoneus; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+TM+TM+PBPB+vWA->

■ **GCF_900119165.1; Amycolatopsis australiensis; counts= 1; multicellularity status: TRUE**

- MFS_1->||<-?||GATase->ABC-ATPase+DUF4162->cNMP_cyclase+TM+TM+TM+TM+TM+TM->EACC1*->CASPASE+TM+TM+TM+TM->EACC1->

■ **GCA_001888885.1; Streptomyces viridifaciens; counts= 1; multicellularity status: TRUE**

- EACC1*->

■ **GCF_001895105.1; Streptomyces sp. NBRC 110465; counts= 1; multicellularity status: TRUE**

- Beta_rich?->EACC1*->CASPASE+TPRs->??->??->

■ **GCA_900141985.1; Nocardiopsis flavescens; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->

■ **GCA_001905125.1; Streptomyces sp. TSRI0281; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+??+SF1-helicase+Vsr(PDDEXK)?->

■ **GCA_001905385.1; Streptomyces sp. CB02414; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+TPRs->

■ **GCF_001905385.1; Streptomyces sp. CB02414; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->

■ **GCA_001905005.1; Streptomyces sp. CB02923; counts= 1; multicellularity status: TRUE**

- SF2-helicase+RecQ_Zn_bind+RQC+HRDC->EACC1*->

■ **GCA_001905425.1; Streptomyces sp. MJM1172; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->

■ **GCA_001905025.1; Streptomyces; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->

■ **GCA_001905465.1; Kitasatospora sp. CB01950; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+TM+TM+TM+TM->

- **GCA_001905755.1; Amycolatopsis sp. CB00013; counts= 1; multicellularity status: TRUE**
  - EACC1*->
- **GCA_001905735.1; Streptomyces sp. CB01249; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+TPRs->
- **GCA_001905575.1; Streptomyces sp. CB00072; counts= 1; multicellularity status: TRUE**
  - EACC1*->
- **GCF_001905725.1; Streptomyces sp. CB02400; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->HTH+N6_Mtase+Methylase_S->
- **GCA_900141745.1; Paraburkholderia phenazinium; counts= 1; multicellularity status: FALSE**
  - EACC1*->CASPASE+TPRs->
- **GCF_900143515.1; Micromonospora cremea; counts= 1; multicellularity status: TRUE**
  - EACC1*->
- **GCA_001941625.1; Actinoalloteichus; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+??->
- **GCA_001940455.1; Actinokineospora bangkokensis; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+GTP_EFTU+GTP_EFTU_D2->
- **GCA_001953885.1; Streptomyces sp. IMTB 2501; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+TM+TM+PBPB+vWA->
- **GCA_001953865.1; Amycolatopsis coloradensis; counts= 1; multicellularity status: TRUE**
  - EACC1*->
- **GCA_001983105.1; Frankia asymbiotica; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->
- **GCA_001970135.1; Streptomyces sp. M1013; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+TPRs->
- **GCA_002006875.1; Micromonospora sp. Rc5; counts= 1; multicellularity status: TRUE**
  - ??+TM+TM+TM+Peptidase_M48+TM+DUF4864+??->?->EACC1*->
- **GCF_000497445.1; Streptomyces roseochromogenus; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+TPRs->
- **GCF_000720185.1; Streptomyces sp. NRRL S-340; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+TM+TM+PBPB+vWA->

- **GCA_002024165.1; Streptomyces scabrisporus; counts= 1; multicellularity status: TRUE**
  - EACC1*->
- **GCF_001572115.1; Streptomyces; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+TPRs->
- **GCF_001735805.1; Streptomyces puniciscabiei; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->
- **GCF_001005085.2; Streptomyces humi; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+TPRs->
- **GCF_900142595.1; Streptomyces yunnanensis; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+TM+MFS_1+TM+TM+TM+TM+TM+TM+TM+TM->
- **GCF_001905365.1; Streptomyces sp. CB02488; counts= 1; multicellularity status: TRUE**
  - MglB->DUF742->sGTP-MglA->?->?->EACC1*->CASPASE+TPRs->||<-?||?->?->DUF664->
- **GCF_001941845.1; Streptomyces sp. TN58; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+RE_Eco29kI+??->
- **GCF_001905885.1; Streptomyces sp. CB03234; counts= 1; multicellularity status: TRUE**
  - FAD_binding_4+??+BBE->EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->
- **GCF_002027195.1; Streptomyces sp. GKU 895; counts= 1; multicellularity status: TRUE**
  - EACC1*->
- **GCA_002027145.1; Microbispora sp. GKU 823; counts= 1; multicellularity status: TRUE**
  - EACC1+CASPASE+TPR_region*->
- **GCA_900129505.1; Bradyrhizobium erythrophlei; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+??+TM->
- **GCA_002754515.1; Streptomyces; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+??->
- **GCA_002057455.1; Nonomuraea sp. ATCC 55076; counts= 1; multicellularity status: TRUE**
  - ARSR-HTH+RHOD-CDC25->??->??->EACC1*->
- **GCF_002078235.1; Streptomyces viridosporus; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+TPRs->??->??->
- **GCA_001298555.1; Actinobacteria bacterium OV450; counts= 1; multicellularity status: NA**

- HATPase_c_2->EACC1*->CASPASE+??+SF1-helicase+Vsr(PDDEXK)?->

■ **GCF_001426245.1; Phycicoccus; counts= 1; multicellularity status: NA**

- EACC1*->CASPASE+??+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM->

■ **GCA_900113515.1; Amycolatopsis regifaucium; counts= 1; multicellularity status: TRUE**

- EACC1*->

■ **GCF_001509495.1; Actinoplanes awajinensis; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+??->

■ **GCA_001567585.1; Micromonospora rosaria; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+TM+TM+TM+TM+TM+TM->

■ **GCA_002082585.1; Kitasatospora albolonga; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+??+SF1-helicase+Vsr(PDDEXK)?->

■ **GCF_001886715.1; Nocardia sp. Y48; counts= 1; multicellularity status: TRUE**

- EACC1*->

■ **GCA_002099185.1; Streptomyces sp. CB03238; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE->

■ **GCA_002114065.1; Streptomyces griseofuscus; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+GAF+PAS->

■ **GCA_002128305.1; Streptomyces sp. SCSIO 03032; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->

■ **GCA_002149035.1; Streptosporangium minutum; counts= 1; multicellularity status: TRUE**

- EACC1+??*->

■ **GCF_002150765.1; Lentzea kentuckyensis; counts= 1; multicellularity status: TRUE**

- TM+TM+BPD_transp_1->OppC_N+TM+TM+BPD_transp_1->ABC-ATPase+ABC-ATPase->PBPB->TM+Beta_rich+TM+Beta_rich+TM+TM->EACC1+CASPASE+TPR_repeats+low_complexity+TM_region*->

■ **GCA_900107925.1; Amycolatopsis pretoriensis; counts= 1; multicellularity status: TRUE**

- GATase->ABC-ATPase+DUF4162->cNMP_cyclase+TM+TM+TM+TM+TM+TM->EACC1*->

■ **GCF_002154415.1; Streptomyces angustmyceticus; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+TPRs->

■ **GCF_002156075.1; Streptomyces scabiei; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+??->

■ **GCF_002154575.1; Streptomyces bobili; counts= 1; multicellularity status: TRUE**

- low-complexity+HD+Tox-RelA+TGS+ACT->Pkinase+TPRs->EACC1*->CASPASE+TPRs->

■ **GCF_002155725.1; Streptomyces scabiei; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+TPRs->

■ **GCA_006539165.1; Streptomyces cacaoi; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+TPRs->

■ **GCA_003937945.1; Amycolatopsis lexingtonensis; counts= 1; multicellularity status: TRUE**

- GATase->ABC-ATPase+DUF4162->cNMP_cyclase+TM+TM+TM+TM+TM+TM->EACC1*->

■ **GCF_002155895.1; Streptomyces rochei; counts= 1; multicellularity status: TRUE**

- low-complexity+HD+Tox-RelA+TGS+ACT->Pkinase+TPRs->EACC1*->CASPASE+TPRs->

■ **GCF_002155885.1; Streptomyces rhizosphaericus; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+STAND+TPRs->

■ **GCA_002188365.1; Streptomyces sp. CS113; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+TPRs->

■ **GCA_900091515.1; Micromonospora purpureochromogenes; counts= 1; multicellularity status: TRUE**

- TM+TM+TM+Peptidase_M48+TM+DUF4864+??->EACC1*->

■ **GCA_002266845.1; Micromonospora echinospora; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+TM+TM+TM+TM+TM+TM->

■ **GCF_900091505.1; Micromonospora chokoriensis; counts= 1; multicellularity status: TRUE**

- EACC1*->

■ **GCA_900090235.1; Micromonospora echinaurantiaca; counts= 1; multicellularity status: TRUE**

- TM+TM+TM+Peptidase_M48+TM+DUF4864+??->EACC1*->TPRs+CASPASE->

■ **GCA_900091455.1; Micromonospora coriariae; counts= 1; multicellularity status: TRUE**

- EACC1*->

■ **GCF_002140155.1; Micromonospora sp. NBS 11-29; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->

■ **GCF_900188345.1; Streptosporangium subroseum; counts= 1; multicellularity status: TRUE**

- EACC1*->

■ **GCA_900188405.1; Streptomyces glauciniger; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+PBPB+vWA->

■ **GCF_900188005.1; Actinoplanes regularis; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+TPRs->

■ **GCF_900188105.1; Actinomadura mexicana; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+TM+TM->

■ **GCF_900188025.1; Blastococcus sp. DSM 44272; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+TM+TM+TM+TM+TM+TM+TM+TM->Aminotran_5->

■ **GCA_000522445.1; Candidatus Entotheonella palauensis; counts= 1; multicellularity status: TRUE**

- RVT_1->23S_rRNA_IVP->EACC1*->

■ **GCA_900110955.1; Lechevalieria xinjiangensis; counts= 1; multicellularity status: TRUE**

- TM+TM+BPD_transp_1->OppC_N+TM+TM+BPD_transp_1->ABC-ATPase+ABC-ATPase->PBPB->TM+Beta_rich+TM+Beta_rich+TM+TM->EACC1+CASPASE+TPR_repeats+low_complexity+TM_region*->

■ **GCA_900100275.1; Lentzea violacea; counts= 1; multicellularity status: TRUE**

- TM+TM+BPD_transp_1->OppC_N+TM+TM+BPD_transp_1->ABC-ATPase+ABC-ATPase->PBPB->TM+Beta_rich+TM+Beta_rich+TM+TM->EACC1+CASPASE+TPR_repeats+low_complexity+TM_region*->

■ **GCA_900100955.1; Lechevalieria fradiae; counts= 1; multicellularity status: TRUE**

- TM+TM+BPD_transp_1->OppC_N+TM+TM+BPD_transp_1->ABC-ATPase+ABC-ATPase->PBPB->TM+Beta_rich+TM+Beta_rich+TM+TM->EACC1+CASPASE+TPR_repeats+low_complexity+TM_region*->

■ **GCA_003350445.1; Lentzea flaviverrucosa; counts= 1; multicellularity status: TRUE**

- TM+TM+BPD_transp_1->OppC_N+TM+TM+BPD_transp_1->ABC-ATPase+ABC-ATPase->PBPB->TM+Beta_rich+TM+Beta_rich+TM+TM->EACC1+CASPASE+TPR_repeats+low_complexity+TM_region*->

■ **GCA_900104175.1; Lentzea jiangxiensis; counts= 1; multicellularity status: TRUE**

- TM+TM+BPD_transp_1->OppC_N+TM+TM+BPD_transp_1->ABC-ATPase+ABC-ATPase->PSE->TM+Beta_rich+TM+Beta_rich+TM+TM->EACC1+CASPASE+TPR_repeats+low_complexity+TM_region*->

■ **GCF_900101745.1; Glycomyces harbinensis; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+TPRs->

■ **GCA_900102815.1; Glycomyces sambucus; counts= 1; multicellularity status: TRUE**

- EACC1*->

■ **GCA_001536285.1; Frankia sp. G2; counts= 1; multicellularity status: TRUE**

- EACC1+EAD1*->CASPASE+STAND+polar_region+TM+BetaPropeller->

■ **GCF_900107045.1; Amycolatopsis xylanica; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->

■ **GCF_900100325.1; Frankineae bacterium MT45; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+low-complexity+DUF4190(has2TM)->

■ **GCA_900091615.1; Micromonospora yangpuensis; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+SF1-helicase->

■ **GCA_900114035.1; Amycolatopsis sacchari; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+TM+TM+TM+TM->

- **GCA_000749465.3; Amycolatopsis lurida; counts= 1; multicellularity status: TRUE**
  - EACC1*->
- **GCA_900110575.1; Amycolatopsis saalfeldensis; counts= 1; multicellularity status: TRUE**
  - EACC1*->
- **GCF_003253475.1; Xiangella phaseoli; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+Pkinase->
- **GCA_900104725.1; Actinoplanes derwentensis; counts= 1; multicellularity status: TRUE**
  - ??+STAND+??->??+STAND+EACC1*->
- **GCF_900114325.1; Rhodanobacter glycinis; counts= 1; multicellularity status: FALSE**
  - EACC1*->
- **GCF_900111175.1; Actinokineospora terrae; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+??+TM+TM+TM+TM+TM+TM+TM+TM+TM->CASPASE+??+TM+TM+TM+TM+TM+TM+TM+TM->
- **GCA_003635025.1; Saccharopolyspora antimicrobica; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+FTSK+FTSK+FTSK+FTSK->
- **GCF_900112555.1; Saccharopolyspora; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+BetaPropeller->
- **GCA_900112325.1; Verrucosispora sediminis; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+TPRs->
- **GCF_900105695.1; Streptomyces melanosporofaciens; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->
- **GCA_002797835.1; Streptomyces; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+??->
- **GCA_003610145.1; Streptomyces sp. 2112.3; counts= 1; multicellularity status: TRUE**
  - EACC1*->
- **GCA_900105755.1; Streptomyces sp. Ag109_O5-10; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+TM+TM+BetaPropeller->
- **GCA_900113015.1; Actinoplanes philippinensis; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+PBPB+vWA->TM+PBPB->
- **GCA_900105515.1; Streptomyces sp. 2131.1; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->

■ **GCF_900112845.1; Streptomyces alni; counts= 1; multicellularity status: TRUE**

- EACC1*->

■ **GCF_900091855.1; Streptomyces sp. DvalAA-14; counts= 1; multicellularity status: TRUE**

- EACC1*->

■ **GCA_900091875.1; Streptomyces sp. BpilaLS-43; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+??+SF1-helicase+Vsr(PDDEXK)?->

■ **GCF_900079415.1; Streptomyces sp. F-7; counts= 1; multicellularity status: TRUE**

- TM+TM+TM+PP2C->??->EACC1*->CASPASE+TM+TM+PBPB+vWA->

■ **GCA_900103985.1; Streptomyces guanduensis; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+TPRs->

■ **GCF_001049855.1; Streptomyces sp. Wb2n-11; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+TM?+Phytase-like->

■ **GCF_900105395.1; Streptomyces sp. TLI_053; counts= 1; multicellularity status: TRUE**

- FAD_binding_4+FAD-oxidase_C->DAGK_cat+DAGK_acc->EACC1*->CASPASE+TPRs->Clp_N+Clp_N+ClpABN-AAA->

■ **GCF_900103585.1; Streptomyces sp. cf386; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+TPRs->

■ **GCA_002234405.1; Amycolatopsis thailandensis; counts= 1; multicellularity status: TRUE**

- EACC1*->

■ **GCA_002234605.1; Amycolatopsis sp. KNN50.9b; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+low-complexity+BetaPropeller->

■ **GCA_001896135.2; Streptomyces phaeoluteigriseus; counts= 1; multicellularity status: TRUE**

- low-complexity+HD+Tox-RelA+TGS+ACT->Pkinase+TPRs->EACC1*->CASPASE+TPRs->

■ **GCA_002242735.1; Streptomyces sp. 2R; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+TPRs+LysM+PG-binding->

■ **GCA_002234475.1; Salmonella enterica; counts= 1; multicellularity status: FALSE**

- EACC1*->

■ **GCA_003428925.1; Streptomyces; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+Trypsin+TPRs->

■ **GCA_002291145.1; Streptomyces sp. SA15; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->

■ **GCF_000220705.2; Streptomyces xinghaiensis; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+PBPB+vWA->

■ **GCA_003633975.1; Streptomyces sp. Ag82_O1-15; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+BetaPropeller->

■ **GCF_001543895.1; Streptomyces thermoautotrophicus; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->

■ **GCF_900230215.1; Jatrophihabitans sp. GAS493; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+low-complexity+DUF4190(has2TM)->?->Glyoxalase->

■ **GCA_002354875.1; Actinosynnema pretiosum; counts= 1; multicellularity status: TRUE**

- EACC1*->

■ **GCA_002411735.1; Klebsiella pneumoniae; counts= 1; multicellularity status: FALSE**

- EACC1*->

■ **GCF_900230245.1; Burkholderia sp. OK806; counts= 1; multicellularity status: FALSE**

- EACC1*->Tnp_DNA_bind+DDE_Tnp_1+Dimer_Tnp_Tn5->CASPASE+TPRs->EACC1->CASPASE(fragment)->EACC1->CASPASE+CASPASE+TM+TPRs->CASPASE(fragment)->

■ **GCA_900215615.1; Streptomyces sp. Ag82_G6-1; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+??+TM+TM+TM->

■ **GCA_900215415.1; Nocardia amikacinitolerans; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+TPRs->

■ **GCF_900215565.1; Streptomyces sp. Ag109_G2-15; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->TM+Acid_phosphat_B->

■ **GCF_002518865.1; Escherichia coli; counts= 1; multicellularity status: FALSE**

- EACC1*->

■ **GCF_002551245.1; Streptomyces sp. rh34; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+??+SF1-helicase+Vsr(PDDEXK)?->

■ **GCF_002551335.1; Streptomyces sp. ms184; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+TPRs->

■ **GCF_002551135.1; Streptomyces sp. st140; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+TPRs->

■ **GCF_002551215.1; Streptomyces; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+STAND+??+TPRs+??->

■ **GCF_002551345.1; Streptomyces sp. ms115; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+TPRs->

■ **GCF_002551305.1; Streptomyces sp. or20; counts= 1; multicellularity status: TRUE**

- HATPase_c_2->EACC1*->CASPASE+Beta_rich_repeat->

■ **GCF_002551435.1; Streptomyces sp. f150; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+TPRs->

■ **GCF_002551475.1; Streptomyces sp. b62; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+TPRs->

■ **GCA_002554515.1; Nocardia sp. FDAARGOS_372; counts= 1; multicellularity status: TRUE**

- DUF2510(W3)+BicD+DUF4041+T5orf172->EACC1*->CASPASE+TPRs->

■ **GCA_003600245.1; Amycolatopsis sulphurea; counts= 1; multicellularity status: TRUE**

- GATase->ABC-ATPase+DUF4162->cNMP_cyclase+TM+TM+TM+TM+TM+TM->EACC1*->

■ **GCF_002551295.1; Streptomyces sp. or3; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+TPRs->

■ **GCF_002551175.1; Streptomyces sp. st77; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->

■ **GCF_002591335.1; Streptomyces malaysiensis; counts= 1; multicellularity status: TRUE**

- TetR_N+TetR_C_6->EACC1*->CASPASE+low-complexity+TM+PBPB->

■ **GCA_900090155.1; Streptomyces sp. ScaeMP-e48; counts= 1; multicellularity status: TRUE**

- EACC1-*->CASPASE+low-complexity+BetaPropeller___*_##->*

■ **GCA_900090175.1; Streptomyces sp. LamerLS-316; counts= 1; multicellularity status: TRUE**

- polar_lead?+TM+TM+TM+polar_tail?+low-complexity->??->EACC1*->CASPASE+TPRs->

■ **GCA_002727115.1; Streptomyces cinnamoneus; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+TM+TM+PBPB+vWA->

■ **GCF_002705975.1; Streptomyces sp. AmelKG-E11A; counts= 1; multicellularity status: TRUE**

- EACC1*->

■ **GCA_002946835.1; Streptomyces; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+TPRs->

■ **GCA_002754655.1; Verrucosispora sp. CNZ293; counts= 1; multicellularity status: TRUE**

- TM+TM+TM+Peptidase_M48+TM+DUF4864+??->EACC1*->

■ **GCF_002754415.1; Micromonospora sp. CNZ299; counts= 1; multicellularity status: TRUE**

- EACC1*->

■ **GCF_002754595.1; Streptomyces sp. 93; counts= 1; multicellularity status: TRUE**

- EACC1*->

■ **GCA_002277855.1; Streptomyces sp. Alain-F2R5; counts= 1; multicellularity status: TRUE**

- low-complexity+HD+Tox-RelA+TGS+ACT->Pkinase+TPRs->EACC1*->CASPASE+TPRs->

■ **GCA_002803075.1; Streptomyces sp. CB01373; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+TM+TM+PBPB+vWA->

■ **GCA_002803085.1; Streptomyces sp. CB01201; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->

■ **GCA_002803145.1; Kitasatospora sp. CB02891; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+PBPB+vWA->

■ **GCF_002812405.1; Streptomyces sp. M56; counts= 1; multicellularity status: TRUE**

- TetR_N+TetR_C_6->EACC1*->CASPASE+low-complexity+TM+PBPB->

■ **GCF_002813405.1; Streptomyces sp. 69; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+STAND->TM+BetaPropeller->TM+Acid_phosphat_B->

■ **GCA_002813165.1; Streptomyces sp. 4121.5; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+TM+TM+??+TM+TM+??+TM+TM+??->

■ **GCA_002844215.1; Streptomyces sp. EAG2; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+TPRs->

■ **GCF_002846295.1; Streptomyces sp. 59; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->TM+Acid_phosphat_B->

■ **GCF_002846355.1; Streptomyces sp. GP55; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+??+STAND+??->

■ **GCF_002846415.1; Streptomyces sp. TLI_146; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+low-complexity+BetaPropeller->

■ **GCF_002846315.1; Streptomyces sp. 73; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->

■ **GCA_002847285.1; Streptomyces sp. CMB-StM0423; counts= 1; multicellularity status: TRUE**

- EACC1+CASPASE+Phytase-like*->Phytase-like->||<-METHYLASE

- **GCA_002846615.1; Amycolatopsis niigatensis; counts= 1; multicellularity status: TRUE**
  - EACC1*->
- **GCA_002846365.1; Nocardia fluminea; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+FTSK+FTSK+FTSK->
- **GCF_002849735.1; Amycolatopsis sp. BJA-103; counts= 1; multicellularity status: TRUE**
  - EACC1*->TM+ZU5+??->
- **GCA_002853675.1; Klebsiella quasipneumoniae; counts= 1; multicellularity status: FALSE**
  - EACC1*->
- **GCA_002891315.1; Streptomyces noursei; counts= 1; multicellularity status: TRUE**
  - low-complexity+HD+Tox-RelA+TGS+ACT->Pkinase+TPRs->EACC1*->CASPASE+TPRs->
- **GCA_002891865.1; Streptomyces malaysiensis; counts= 1; multicellularity status: TRUE**
  - TetR_N+TetR_C_6->EACC1*->CASPASE+low-complexity+TM+PBPB->
- **GCF_002904295.1; Amycolatopsis sp. CA-128772; counts= 1; multicellularity status: TRUE**
  - GATase->ABC-ATPase+DUF4162->cNMP_cyclase+TM+TM+TM+TM+TM+TM->EACC1*->
- **GCA_002910775.2; Streptomyces; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+TPRs->
- **GCA_001577385.1; Streptomyces; counts= 1; multicellularity status: TRUE**
  - TM+REase->EACC1*->CASPASE+??+SF1-helicase+Vsr(PDDEXK)?->
- **GCF_002920535.1; Streptomyces sp. Ru71; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+TPRs->Clp_N+Clp_N+ClpABN-AAA->
- **GCA_002920615.1; Streptomyces sp. Ru62; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+TM?+Phytase-like->MDMPI_N+MDMPI_C->META->
- **GCF_002920575.1; Streptomyces sp. Ru73; counts= 1; multicellularity status: TRUE**
  - EACC1*->
- **GCA_900099115.2; Thiotrichales bacterium HS_08; counts= 1; multicellularity status: TRUE**
  - RVT_1->?->EACC1*->
- **GCA_002933535.1; Nocardia nova; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+TPRs->
- **GCF_002934265.1; Actinokineospora auranticolor; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+TM+TM->TM+PBPB->

- **GCA_003002815.1; Umezawaea tangerina; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+TM+TM+TM+TM->
- **GCF_003001935.1; Nonomuraea fuscirosea; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+PBPB->
- **GCA_003011965.1; Streptosporangium nondiastaticum; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->
- **GCA_003023875.1; Nocardia sp. MDA0666; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+TM+TM+TM+TM->
- **GCF_000156695.2; Streptomyces; counts= 1; multicellularity status: TRUE**
  - EACC1*->
- **GCA_003013775.1; Micromonospora sp. MH33; counts= 1; multicellularity status: TRUE**
  - EACC1*->
- **GCF_000412265.2; Streptomyces sp. Mg1; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->
- **GCF_001279685.1; Streptomyces sp. WM6373; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+??+SF1-helicase+Vsr(PDDEXK)?->
- **GCF_001426405.1; Streptomyces; counts= 1; multicellularity status: TRUE**
  - low_complexity+EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->||<-MFS_1
- **GCA_003030385.1; Plantactinospora sp. BB1; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+TPRs->
- **GCA_003030345.1; Plantactinospora sp. BC1; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+TPRs->
- **GCF_001590865.1; Streptomyces sp. NBRC 110611; counts= 1; multicellularity status: TRUE**
  - EACC1*->
- **GCF_003041235.1; Streptomyces sp. A244; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+??->
- **GCF_002251155.1; Streptomyces sp. FBKL.4005; counts= 1; multicellularity status: TRUE**
  - EACC1*->CASPASE+TM?+DUF3558+DUF3558->
- **GCF_900269665.1; Nocardia suismassiliense; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+STAND+BetaPropeller+BetaPropeller->

■ **GCA_003097515.1; Streptomyces sp. HNM0039; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+STAND+??->

■ **GCA_003116775.1; Streptomyces sp. CS147; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->

■ **GCA_003116715.1; Streptomyces sp. CS081A; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->

■ **GCF_003121295.1; Streptomyces orinoci; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->

■ **GCF_001756925.1; Streptomyces xinghaiensis; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+PBPB+vWA->

■ **GCA_003143855.1; Streptomyces sp. NWU339; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+STAND+polar_region+TM+BetaPropeller->

■ **GCA_003143935.1; Streptomyces sp. Act143; counts= 1; multicellularity status: TRUE**

- EACC1*->CASPASE+TPRs->

■ **GCF_003121585.1; Nocardioides sp. YIM ART13; counts= 1; multicellularity status: TRUE**

- EACC1*->

■ **GCF_003123685.1; Nocardia sp. SYSU K10002; counts= 1; multicellularity status: TRUE**

- EACC1+CASPASE*->

■ **GCA_003148865.1; Lechevalieria deserti; counts= 1; multicellularity status: TRUE**

- TM+TM+BPD_transp_1->OppC_N+TM+TM+BPD_transp_1->ABC-ATPase+ABC-ATPase->PBPB->TM+Beta_rich+TM+Beta_rich+TM+TM->EACC1+CASPASE+TPR_repeats+low_complexity+TM_region*->

■ **GCA_006471505.1; Escherichia coli; counts= 1; multicellularity status: FALSE**

- EACC1*->

■ **GCA_003176715.1; Micromonospora sp. S4605; counts= 1; multicellularity status: TRUE**

- TM+TM+TM+Peptidase_M48+TM+DUF4864+??->EACC1*->TPRs+CASPASE->

■ **GCF_003182135.1; Nocardia neocaledoniensis; counts= 1; multicellularity status: TRUE**

- EACC1*->

II. Source data - domain architectures, genome identifiers, gene neighborhoods

VMAP-ternary systems

acc	architecture	operon	len	species	gca	taxend
AAZ54441.1	vWA+APATPase+wHTH+TPRs	Trypsin+EAD2→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ Trypco1→	1523	Thermobifida fusca YX	GCA_000012405.1	actinobacteria
ABG51370.1	vWA+HTH+HTH+HTH+HTH+HTH+HTH+HTH+HTH+HTH+FGS-fold_domain	CASPASE+VMAP-C→ MoxR→ ?→ vWA(partial)→ vWA+HTH+HTH+HTH+HTH+HTH+HTH+HTH+HTH+HTH+FGS-fold_domain*→	1911	Trichodesmium erythraeum IMS101	GCA_000014265.1	cyanobacteria
ABG51457.1	vWA+FGS-fold_domain+FGS-fold_domain	EAD6+VMAP-M12+VMAP-C→ MoxR→ vWA+FGS-fold_domain+FGS-fold_domain*→	1196	Trichodesmium erythraeum IMS101	GCA_000014265.1	cyanobacteria
ABG53299.1	vWA+FGS-fold_domain	EAD1+Trypsin→ ?→ EAD1+VMAP-M0+VMAP-C→ MoxR→ ?→ ‖← ?‖vWA+FGS-fold_domain*→	862	Trichodesmium erythraeum IMS101	GCA_000014265.1	cyanobacteria
ABW16290.1	vWA+APATPase+wHTH+TPRs	EAD2+EAD1→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ‖← METALLOPROTEASE+TPRs	1500	Frankia sp. EAN1pec	GCA_000018005.1	actinobacteria
ABW33201.1	vWA+FGS-fold_domain	Trypco1→ Trypsin+VMAP-M1+VMAP-C→ MoxR→ vWA+FGS-fold_domain*→ FGS-fold_domain→ FGS-fold_domain→	955	Acaryochloris marina MBIC11017	GCA_000018105.1	cyanobacteria
ACC85234.1	vWA+Calcineurin-like+SAVED	VMAP-M1+VMAP-C→ MoxR→ vWA+Calcineurin-like+SAVED*→	1237	Nostoc punctiforme PCC 73102	GCA_000020025.1	cyanobacteria
ACL45435.1	vWA	FGS-fold_domain← ?← ?← ?‖VMAP-M1+VMAP-C→ MoxR→ vWA*→ ‖← zf-IS66+DDE_Tnp_IS66← TIR+EAD9← ?← Trypsin← Trypco1	745	Cyanothece sp. PCC 7425	GCA_000022045.1	cyanobacteria
ACY97176.1	vWA+APATPase+wHTH+TPRs	Radical_SAM→ METALLOPROTEASE+TPRs→ ‖← TIR+APATPase+TPRs‖EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→	1383	Thermomonospora curvata DSM 43183	GCA_000024385.1	actinobacteria
ADH69904.1	vWA+APATPase+wHTH+TPRs	Trypsin+EAD2→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ‖← DUF397	1509	Nocardiopsis dassonvillei subsp. dassonvillei DSM 43111	GCA_000092985.1	actinobacteria
ADI03786.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ‖← METALLOPROTEASE+TPRs← FXSXX-COOH-like← ?← ?← Na_H_Exchanger	1376	Streptomyces bingchenggensis BCW-1	GCA_000092385.1	actinobacteria
ADO19142.1	vWA	vWA*→ ?→ ?→ FGS-fold_domain→	609	Nostoc flagelliforme str. Sunitezuoqi	-	cyanobacteria
AEV84216.1	vWA+TPRs	EAD1+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→	915	Actinoplanes sp. SE50/110	GCA_000237145.1	actinobacteria
AFY58464.1	vWA+FGS-fold_domain	EAD1+VMAP-M1+VMAP-C→ MoxR→ ?→ vWA+FGS-fold_domain*→ FGS-fold_domain→	879	Rivularia sp. PCC 7116	GCA_000316665.1	cyanobacteria
AFZ01290.1	vWA+AP-GTPase+COR	vWA+MNS+CASPASE+MNS← MoxR← EAD10+VMAP-M1+VMAP-C‖?→ CASPASE→ EAD10+VMAP-M1+VMAP-C→ MoxR→ vWA+AP-GTPase+COR*→	1196	Calothrix sp. PCC 6303	GCA_000317435.1	cyanobacteria
AGI87916.1	vWA+TPRs	TCAD15‖Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1108	Streptomyces albus J1074	GCA_000359525.1	actinobacteria
AGM04021.1	vWA+APATPase+wHTH+TPRs	VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ‖← METALLOPROTEASE+TPRs← FXSXX-COOH-like← cNMP_binding+HTH_Crp_2	1449	Amycolatopsis orientalis HCCB10007	GCA_000400635.2	actinobacteria
AGP53016.1	vWA+APATPase+wHTH+TPRs	PNP_UDP_1+EAD2→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ‖← METALLOPROTEASE+TPRs← FXSXX-COOH-like	1194	Streptomyces rapamycinicus NRRL 5491	GCA_000418455.1	actinobacteria
AGS71776.1	vWA+TPRs	TCAD15→ Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1323	Streptomyces collinus Tu 365	GCA_000444875.1	actinobacteria
AHH96337.1	vWA+TIR+BetaPropeller	EAD2+VMAP-M0+VMAP-C→ MoxR→ ?→ vWA+TIR+BetaPropeller*→ ?→ ?→ ‖← cNMP_cyclase+EAD2‖cNMP_binding+HTH_Crp_2→ ?→ SIR2→	1185	Kutzneria albida DSM 43870	GCA_000525635.1	actinobacteria
AHJ30118.1	vWA+beta-rich-region+HTH+FGS-fold_domain	TIR+EAD6→ EAD6+VMAP-M5→ VMAP-C→ MoxR→ vWA+beta-rich-region+HTH+FGS-fold_domain*→ four_helix_bundle_protein→ RVT_1→	1076	Nodularia spumigena CCY9414	GCA_000340565.3	cyanobacteria
AIG79293.1	vWA+APATPase+wHTH+TPRs	cNMP_cyclase+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ‖← METALLOPROTEASE+TPRs← FXSXX-COOH-like← cNMP_binding+HTH_Crp_2	1458	Amycolatopsis japonica	GCA_000732925.1	actinobacteria
AIJ13394.1	vWA+TPRs	TCAD15‖Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→ Trypco1→	1147	Streptomyces lividans TK24	GCA_000739105.1	actinobacteria
AIS01610.1	vWA+TIR+APATPase+wHTH+TPRs	DRHyd+VMAP-M0+VMAP-C→ MoxR→ vWA+TIR+APATPase+wHTH+TPRs*→	1416	Streptomyces glaucescens	GCA_000761215.1	actinobacteria
AIV38673.1	vWA+TPRs	TCAD15‖Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→ Trypco1→	1102	Streptomyces sp. CCM_MD2014	GCA_000772045.1	actinobacteria
AJK55727.1	vWA+APATPase+wHTH+TPRs	cNMP_cyclase+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ‖← ?‖?→ ‖← FXSXX-COOH-like← cNMP_binding+HTH_Crp_2	1463	Amycolatopsis lurida NRRL 2430	GCA_000749465.2	actinobacteria
AJP03761.1	vWA+TPRs	TCAD15‖Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1118	Streptomyces cyaneogriseus subsp. noncyanogenus	GCA_000931445.1	actinobacteria
AKI98917.1	vWA+SLOG+SLOG+TPRs	EAD1+VMAP-M1+VMAP-C→ MoxR→ vWA+SLOG+SLOG+TPRs*→ EAD1+Trypsin→	1959	Archangium gephyra	GCA_001027285.1	deltaproteobacteria
AKJ08455.1	vWA+SLOG	EAD1+VMAP-M1+VMAP-C→ vWA+SLOG*→	1054	Archangium gephyra	GCA_001027285.1	deltaproteobacteria
AKJ10474.1	vWA+APATPase+wHTH+TPRs	Trypco2→ EAD2+VMAP-M0+VMAP-C→ vWA+APATPase+wHTH+TPRs*→ ‖← FXSXX-COOH-like← Trypsin+EAD2‖?→ ?→ ?→ ?→ DUF397→	1201	Streptomyces incarnatus	GCA_001027185.1	actinobacteria

acc	architecture	operon	len	species	gca	taxend
AKN68644.1	vWA+TPRs	TCAD15→ Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH-like→	1261	Streptomyces sp. PBH53	GCA_001040905.1	actinobacteria
AKN69695.1	vWA+wHTH+cNMP_cyclase+Band7+HAD	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+wHTH+cNMP_cyclase+Band7+HAD*→	1303	Streptomyces sp. PBH53	GCA_001040905.1	actinobacteria
AKV66222.1	vWA+FGS-fold_domain	AB_hydrolase→ CASPASE+VMAP-M14+VMAP-C→ MoxR→ vWA+FGS-fold_domain*→	842	Microcystis panniformis FACHB-1757	GCA_001264245.1	cyanobacteria
AKV67733.1	vWA+FGS-fold_domain	HTH+VMAP-M9+VMAP-C→ MoxR→ vWA+FGS-fold_domain*→ ?→ ‖← ?‖FGS-fold_domain→	961	Microcystis panniformis FACHB-1757	GCA_001264245.1	cyanobacteria
AKV70250.1	vWA+FGS-fold_domain	Trypco1→ Trypsin+VMAP-M1+VMAP-C→ MoxR→ vWA+FGS-fold_domain*→ ?→ ‖← ?← ?‖FGS-fold_domain→	884	Microcystis panniformis FACHB-1757	GCA_001264245.1	cyanobacteria
ALB40811.1	vWA+FGS-fold_domain	EAD6+VMAP-C→ MoxR→ vWA+FGS-fold_domain*→ FGS-fold_domain→	880	Anabaena sp. WA102	GCA_001277295.1	cyanobacteria
ALC19574.1	vWA+Tubulin	Trypco1→ Trypsin+VMAP-M7+VMAP-C→ MoxR→ vWA+Tubulin*→	1629	Streptomyces pristinaespiralis	GCA_001278075.1	actinobacteria
ALC31298.1	vWA+REase+SWACOS+TPRs+cNMP_cyclase	CASPASE+VMAP-M2+VMAP-C→ MoxR→ vWA+REase+SWACOS+TPRs+cNMP_cyclase*→	1713	Streptomyces sp. CFMR 7	GCA_001278095.1	actinobacteria
ALG12738.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs→ ‖← METALLOPROTEASE+TPRs← FXSXX-COOH-like‖EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ‖← METALLOPROTEASE+TPRs← FXSXX-COOH-like	1395	Kibdelosporangium phytohabitans	GCA_001302585.1	actinobacteria
ALM38630.1	vWA+TPRs	low-complexity+HDxxH+VMAP-M0→ VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ ?→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1137	Streptomyces sp. FR-008	GCA_001431765.1	actinobacteria
ALO96113.1	vWA+TPRs	TCAD15→ Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1160	Streptomyces hygroscopicus subsp. limoneus	GCA_001447075.1	actinobacteria
ALV33603.1	vWA+TPRs	TCAD15‖Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1125	Streptomyces sp. CdTB01	GCA_001484565.1	actinobacteria
AMM08319.1	vWA+TPRs	TCAD15‖Trypco1→ VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1039	Streptomyces albus	GCA_001577385.1	actinobacteria
AMV25224.1	EAD1+HD+vWA+NEFF1	EAD1+HD← EAD1+Trypsin‖VMAP-M21+VMAP-C→ MoxR→ EAD1+HD+vWA+NEFF1*→	1336	Gemmata sp. SH-PL17	GCA_001610855.1	planctomycetes
AMW10311.1	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD*→	1423	Streptomyces sp. S10(2016)	GCA_001611795.1	actinobacteria
AMW13454.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ AB_hydrolase→ CASPASE+EAD2→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→	1500	Streptomyces sp. S10(2016)	GCA_001611795.1	actinobacteria
ANJ11717.1	vWA+APATPase+wHTH+TPRs	Trypco2→ EAD2+VMAP-M0+VMAP-C→ vWA+APATPase+wHTH+TPRs*→ ‖← METALLOPROTEASE+TPRs← FXSXX-COOH-like← Trypsin+EAD2	1201	Streptomyces parvulus	GCA_001660045.1	actinobacteria
ANL87877.1	vWA+REC+SLOG+CASPASE	EAD5+Trypsin→ EAD5+VMAP-M4+VMAP-C→ MoxR→ vWA+REC+SLOG+CASPASE*→	1509	Rhizobium phaseoli	GCA_001664405.1	alphaproteobacteria
ANN22215.1	vWA+APATPase+wHTH+TPRs	cNMP_cyclase+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ‖← METALLOPROTEASE+TPRs← FXSXX-COOH-like← cNMP_binding+HTH_Crp_2	1202	Amycolatopsis orientalis	GCA_000943515.2	actinobacteria
ANP56390.1	vWA+APATPase+wHTH+TPRs	Trypco2→ EAD2+VMAP-M0+VMAP-C→ vWA+APATPase+wHTH+TPRs*→ ‖← METALLOPROTEASE+TPRs← Trypsin+EAD2‖?→ Trypco2→	1201	Streptomyces griseochromogenes	GCA_001542625.2	actinobacteria
ANS63696.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ‖← CASPASE+EAD2	1315	Streptomyces lincolnensis	GCA_001685355.1	actinobacteria
ANS68576.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ‖← Na_H_Exchanger‖AB_hydrolase→ CASPASE+EAD2→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→	1508	Streptomyces lincolnensis	GCA_001685355.1	actinobacteria
ANS69559.1	vWA+SFII-helicase+Z1	AB_hydrolase→ CASPASE+VMAP-M2+VMAP-C→ MoxR→ vWA+SFII-helicase+Z1*→	1269	Streptomyces lincolnensis	GCA_001685355.1	actinobacteria
ANS70744.1	vWA+STAND_NTPase+Trypsin+TIR+CASPASE+EAD2	AB_hydrolase→ CASPASE+VMAP-M0+VMAP-C→ MoxR→ vWA+STAND_NTPase+Trypsin+TIR+CASPASE+EAD2*→	1564	Streptomyces lincolnensis	GCA_001685355.1	actinobacteria
AOR30905.1	vWA+APATPase+wHTH+TPRs	Trypsin+EAD2+VMAP-M0+VMAP-C→ vWA+APATPase+wHTH+TPRs*→	779	Streptomyces punicicsabiei	GCA_001735805.1	actinobacteria
AOR34174.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→	1190	Streptomyces punicicsabiei	GCA_001735805.1	actinobacteria
AOT62241.1	vWA+APATPase+wHTH+TPRs+cNMP_cyclase+NaeI	Trypco1→ ?→ ?→ AB_hydrolase→ CASPASE+VMAP-M2+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs+cNMP_cyclase+NaeI*→	1810	Streptomyces rubrolavendulae	GCA_001750785.1	actinobacteria
APC37890.1	vWA+APATPase+wHTH+TPRs	Trypsin+EAD2→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ‖← DUF397	1509	Nocardiopsis dassonvillei	GCA_001877055.1	actinobacteria
APU44607.1	vWA+TPRs	TCAD15‖Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1088	Streptomyces sp. TN58	GCA_001941845.1	actinobacteria
AQA11755.1	vWA+TPRs	AB_hydrolase→ CASPASE+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→	1171	Streptomyces autolyticus	GCA_001983975.1	actinobacteria
AQT76777.1	vWA+TPRs	TCAD15‖Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1093	Streptomyces sp. fd1-xmd	GCA_002007685.1	actinobacteria
ARF57533.1	vWA+APATPase+wHTH+TPRs	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→	1334	Streptomyces gilvosporeus	GCA_002082195.1	actinobacteria
ARH93170.1	vWA+TPRs	TCAD15‖Trypco1→ PSE→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ TIR+APATPase+TPRs→	1134	Streptomyces sp. MOE7	GCA_002090335.1	actinobacteria
ARH94837.1	vWA	EAD2+VMAP-M0+VMAP-C→ vWA(partial)→ vWA*→	335	Streptomyces sp. MOE7	GCA_002090335.1	actinobacteria
ARQ68581.1	vWA+TPRs	TCAD15‖PSE→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1094	Streptomyces sp. SCSIO 03032	GCA_002128305.1	actinobacteria
BAE95415.1	vWA+APATPase+wHTH+TPRs	Trypco1→ Trypsin+VMAP-M8+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→	1111	Streptomyces kanamyceticus	-	actinobacteria
BAG18883.1	vWA+TIR+FxsC_Cter	AB_hydrolase→ CASPASE+VMAP-M2+VMAP-C→ MoxR→ vWA+TIR+FxsC_Cter*→	1001	Streptomyces griseus subsp. griseus NBRC 13350	GCA_000010605.1	actinobacteria
BAS55188.1	vWA+FGS-fold_domain	TIR+EAD9→ EAD9+VMAP-M1+VMAP-C→ MoxR→ vWA+FGS-fold_domain*→	1083	Leptolyngbya boryana IAM M-101	GCA_002142475.1	cyanobacteria
BAU85996.1	vWA+TPRs	TCAD15‖Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1091	Streptomyces laurentii	GCA_002355495.1	actinobacteria
BAU87440.1	vWA+APATPase+wHTH+TPRs+cNMP_cyclase+NaeI	AB_hydrolase→ CASPASE+VMAP-M2+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs+cNMP_cyclase+NaeI*→	1575	Streptomyces laurentii	GCA_002355495.1	actinobacteria
BAY12967.1	vWA+MNS	EAD8+VMAP-M1+VMAP-C→ MoxR→ ?→ vWA+MNS*→	1139	Calothrix sp. NIES-2098	GCA_002368175.1	cyanobacteria
BAZ13460.1	vWA+GUN4+FGS-fold_domain	EAD1+Trypsin→ EAD1+VMAP-M1+VMAP-C→ MoxR→ vWA+GUN4+FGS-fold_domain*→	1035	Calothrix sp. NIES-4071	GCA_002368455.1	cyanobacteria
BAZ33904.1	vWA+Glyco_trans_4_4+Glycos_transf_1	cNMP_cyclase+VMAP-M1+VMAP-C→ MoxR→ vWA+Glyco_trans_4_4+Glycos_transf_1*→ FGS-fold_domain→	1018	Cylindrospermum sp. NIES-4074	GCA_003994795.1	cyanobacteria

acc	architecture	operon	len	species	gca	taxend
CAF33302.1	vWA+APATPase+wHTH+TPRs+cNMP_cyclase+NaeI	CASPASE+VMAP-M2+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs+cNMP_cyclase+NaeI*→	1793	Streptomyces fradiae	-	actinobacteria
CAH05112.1	vWA+APATPase+wHTH+TPRs+cNMP_cyclase+NaeI	AB_hydrolase→ CASPASE+VMAP-M2+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs+cNMP_cyclase+NaeI*→	1796	Streptomyces fradiae	-	actinobacteria
CAO86961.1	vWA+FGS-fold_domain	HTH+VMAP-M9+VMAP-C→ MoxR→ vWA+FGS-fold_domain*→ ||← ?||?→ ||← ?← ?||?→ FGS-fold_domain→	964	Microcystis aeruginosa PCC 7806	-	cyanobacteria
CBG74991.1	vWA+APATPase+wHTH+TPRs	TCAD9+Pkinase+NACHT+HEAT_repeats→ EAD2+VMAP-M0+VMAP-C→ vWA→ MoxR→ vWA+APATPase+TPRs*→	1029	Streptomyces scabiei 87.22	GCA_000091305.1	actinobacteria
CBG74993.1	vWA	TCAD9+Pkinase+NACHT+HEAT_repeats→ EAD2+VMAP-M0+VMAP-C→ vWA*→ MoxR→ vWA+APATPase+TPRs→	460	Streptomyces scabiei 87.22	GCA_000091305.1	actinobacteria
CCH29662.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs←- FXSXX-COOH-like←- cNMP_cyclase+EAD2	1326	Saccharothrix espanaensis DSM 44229	GCA_000328705.1	actinobacteria
CCH33419.1	vWA+APATPase+wHTH+TPRs	cNMP_cyclase+EAD2→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs	1447	Saccharothrix espanaensis DSM 44229	GCA_000328705.1	actinobacteria
CCH34758.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← ?← ?← TCAD15	1335	Saccharothrix espanaensis DSM 44229	GCA_000328705.1	actinobacteria
CCI02683.1	vWA	Trypsin+VMAP-M1+VMAP-C→ MoxR→ vWA*→	583	Microcystis aeruginosa PCC 9443	GCA_000312185.1	cyanobacteria
CCI03549.1	vWA+FGS-fold_domain	HTH+VMAP-M9+VMAP-C→ MoxR→ vWA+FGS-fold_domain*→ ?→ ?→ FGS-fold_domain→	930	Microcystis aeruginosa PCC 9443	GCA_000312185.1	cyanobacteria
CCK25370.1	vWA+HTH	CASPASE+VMAP-M0+VMAP-C→ vWA+HTH*→	762	Streptomyces davawensis JCM 4913	GCA_000349325.1	actinobacteria
CCK29233.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs←- FXSXX-COOH-like←- Trypsin+EAD2||FXSXX-COOH-like→ METALLOPROTEASE+TPRs→	1276	Streptomyces davawensis JCM 4913	GCA_000349325.1	actinobacteria
CEL17030.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs←- FXSXX-COOH-like||?→ ||← ?||EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs→	1441	Kibdelosporangium sp. MJ126-NF4	GCA_000826545.1	actinobacteria
CEL17037.1	vWA+APATPase+wHTH+TPRs	vWA+APATPase+wHTH+TPRs→ ||← METALLOPROTEASE+TPRs←- FXSXX-COOH-like||?→ ||← ?||EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs	1403	Kibdelosporangium sp. MJ126-NF4	GCA_000826545.1	actinobacteria
CNF91710.1	vWA+FtsK+FtsK+CASPASE+FtsK	Trypco1→ Trypsin+VMAP-M8+VMAP-C→ MoxR→ vWA+FtsK+FtsK+CASPASE+FtsK*→	1677	Mycobacterium tuberculosis	GCA_001160225.1	actinobacteria
CQR61924.1	vWA+TPRs	← TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1118	Streptomyces leeuwenhoekii	GCA_001013905.1	actinobacteria
CQR62799.1	vWA+Pkinase+NUDIX	VMAP-M2+VMAP-C→ MoxR→ vWA+Pkinase+NUDIX*→	1271	Streptomyces leeuwenhoekii	GCA_001013905.1	actinobacteria
CUM41332.1	vWA+TPRs	AB_hydrolase→ CASPASE+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→	1193	Streptomyces venezuelae	GCA_001406115.1	actinobacteria
CUM41527.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← Na_H_Exchanger||AB_hydrolase→ CASPASE+EAD2→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→	1526	Streptomyces venezuelae	GCA_001406115.1	actinobacteria
CUU60227.1	vWA+APATPase+wHTH+TPRs	EAD2+EAD1→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs←- FXSXX-COOH-like	1582	Frankia sp. G2	GCA_001536285.1	actinobacteria
CUW28293.1	vWA+wHTH+cNMP_cyclase+Band7+HAD	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+wHTH+cNMP_cyclase+Band7+HAD*→	1288	Streptomyces reticuli	GCA_001511815.1	actinobacteria
CUW31051.1	vWA+TPRs	TCAD15→ Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1217	Streptomyces reticuli	GCA_001511815.1	actinobacteria
EAW35097.1	vWA+FGS-fold_domain	EAD4+VMAP-M3+VMAP-C→ MoxR→ vWA+FGS-fold_domain*→ FGS-fold_domain→	894	Lyngbya sp. PCC 8106	GCA_000169095.1	cyanobacteria
EDX26496.1	vWA	← cNMP_binding+HTH_Crp_2←- ?← ?||EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA*→	537	Streptomyces sp. Mg1	GCA_000154885.1	actinobacteria
EFC84333.1	vWA+O-GTPase2	TIR+VMAP-M2+VMAP-C→ MoxR→ vWA+DO-GTPase2*→	1017	Frankia sp. EUN1f	GCA_000177675.1	actinobacteria
EFD69442.1	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA→ vWA+Pkinase+HTH+TPRs+cNMP_cyclase*→	1038	Streptomyces lividans TK24	GCA_000158935.1	actinobacteria
EFD69443.1	vWA_protein	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA*→ vWA+Pkinase+HTH+TPRs+cNMP_cyclase→	296	Streptomyces lividans TK24	GCA_000158935.1	actinobacteria
EFE78827.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ AB_hydrolase→ CASPASE+EAD2→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→	1347	Streptomyces roseosporus NRRL 15998	GCA_000156455.1	actinobacteria
EFH31709.1	vWA+TIR+FxsC_Cter	AB_hydrolase→ CASPASE+VMAP-M2+VMAP-C→ MoxR→ vWA+TIR+FxsC_Cter*→ ||← DUF397	967	Streptomyces pristinaespiralis ATCC 25486	GCA_000154945.1	actinobacteria
EFL17576.1	vWA	← TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	583	Streptomyces sp. C	GCA_000158895.1	actinobacteria
EFL20927.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs←- FXSXX-COOH-like	1469	Streptomyces himastatinicus ATCC 53653	GCA_000158915.1	actinobacteria
EFL31903.1	vWA	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA*→	570	Streptomyces viridochromogenes DSM 40736	GCA_000158955.1	actinobacteria
EFL34810.1	vWA+TPRs	← TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→	1000	Streptomyces viridochromogenes DSM 40736	GCA_000158955.1	actinobacteria
EFL35514.1	vWA	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA*→ TIR+APATPase+TPRs→ ?→ CASPASE+EAD2→ METALLOPROTEASE+TPRs→	464	Streptomyces viridochromogenes DSM 40736	GCA_000158955.1	actinobacteria
EFO80365.1	vWA+TPRs	← CASPASE+TCAD1+TCAD2||CASPASE+TCAD1+DUF4404→ VMAP-M13+VMAP-C→ MoxR→ vWA+TPRs*→	1062	Oscillochloris trichoides DG-6	GCA_000152145.1	chloroflexi
EGE41651.1	vWA+TIR+FxsC_Cter	AB_hydrolase→ CASPASE+VMAP-M2+VMAP-C→ MoxR→ vWA+TIR+FxsC_Cter*→	1001	Streptomyces sp. ACT-1	GCA_000177175.2	actinobacteria

acc	architecture	operon	len	species	gca	taxend
EHM30204.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ AB_hydrolase→ CASPASE+EAD2→ METALLOPROTEASE+TPRs→	1329	Streptomyces sp. W007	GCA_000239075.2	actinobacteria
EHR73674.1	vWA+HTH	AB_hydrolase→ CASPASE+VMAP-M15+VMAP-C→ MoxR→ vWA+HTH*→	881	Burkholderiales bacterium JOSHI_001	GCA_000244995.1	betaproteobacteria
EIF91212.1	vWA+Pkinase	vWA+Pkinase*→	686	Streptomyces tsukubensis NRRL18488	GCA_000297155.2	actinobacteria
EIP98807.1	vWA+REC+HTH+SLOG	TCAD5+AB_hydrolase+TCAD7+macroglobulin-like+CASPASE→ CASPASE+VMAP-C→ MoxR→ vWA+REC+HTH+SLOG*→	1192	Opitutaceae bacterium TAV1	GCA_000243495.3	verrucomicrobia
EIV90731.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← ?← EAD5+TIR	1480	Frankia sp. QA3	GCA_000262465.1	actinobacteria
EKC91743.1	vWA+TPRs	VMAP-C(partial)→ MoxR→ vWA+TPRs*→	899	Streptomyces sp. SM8	-	actinobacteria
EKU96832.1	vWA+FGS-fold_domain	AB_hydrolase→ CASPASE+EAD9→ EAD9+VMAP-M1+VMAP-C→ MoxR→ vWA+FGS-fold_domain*→ FGS-fold_domain→ four_helix_bundle_protein→ RVT_1→ FGS-fold_domain→	926	Leptolyngbya sp. PCC 7375	GCA_000316115.1	cyanobacteria
EKU96985.1	vWA+BetaPropeller+FGS-fold_domain	FGS-fold_domain→ EAD1+Trypsin→ ?→ EAD1+VMAP-M1+VMAP-C→ MoxR→ vWA+BetaPropeller+FGS-fold_domain*→ FGS-fold_domain→ ||← RVT_1← four_helix_bundle_protein	1247	Leptolyngbya sp. PCC 7375	GCA_000316115.1	cyanobacteria
ELQ77549.1	vWA	← TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA*→	345	Streptomyces rimosus subsp. rimosus ATCC 10970	GCA_000331185.1	actinobacteria
EME53021.1	vWA+APATPase+wHTH+TPRs	cNMP_cyclase+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like← cNMP_binding+HTH_Crp_2	1468	Amycolatopsis decaplanina DSM 44594	GCA_000342005.1	actinobacteria
EMF02657.1	vWA+TPRs	← TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1056	Streptomyces mobaraensis NBRC 13819 = DSM 40847	GCA_000342125.1	actinobacteria
EOY47501.1	vWA+Pkinase	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase*→	449	Streptomyces lividans 1326	GCA_000403665.1	actinobacteria
EOY50271.1	vWA	← TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA*→ ?→ ?→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→ Trypco1→	356	Streptomyces lividans 1326	GCA_000403665.1	actinobacteria
EPD55277.1	vWA+TPRs	← TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1151	Streptomyces sp. HGB0020	GCA_000411315.1	actinobacteria
EPF21804.1	vWA+FGS-fold_domain	AB_hydrolase→ CASPASE+VMAP-M14+VMAP-C→ MoxR→ vWA(partial)→ vWA+FGS-fold_domain*→	706	Microcystis aeruginosa SPC777	GCA_000412595.1	cyanobacteria
EPH45106.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ ?→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→	1092	Streptomyces aurantiacus JA 4570	GCA_000414115.1	actinobacteria
EPH45390.1	vWA+APATPase+wHTH+TPRs	vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like← CASPASE+EAD2	1294	Streptomyces aurantiacus JA 4570	GCA_000414115.1	actinobacteria
EPJ42712.1	vWA+EAD2+CASPASE+EAD2	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+EAD2+CASPASE+EAD2*→	997	Streptomyces afghaniensis 772	GCA_000415505.1	actinobacteria
ESP99762.1	vWA+TPRs	← TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1106	Streptomyces sp. GBA 94-10	GCA_000495635.1	actinobacteria
ESQ05820.1	vWA+TPRs	← TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1106	Streptomyces sp. PVA 94-07	GCA_000495755.1	actinobacteria
ESQ11649.1	vWA_protein	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA_protein*→	586	uncultured Thiohalocapsa sp. PB-PSB1	GCA_000495615.1	gammaproteobacteria
EST31053.1	vWA+Pkinase+TPRs	Trypco2→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+TPRs*→	1121	Streptomyces niveus NCIMB 11891	GCA_000497425.1	actinobacteria
EST34701.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like	1484	Streptomyces roseochromogenus subsp. oscitans DS 12.976	GCA_000497445.1	actinobacteria
EWM11539.1	vWA+TIR+BetaPropeller	EAD2+VMAP-M0+VMAP-C→ vWA+TIR+BetaPropeller*→ ?→ ?→ cNMP_binding+HTH_Crp_2→	1096	Kutzneria sp. 744	GCA_000568255.1	actinobacteria
EXU70110.1	vWA+TPRs	AB_hydrolase→ CASPASE+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→	1172	Streptomyces sp. PRh5	GCA_000590515.1	actinobacteria
EYU68527.1	vWA+TIR+FxsC_Cter	AB_hydrolase→ CASPASE+VMAP-M2+VMAP-C→ MoxR→ vWA+TIR+FxsC_Cter*→	839	Streptomyces sp. PCS3-D2	GCA_000612545.1	actinobacteria
EYU71427.1	vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats	AB_hydrolase→ CASPASE+VMAP-M0+VMAP-C→ MoxR→ vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats*→	1196	Streptomyces sp. PCS3-D2	GCA_000612545.1	actinobacteria
GAO06359.1	vWA+TPRs	← TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ TIR+APATPase+TPRs→	1127	Streptomyces sp. NBRC 110027	GCA_000829715.2	actinobacteria
GAO06532.1	vWA+wHTH+TPRs+APATPase+wHTH+TPRs	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+wHTH+TPRs+APATPase+wHTH+TPRs*→ ||← ?||?→ ||← AB_hydrolase	1588	Streptomyces sp. NBRC 110027	GCA_000829715.2	actinobacteria
GAP48484.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ AB_hydrolase→ CASPASE+EAD2→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→	1477	Streptomyces azureus	GCA_001270025.1	actinobacteria
GAP50094.1	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD*→	1448	Streptomyces azureus	GCA_001270025.1	actinobacteria
GAQ55305.1	vWA+Pkinase+wHTH+cNMP_cyclase+Band7+HAD	vWA+Pkinase+wHTH+cNMP_cyclase+Band7+HAD*→	1190	Streptomyces acidiscabies	GCA_001485105.1	actinobacteria
GAQ56299.1	vWA+TPRs	vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1047	Streptomyces acidiscabies	GCA_001485105.1	actinobacteria
GAQ67487.1	vWA+SFII-helicase+Trypsin+cNMP_cyclase+Coiled-coil+CASPASE	AB_hydrolase→ CASPASE+VMAP-M2+VMAP-C→ MoxR→ vWA+SFII-helicase+Trypsin+cNMP_cyclase+Coiled-coil+CASPASE*→ ||← ?← ?← TIR+APATPase+TPRs	1797	Streptomyces scabiei	GCA_001485125.1	actinobacteria
GAT82291.1	vWA+APATPase+wHTH+TPRs	Trypsin+EAD2→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs||?→ Trypco1→	1628	Streptomyces sp. F-3	GCA_001653115.1	actinobacteria
GAV40520.1	vWA+Pkinase+wHTH+cNMP_cyclase+Band7+HAD	vWA+Pkinase+wHTH+cNMP_cyclase+Band7+HAD*→	1258	Streptomyces acidiscabies	GCA_001949645.1	actinobacteria
GAV42170.1	vWA+TPRs	vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1017	Streptomyces acidiscabies	GCA_001949645.1	actinobacteria
GAV44387.1	vWA+TIR+FxsC_Cter(partial)	vWA+TIR+FxsC_Cter(partial)*→	765	Streptomyces acidiscabies	GCA_001949645.1	actinobacteria

acc	architecture	operon	len	species	gca	taxend
KDR57872.1	vWA	VMAP-C_protein→ MoxR→ vWA*→	569	Arthrospira platensis str. Paraca	GCA_000175415.3	cyanobacteria
KDS87355.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	NUDIX→ Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→ SIR2→	1158	Streptomyces fradiae	-	actinobacteria
KES08164.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→	1111	Streptomyces toyocaensis	GCA_000725125.1	actinobacteria
KIF16909.1	vWA+FGS-fold_domain	Trypco1→ Trypsin+VMAP-M1+VMAP-C→ MoxR→ vWA+FGS-fold_domain*→ FGS-fold_domain→	878	Aphanocapsa montana BDHKU210001	GCA_000817745.1	cyanobacteria
KIF79231.1	vWA+TPRs	← TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1108	Streptomyces sp. 150FB	GCA_000818195.1	actinobacteria
KIH98248.1	vWA+APATPase+wHTH+TPRs	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← Radical_SAM← FXSXX-COOH-like	1426	Streptomonospora alba	GCA_000826685.1	actinobacteria
KIR65538.1	vWA+TPRs	Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ ?→ TIR+APATPase+TPRs→	1129	Micromonospora carbonacea	GCA_000876225.1	actinobacteria
KIX48996.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ AB_hydrolase→ CASPASE+EAD2→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→	1463	Streptomyces griseus	-	actinobacteria
KJK39591.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ AB_hydrolase→ CASPASE+EAD2→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→	1508	Streptomyces variegatus	GCA_000955965.1	actinobacteria
KJK41459.1	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD*→	1423	Streptomyces variegatus	GCA_000955965.1	actinobacteria
KJK51066.1	vWA+APATPase+wHTH+TPRs	← cNMP_binding+HTH_Crp_2||MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like	1204	Lechevalieria aerocolonigenes	GCA_000955955.1	actinobacteria
KJY16212.1	vWA+TPRs	← TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→	1077	Streptomyces sp. NRRL S-104	GCA_000966965.1	actinobacteria
KJY21448.1	vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats	VMAP-M0+VMAP-C→ MoxR→ vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats*→	1198	Streptomyces sp. NRRL S-104	GCA_000966965.1	actinobacteria
KJY37233.1	vWA	vWA*→	346	Streptomyces katrae	GCA_000966975.1	actinobacteria
KJY41391.1	vWA	← TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA*→	467	Streptomyces sp. NRRL S-444	GCA_000966985.1	actinobacteria
KMO98800.1	vWA+TPRs	← TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1071	Streptomyces roseus	GCA_001044425.1	actinobacteria
KMS71131.1	vWA+APATPase+wHTH+TPRs	Trypco2→ EAD2+VMAP-M0+VMAP-C→ vWA+APATPase+wHTH+TPRs*→ ||← FXSXX-COOH-like← Trypsin+EAD2	1201	Streptomyces viridochromogenes	GCA_001047325.1	actinobacteria
KMS80645.1	vWA+TPRs	← TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1118	Streptomyces leeuwenhoekii	GCA_001047315.1	actinobacteria
KMS83272.1	vWA+TPRs	Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1238	Streptomyces regensis	GCA_001047335.1	actinobacteria
KMS84544.1	vWA+Pkinase+cNMP_cyclase+Band7+HAD	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+cNMP_cyclase+Band7+HAD*→	1313	Streptomyces regensis	GCA_001047335.1	actinobacteria
KMW70431.1	vWA+FGS-fold_domain	FGS-fold_domain→ ||← ?← ?||EAD4+VMAP-M3+VMAP-C→ MoxR→ vWA+FGS-fold_domain*→ ?→ FGS-fold_domain→	884	Limnoraphis robusta CS-951	GCA_000972705.2	cyanobacteria
KMW70584.1	vWA_protein	FGS-fold_domain→ ||← ?← ?||EAD4+VMAP-M3+VMAP-C→ MoxR→ vWA_protein*→	354	Limnoraphis robusta CS-951	GCA_000972705.2	cyanobacteria
KND29573.1	vWA+Pkinase+wHTH+cNMP_cyclase+Band7+HAD	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ ?→ vWA+Pkinase+wHTH+cNMP_cyclase+Band7+HAD*→	1217	Streptomyces aciduscabies	GCA_001189015.1	actinobacteria
KND32413.1	vWA+TPRs	← TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1100	Streptomyces aciduscabies	GCA_001189015.1	actinobacteria
KND33426.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ AB_hydrolase→ CASPASE+EAD2→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→	1329	Streptomyces europaeiscabiei	GCA_001189025.1	actinobacteria
KOG25205.1	vWA_protein	Trypco2→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA_protein*→	277	Streptomyces viridochromogenes	GCA_001270515.1	actinobacteria
KOG25691.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ AB_hydrolase→ CASPASE+EAD2→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→	1355	Streptomyces viridochromogenes	GCA_001270515.1	actinobacteria
KOG44801.1	vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats	vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats*→	1144	Streptomyces virginiae	GCA_001270565.1	actinobacteria
KOG57815.1	vWA+TPRs	← TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1098	Streptomyces virginiae	GCA_001270565.1	actinobacteria
KOG73838.1	vWA+TPRs	TCAD15→ Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1235	Streptomyces antibioticus	GCA_001270635.1	actinobacteria
KOT34693.1	vWA+wHTH+TPRs+wHTH+TPRs+APATPase+wHTH+TPRs	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+wHTH+TPRs+wHTH+TPRs+APATPase+wHTH+TPRs*→ ||← AB_hydrolase	1732	Streptomyces sp. NRRL WC-3701	GCA_001279025.1	actinobacteria
KOT44382.1	vWA+TPRs	← TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ Radical_SAM→ TIR+APATPase+TPRs→	1085	Streptomyces rimosus subsp. rimosus	GCA_001279015.1	actinobacteria
KOT47672.1	vWA+TPRs	← TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ Radical_SAM→ TIR+APATPase+TPRs→	1085	Streptomyces rimosus subsp. rimosus	GCA_001279065.1	actinobacteria
KOT61113.1	vWA+wHTH+TPRs+wHTH+TPRs+APATPase+wHTH+TPRs	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+wHTH+TPRs+wHTH+TPRs+APATPase+wHTH+TPRs*→ ||← AB_hydrolase	1742	Streptomyces rimosus subsp. rimosus	GCA_001279065.1	actinobacteria
KOT93823.1	vWA+wHTH+TPRs+wHTH+TPRs+APATPase+wHTH+TPRs	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+wHTH+TPRs+wHTH+TPRs+APATPase+wHTH+TPRs*→ ||← AB_hydrolase	1733	Streptomyces sp. NRRL F-5755	GCA_001279365.1	actinobacteria
KOT96760.1	vWA+TPRs	← TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ Radical_SAM→ TIR+APATPase+TPRs→	1085	Streptomyces rimosus subsp. pseudoverticillatus	GCA_001279345.1	actinobacteria
KOT99550.1	vWA+wHTH+TPRs+wHTH+TPRs+APATPase+wHTH+TPRs	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+wHTH+TPRs+wHTH+TPRs+APATPase+wHTH+TPRs*→ ||← AB_hydrolase	1732	Streptomyces rimosus subsp. pseudoverticillatus	GCA_001279345.1	actinobacteria
KOU00046.1	vWA+TPRs	← TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ Radical_SAM→ TIR+APATPase+TPRs→ TIR+APATPase+TPRs→	1094	Streptomyces sp. NRRL F-5755	GCA_001279365.1	actinobacteria
KOU06764.1	vWA+TPRs	← TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→ Trypco1→	1125	Streptomyces sp. NRRL F-4711	GCA_001279355.1	actinobacteria

acc	architecture	operon	len	species	gca	taxend
KOU20535.1	vWA+TPRs	TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→	1098	Streptomyces sp. WM6368	GCA_001279625.1	actinobacteria
KOU20844.1	vWA+TPRs	TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→	1076	Streptomyces sp. WM6349	GCA_001279445.1	actinobacteria
KOU33656.1	vWA+CASPASE+TCAD12	AB_hydrolase→ CASPASE+VMAP-M2+VMAP-C→ MoxR→ vWA+CASPASE+TCAD12*→	1107	Streptomyces sp. WM6373	GCA_001279685.1	actinobacteria
KOU34863.1	vWA+TPRs	TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→	1077	Streptomyces sp. WM6373	GCA_001279685.1	actinobacteria
KOU55156.1	vWA+APATPase+Trypsin+TIR+FxsC_Cter(partial)	vWA+APATPase+Trypsin+TIR+FxsC_Cter(partial)*→ ||← DUF397	1147	Streptomyces sp. MMG1533	GCA_001279775.1	actinobacteria
KOU62395.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← Na_H_Exchanger||AB_hydrolase→ CASPASE+EAD2→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→	1532	Streptomyces sp. MMG1533	GCA_001279775.1	actinobacteria
KOU66101.1	vWA+TPRs	TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C→ vWA+TPRs*→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1041	Streptomyces sp. WM4235	GCA_001279725.1	actinobacteria
KOU66771.1	vWA+TPRs	TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→	1077	Streptomyces sp. IGB124	GCA_001279935.1	actinobacteria
KOU75547.1	vWA+TPRs	TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→	1077	Streptomyces sp. XY66	GCA_001279905.1	actinobacteria
KOU88266.1	vWA+TPRs	TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→	1077	Streptomyces sp. XY58	GCA_001279855.1	actinobacteria
KOU97671.1	vWA+TPRs	TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→	1076	Streptomyces sp. XY511	GCA_001279485.1	actinobacteria
KOV10493.1	vWA+TPRs	AB_hydrolase→ CASPASE+EAD2+VMAP-C→ MoxR→ vWA+TPRs*→	2147	Streptomyces sp. XY431	GCA_001279805.1	actinobacteria
KOV19775.1	vWA+TPRs	TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→	1077	Streptomyces sp. XY413	GCA_001279765.1	actinobacteria
KOV37678.1	vWA+TPRs	TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1077	Streptomyces sp. H021	GCA_001279495.1	actinobacteria
KOV64928.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like← Trypsin+EAD2← Trypco2||METALLOPROTEASE+TPRs→	1186	Streptomyces sp. AS58	GCA_001279985.1	actinobacteria
KOV86253.1	vWA+TPRs	MoxR→ vWA+TPRs*→ Radical_SAM→ TIR+APATPase+TPRs→ Radical_SAM→ ?→ STAND_NTPase→ TIR+APATPase+TPRs→ ||← DUF397	1078	Streptomyces sp. NRRL WC-3618	GCA_001280005.1	actinobacteria
KOV97699.1	vWA+Pkinase+cNMP_cyclase+Band7+HAD	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+cNMP_cyclase+Band7+HAD*→	1313	Streptomyces sp. NRRL WC-3723	GCA_001280045.1	actinobacteria
KOV97767.1	vWA+TPRs	TCAD15→ Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1235	Streptomyces sp. NRRL WC-3723	GCA_001280045.1	actinobacteria
KOX08458.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs	1254	Micromonospora sp. NRRL B-16802	GCA_001279555.1	actinobacteria
KOX39399.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→ ?→ ?→ CASPASE→	1125	Streptomyces sp. NRRL F-4707	GCA_001279605.1	actinobacteria
KOX52870.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→ ?→ CASPASE→ TIR+APATPase+TPRs→	1125	Streptomyces sp. NRRL F-7442	GCA_001279615.1	actinobacteria
KPC67231.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ TIR+APATPase+TPRs→	1077	Streptomyces chattanoogensis	GCA_001294335.1	actinobacteria
KPC72055.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← Na_H_Exchanger||AB_hydrolase→ CASPASE+EAD2→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→	1503	Streptomyces sp. NRRL WC-3753	GCA_001294395.1	actinobacteria
KPC90543.1	vWA+TPRs	TCAD15→ ?→ ?→ Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1054	Streptomyces sp. NRRL F-6602	GCA_001294325.1	actinobacteria
KPH99459.1	vWA+BetaPropeller	AB_hydrolase→ CASPASE+VMAP-M2+VMAP-C→ MoxR→ vWA+BetaPropeller*→	852	Actinobacteria bacterium OK006	GCA_001298565.1	actinobacteria
KPH99925.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← Na_H_Exchanger||AB_hydrolase→ CASPASE+EAD2→ METALLOPROTEASE+TPRs→	1498	Actinobacteria bacterium OV450	GCA_001298555.1	actinobacteria
KPI09079.1	vWA+APATPase+wHTH+TPRs	EAD2+TIR→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs	1290	Actinobacteria bacterium OK006	GCA_001298565.1	actinobacteria
KPI10108.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like← Trypsin+EAD2← Trypco2||FXSXX-COOH-like→ METALLOPROTEASE+TPRs→	1317	Actinobacteria bacterium OK006	GCA_001298565.1	actinobacteria
KPI17053.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	NUDIX→ Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→ SIR2→	1168	Actinobacteria bacterium OK074	GCA_001298575.1	actinobacteria
KPI25952.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1165	Actinobacteria bacterium OV320	GCA_001298545.1	actinobacteria
KPI32272.1	vWA+cNMP_cyclase+Band7+HAD	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+cNMP_cyclase+Band7+HAD*→	1122	Actinobacteria bacterium OV320	GCA_001298545.1	actinobacteria
KPQ32127.1	vWA+FGS-fold_domain	Trypco1→ Trypsin+VMAP-M1+VMAP-C→ MoxR→ vWA+FGS-fold_domain*→ FGS-fold_domain→ ||← RVT_1← four_helix_bundle_protein	920	Phormidesmis priestleyi Ana	GCA_001314865.1	cyanobacteria
KPQ33019.1	vWA+FGS-fold_domain	EAD1+Trypsin→ ?→ EAD1+VMAP-M1+VMAP-C→ MoxR→ vWA+FGS-fold_domain*→ FGS-fold_domain→ FGS-fold_domain→	1004	Phormidesmis priestleyi Ana	GCA_001314865.1	cyanobacteria
KQC35451.1	vWA+APATPase+wHTH+TPRs	EAD2+EAD1→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← FXSXX-COOH-like	1199	Frankia sp. ACN1ag	GCA_001414035.1	actinobacteria
KQM03129.1	vWA+APATPase+wHTH+TPRs	EAD2+EAD1→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like	1380	Frankia sp. CpI1-P	GCA_001421075.1	actinobacteria
KRD17930.1	vWA+APATPase+wHTH+TPRs	DUF397→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← vWA← EAD2+VMAP-M0+VMAP-C	870	Streptomyces sp. Root264	GCA_001428885.1	actinobacteria
KST64955.1	vWA+Ntox3+MACRODOMAIN+FGS-fold_domain	EAD1+VMAP-M1+VMAP-C→ MoxR→ vWA+Ntox3+MACRODOMAIN+FGS-fold_domain*→	1071	Mastigocoleus testarum BC008	GCA_001456025.1	cyanobacteria
KUF20465.1	vWA+TPRs	Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→	1213	Streptomyces silvensis	GCA_001482415.1	actinobacteria

acc	architecture	operon	len	species	gca	taxend
KUH39613.1	vWA_protein	AB_hydrolase→ CASPASE+VMAP-M2+VMAP-C→ MoxR→ vWA_protein*→ vWA(partial)+APATPase+wHTH+cNMP_cyclase+NaeI→	502	Streptomyces kanasensis	GCA_001484625.1	actinobacteria
KUJ68393.1	vWA+APATPase+wHTH+TPRs	PNP_UDP_1+EAD2→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ‖← PSE← FXSXX-COOH-like	1473	Streptomyces albus subsp. albus	GCA_001507455.1	actinobacteria
KUL22000.1	vWA+APATPase+wHTH+TPRs	FXSXX-COOH-like→ METALLOPROTEASE+TPRs→ PNP_UDP_1+VMAP-M0+VMAP-C→ vWA+APATPase+wHTH+TPRs*→	1255	Actinoplanes awajinensis subsp. mycoplanecinus	GCA_001509495.1	actinobacteria
KUL67220.1	vWA+Pkinase+ZNR+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	SIR2→ ‖← ?← ?‖Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ZNR+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→ Porphobil_deam+Porphobil_deamC→	1367	Streptomyces violaceusniger	GCA_001509775.1	actinobacteria
KUN02935.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→	1115	Streptomyces yokosukanensis	GCA_001514035.1	actinobacteria
KUN19774.1	vWA+TIR+APATPase+wHTH+TPRs	DRHyd+VMAP-M0+VMAP-C→ MoxR→ vWA+TIR+APATPase+wHTH+TPRs*→	1340	Streptomyces antibioticus	GCA_001514065.1	actinobacteria
KUN28796.1	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD	Trypco1→ PSE→ MoxR→ vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD*→	1412	Streptomyces antibioticus	GCA_001514065.1	actinobacteria
KUN39593.1	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD*→	1526	Streptomyces longwoodensis	GCA_001514125.1	actinobacteria
KUN44905.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ vWA+APATPase+wHTH+TPRs*→ ‖← METALLOPROTEASE+TPRs← Trypsin+EAD2← Trypco2‖METALLOPROTEASE+TPRs→	1296	Streptomyces olivochromogenes	GCA_001514115.1	actinobacteria
KUN49123.1	vWA+APATPase+wHTH+TPRs+cNMP_cyclase+NaeI	AB_hydrolase→ CASPASE+VMAP-M2+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs+cNMP_cyclase+NaeI*→	1667	Streptomyces avermitilis	GCA_001514135.1	actinobacteria
KUN87228.1	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD*→	1443	Streptomyces griseoruber	GCA_001514205.1	actinobacteria
KUN89326.1	vWA+APATPase+wHTH+TPRs	Trypsin+EAD2+VMAP-M0+VMAP-C→ vWA+APATPase+wHTH+TPRs*→ KAP_NTPase→	806	Streptomyces griseoruber	GCA_001514205.1	actinobacteria
KUN98985.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→	1105	Streptomyces caeruleatus	GCA_001514235.1	actinobacteria
KUO22454.1	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD*→	1396	Streptomyces sp. RV15	GCA_001514305.1	actinobacteria
KYK10151.1	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase	Trypco1→ MoxR→ vWA+Pkinase+wHTH+TPRs+cNMP_cyclase*→	991	Streptomyces sp. CC71	GCA_001595515.1	actinobacteria
KYK14919.1	vWA+APATPase+wHTH+TPRs	vWA+APATPase+wHTH+TPRs*→ ‖← Na_H_Exchanger	1391	Streptomyces sp. CC71	GCA_001595515.1	actinobacteria
OBQ03799.1	vWA+FGS-fold_domain	Trypco1→ Trypsin+VMAP-M1+VMAP-C→ MoxR→ vWA+FGS-fold_domain*→	870	Anabaena sp. AL09	GCA_001672255.1	cyanobacteria
OBQ11326.1	vWA+FGS-fold_domain	Trypco1→ Trypsin+VMAP-M1+VMAP-C→ MoxR→ vWA+FGS-fold_domain*→	871	Anabaena sp. LE011-02	GCA_001672225.1	cyanobacteria
OBQ20858.1	vWA+FGS-fold_domain	vWA+FGS-fold_domain*→	880	Anabaena sp. AL93	GCA_001672085.1	cyanobacteria
OBQ35051.1	vWA+FGS-fold_domain	Trypco1→ VMAP-M1+EAD6+VMAP-C→ MoxR→ vWA+FGS-fold_domain*→	789	Anabaena sp. CRKS33	GCA_001672075.1	cyanobacteria
OBQ40142.1	vWA+FGS-fold_domain	Trypco1→ MoxR→ vWA+FGS-fold_domain*→	870	Anabaena sp. MDT14b	GCA_001672195.1	cyanobacteria
OBQ42247.1	vWA+beta-rich-region+HTH+FGS-fold_domain	cNMP_cyclase+EAD1→ EAD1+VMAP-M24+VMAP-C→ MoxR→ vWA+beta-rich-region+HTH+FGS-fold_domain*→ ?→ ‖← RVT_1← four_helix_bundle_protein← FGS-fold_domain	1075	Aphanizomenon flos-aquae WA102	GCA_001672105.1	cyanobacteria
OEV11574.1	vWA	TCAD15‖Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA*→	299	Streptomyces nanshensis	GCA_001751255.1	actinobacteria
OEV17914.1	vWA	AB_hydrolase→ CASPASE+VMAP-M2+VMAP-C→ MoxR→ vWA→ vWA*→	369	Streptomyces nanshensis	GCA_001751305.1	actinobacteria
OEV17915.1	vWA	AB_hydrolase→ CASPASE+VMAP-M2+VMAP-C→ MoxR→ vWA*→ vWA→	354	Streptomyces nanshensis	GCA_001751305.1	actinobacteria
OEV28767.1	vWA	Trypsin+HDxxH+VMAP-M0→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA*→ ?→ TIR+APATPase+TPRs→	606	Streptomyces nanshensis	GCA_001751265.1	actinobacteria
OHV36996.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ‖← ?‖EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs→ ‖← METALLOPROTEASE+TPRs	1397	Frankia sp. EUN1h	GCA_001854645.1	actinobacteria
OHV37160.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs→ ‖← ?‖EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ‖← METALLOPROTEASE+TPRs	1281	Frankia sp. EUN1h	GCA_001854645.1	actinobacteria
OIJ95017.1	vWA+SFII-helicase+DUF3427	AB_hydrolase→ CASPASE+VMAP-M2+VMAP-C→ MoxR→ vWA+SFII-helicase+DUF3427*→	1325	Streptomyces sp. MUSC 93	GCA_001866645.1	actinobacteria
OIK25119.1	vWA+APATPase+wHTH+TPRs	Trypco2→ EAD2+VMAP-M0+VMAP-C→ vWA+APATPase+wHTH+TPRs*→ ‖← PSE← FXSXX-COOH-like← Trypsin+EAD2	1218	Streptomyces malaysiense	GCA_000980885.2	actinobacteria
OKH35591.1	vWA+FGS-fold_domain	cNMP_cyclase+VMAP-M1+VMAP-C→ MoxR→ vWA+FGS-fold_domain*→ FGS-fold_domain→	863	Phormidium ambiguum IAM M-71	GCA_001904725.1	cyanobacteria
OKI00871.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→ ?→ NUDIX→	1137	Streptomyces sp. CB02923	GCA_001905005.1	actinobacteria
OKI13910.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ‖← METALLOPROTEASE+TPRs← FXSXX-COOH-like	1444	Saccharothrix sp. CB00851	GCA_001905065.1	actinobacteria
OKI29456.1	vWA+TPRs	TCAD15‖Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1076	Streptomyces sp. CB03578	GCA_001905025.1	actinobacteria
OKI29918.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ vWA+APATPase+wHTH+TPRs*→ ‖← METALLOPROTEASE+TPRs← cNMP_cyclase+EAD2	1294	Saccharothrix sp. CB00851	GCA_001905065.1	actinobacteria
OKI39951.1	vWA+APATPase+wHTH+TPRs	cNMP_binding+HTH_Crp_2← ?‖EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ‖← Na_H_Exchanger‖AB_hydrolase→ CASPASE+EAD2→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→	1508	Streptomyces sp. CB03578	GCA_001905025.1	actinobacteria
OKI55839.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ AB_hydrolase→ CASPASE+EAD2→ METALLOPROTEASE+TPRs→	1328	Streptomyces sp. CB00072	GCA_001905575.1	actinobacteria
OKI62008.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ‖← Na_H_Exchanger‖AB_hydrolase→ CASPASE+EAD2→ METALLOPROTEASE+TPRs→	1522	Streptomyces sp. MJM1172	GCA_001905425.1	actinobacteria
OKI68699.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ AB_hydrolase→ CASPASE+EAD2→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→	1347	Streptomyces sp. TSRI0445	GCA_001905405.1	actinobacteria
OKI79079.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ AB_hydrolase→ CASPASE+EAD2→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→	1329	Streptomyces sp. TSRI0395	GCA_001905525.1	actinobacteria
OKJ43967.1	vWA+TPRs	TCAD15‖Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1132	Streptomyces sp. CB01580	GCA_001905795.1	actinobacteria
OKJ54712.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ AB_hydrolase→ CASPASE+EAD2→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→	1329	Streptomyces sp. CB02115	GCA_001905645.1	actinobacteria
OKJ83696.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ AB_hydrolase→ CASPASE+EAD2→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→	1358	Streptomyces sp. CB01883	GCA_001905855.1	actinobacteria
OKJ89683.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ‖← Na_H_Exchanger‖AB_hydrolase→ CASPASE+EAD2→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→	1489	Streptomyces sp. TSRI0107	GCA_001905845.1	actinobacteria
OKK02915.1	vWA+APATPase+wHTH+TPRs	AB_hydrolase→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ‖← METALLOPROTEASE+TPRs← FXSXX-COOH-like	1279	Streptomyces sp. CB03234	GCA_001905885.1	actinobacteria
OKK13505.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→	1426	Streptomyces sp. CB02400	GCA_001905725.1	actinobacteria
OKK20627.1	vWA+TPRs	TCAD15‖Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1122	Streptomyces sp. CB00455	GCA_001905445.1	actinobacteria

acc	architecture	operon	len	species	gca	taxend
OLC62284.1	vWA+Glyco_transf_20	MoxR→ vWA+Glyco_transf_20*→	1123	Ktedonobacter sp. 13_1_40CM_4_52_4	GCA_001918255.1	chloroflexi
OLO30728.1	vWA+TIR+FxsC_Cter	← PNP_UDP_1+EAD2||AB_hydrolase→ CASPASE+VMAP-M2+VMAP-C→ MoxR→ vWA+TIR+FxsC_Cter*→	1009	Streptomyces sp. MNU77	GCA_000935135.2	actinobacteria
OLZ67587.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like	1282	Streptomyces sp. IMTB 2501	GCA_001953885.1	actinobacteria
OLZ74128.1	vWA+TPRs	← TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1094	Streptomyces amritsarensis	GCA_001953875.1	actinobacteria
OMI34266.1	vWA+APATPase+wHTH+TPRs	PNP_UDP_1+EAD2→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like	1440	Streptomyces sparsogenes DSM 40356	GCA_001969965.1	actinobacteria
OMI41127.1	vWA+Pkinase+Pkinase	vWA+Pkinase+Pkinase*→ Porphobil_deam+Porphobil_deamC→	836	Streptomyces sparsogenes DSM 40356	GCA_001969965.1	actinobacteria
ONH30898.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ TIR+APATPase+TPRs→ ||← METALLOPROTEASE+TPRs	1329	Frankia sp. M16386	GCA_001983105.1	actinobacteria
OOC02455.1	vWA+APATPase+wHTH+TPRs	cNMP_cyclase+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like← cNMP_binding+HTH_Crp_2	1202	Amycolatopsis azurea DSM 43854	GCA_001995215.1	actinobacteria
OOQ46879.1	vWA+APATPase+wHTH+TPRs	Trypsin+EAD2+VMAP-C→ vWA+APATPase+wHTH+TPRs*→ KAP_NTPase→	805	Streptomyces antibioticus	GCA_002019855.1	actinobacteria
OOQ51257.1	vWA+APATPase+wHTH+TPRs	vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like← Trypsin+EAD2||METALLOPROTEASE+TPRs→	1250	Streptomyces antibioticus	GCA_002019855.1	actinobacteria
OOQ52337.1	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD*→	1161	Streptomyces antibioticus	GCA_002019855.1	actinobacteria
OQY51160.1	vWA_protein	VMAP-C(partial)→ VMAP-C(partial)→ ?→ ?→ ?→ MoxR→ vWA_protein*→	588	Beggiatoa sp. 4572_84	GCA_002085445.1	gammaproteobacteria
OSC70555.1	vWA+TPRs	AB_hydrolase→ CASPASE+EAD2→ VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→	1178	Streptomyces sp. 4F	GCA_002104855.1	actinobacteria
OSC74050.1	vWA(partial)+REase+STAND_NTPase+TPRs+cNMP_cyclase	vWA(partial)+REase+STAND_NTPase+TPRs+cNMP_cyclase*→	1256	Streptomyces sp. BF-3	GCA_002104865.1	actinobacteria
OSZ59308.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→	1106	Streptomyces pharetrae CZA14	GCA_002128465.1	actinobacteria
OSZ60893.1	vWA+TIR+APATPase+Trypsin+HDxxH+VMAP-M0+VMAP-C	← TCAD15||PSE→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TIR+APATPase+Trypsin+HDxxH+VMAP-M0+VMAP-C*→	1351	Streptomyces pharetrae CZA14	GCA_002128465.1	actinobacteria
OUC12065.1	vWA_protein	Trypsin+VMAP-M1+VMAP-C→ MoxR→ vWA_protein*→ FGS-fold_domain→ FGS-fold_domain→	410	Alkalinema sp. CACIAM 70d	GCA_002148405.1	cyanobacteria
PBC92565.1	vWA+cNMP_binding+HTH_Crp_2+TerD	AB_hydrolase→ CASPASE+VMAP-M0+VMAP-C→ MoxR→ vWA+cNMP_binding+HTH_Crp_2+TerD*→	1494	Streptomyces sp. Ag82_O1-15	GCA_002300485.1	actinobacteria
PDW02245.1	vWA+Pkinase+REC+TCAD9+APHkinase	vWA+Pkinase+REC+TCAD9+APHkinase*→	1297	Chloroflexi bacterium Kir15-3F	GCA_002532535.1	chloroflexi
PJN27976.1	vWA+BetaPropeller+Pkinase+TIR	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+BetaPropeller+Pkinase+TIR*→	1356	Kitasatospora sp. CB02891	GCA_002803145.1	actinobacteria
SBT88418.1	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD*→	1567	Streptomyces sp. DI166	GCA_900091315.1	actinobacteria
SBT93465.1	vWA+HTH	CASPASE+VMAP-M0+VMAP-C→ vWA+HTH*→	729	Streptomyces sp. DI166	GCA_900091315.1	actinobacteria
SBT93723.1	vWA_protein	AB_hydrolase→ CASPASE+VMAP-M0+VMAP-C→ MoxR→ vWA_protein*→ Trypsin+CASPASE+S1COLD→	608	Streptomyces sp. DI166	GCA_900091315.1	actinobacteria
SBT94501.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ vWA+APATPase+wHTH+TPRs*→	1320	Streptomyces sp. DI166	GCA_900091315.1	actinobacteria
SBU89710.1	vWA+TIR+FxsC_Cter	AB_hydrolase→ CASPASE+VMAP-M2+VMAP-C→ MoxR→ vWA+TIR+FxsC_Cter*→	1001	Streptomyces sp. MnatMP-M77	GCA_900090075.1	actinobacteria
SBU92090.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→	1070	Streptomyces sp. MnatMP-M77	GCA_900090075.1	actinobacteria
SBU92604.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ AB_hydrolase→ CASPASE+EAD2→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→	1457	Streptomyces sp. OspMP-M45	GCA_900090065.1	actinobacteria
SBV04727.1	vWA+REase+STAND_NTPase+SFI-helicase	DUF397→ Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+REase+STAND_NTPase+SFI-helicase*→	1640	Streptomyces sp. Ncost-T6T-1	GCA_900090085.1	actinobacteria
SBV07778.1	vWA+TPRs+TIR+FxsC_Cter(partial)	AB_hydrolase→ CASPASE+VMAP-M2+VMAP-C→ MoxR→ vWA+TPRs+TIR+FxsC_Cter(partial)*→	1422	Streptomyces sp. MnatMP-M77	GCA_900090075.1	actinobacteria
SCD36331.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ AB_hydrolase→ CASPASE+EAD2→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→	1457	Streptomyces sp. PalvLS-984	GCA_900091765.1	actinobacteria
SCD66673.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ AB_hydrolase→ CASPASE+EAD2→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→	1457	Streptomyces sp. PpalLS-921	GCA_900091835.1	actinobacteria
SCD67020.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ ?→ vWA+APATPase+wHTH+TPRs*→ AB_hydrolase→	1364	Streptomyces sp. BpilaLS-43	GCA_900091875.1	actinobacteria
SCD89054.1	vWA+REase+SWACOS+TPRs+cNMP_cyclase	AB_hydrolase→ CASPASE+VMAP-M2+VMAP-C→ MoxR→ vWA+REase+SWACOS+TPRs+cNMP_cyclase*→	1705	Streptomyces sp. BvalAA-19	GCA_900091865.1	actinobacteria
SCD99771.1	vWA_protein	VMAP-C→ MoxR→ vWA_protein*→	835	Streptomyces sp. TverLS-915	GCA_900091755.1	actinobacteria
SCE03681.1	vWA+TPRs	vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→	1026	Streptomyces sp. BvitLS-983	GCA_900091785.1	actinobacteria
SCE24206.1	vWA+TPRs	← TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→	1137	Streptomyces sp. ScaeMP-6W	GCA_900091885.1	actinobacteria
SCE36538.1	vWA+APATPase+wHTH+TPRs	vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like||Trypco1→	1363	Streptomyces sp. SolWspMP-5a-2	GCA_900091845.1	actinobacteria
SCE53113.1	vWA+TPRs	vWA+TPRs*→	1050	Streptomyces sp. DvalAA-14	GCA_900091855.1	actinobacteria
SCE55987.1	vWA+TPRs	AB_hydrolase→ CASPASE+VMAP-M2+VMAP-C→ MoxR→ vWA+TPRs*→	666	Streptomyces sp. OspMP-M43	GCA_900091905.1	actinobacteria
SCE56241.1	vWA+TPRs	← TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→ Trypco1→	1134	Streptomyces sp. DvalAA-43	GCA_900091725.1	actinobacteria
SCE64837.1	vWA+TPRs	Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ ?→ Radical_SAM→ TIR+APATPase+TPRs→ ||← Voltage_CLC	1129	Micromonospora haikouensis	GCA_900091595.1	actinobacteria
SCF42109.1	vWA_protein	CASPASE(partial)+VMAP-M2+VMAP-C→ MoxR→ vWA_protein*→	1041	Micromonospora matsumotoense	GCA_900091525.1	actinobacteria
SCF49061.1	vWA+TPRs	VMAP-C→ MoxR→ ?→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→ Trypco1→	1042	Streptomyces sp. LcepLS	GCA_900091485.1	actinobacteria
SCF56449.1	vWA+STAND_NTPase+BetaPropeller+REase(Mrr_cat-PDDEXK)	AB_hydrolase→ CASPASE+VMAP-M0+VMAP-C→ MoxR→ vWA+STAND_NTPase+BetaPropeller+REase(Mrr_cat-PDDEXK)*→	1067	Streptomyces sp. Ncost-T10-10d	GCA_900091955.1	actinobacteria
SCF58287.1	vWA+Pkinase+cNMP_cyclase+Band7+HAD	VMAP-C(partial)→ MoxR→ vWA+Pkinase+cNMP_cyclase+Band7+HAD*→	1314	Streptomyces sp. LamerLS-31b	GCA_900091975.1	actinobacteria

acc	architecture	operon	len	species	gca	taxend
SCF72582.1	vWA+TPRs	vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	980	Streptomyces sp. Ncost-T10-10d	GCA_900091955.1	actinobacteria
SCF77036.1	vWA+TIR+FxsC_Cter	AB_hydrolase→ CASPASE+VMAP-M2+VMAP-C→ MoxR→ vWA+TIR+FxsC_Cter*→	1071	Streptomyces sp. MnatMP-M17	GCA_900091995.1	actinobacteria
SCF89167.1	vWA+APATPase+wHTH+TPRs	Trypco2→ EAD2+VMAP-M0+VMAP-C→ vWA+APATPase+wHTH+TPRs*→ ‖← METALLOPROTEASE+TPRs← FXSXX-COOH-like← Trypsin+EAD2← HTH_31	1321	Streptomyces sp. LamerLS-31b	GCA_900091975.1	actinobacteria
SCF93414.1	vWA+REase+SWACOS+TPRs+cNMP_cyclase	AB_hydrolase→ CASPASE+VMAP-M2+VMAP-C→ MoxR→ vWA+REase+SWACOS+TPRs+cNMP_cyclase*→	1650	Streptomyces sp. Cmuel-A718b	GCA_900092005.1	actinobacteria
SCF93674.1	vWA+Pkinase+cNMP_cyclase+Band7	vWA+Pkinase+cNMP_cyclase+Band7*→	1181	Streptomyces sp. DconLS	GCA_900091985.1	actinobacteria
SCF98831.1	vWA+REase+SFI-helicase+DUF4729	Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+REase+SFI-helicase+DUF4729*→	1616	Streptomyces sp. Ncost-T10-10d	GCA_900091955.1	actinobacteria
SCG16381.1	vWA+SWACOS+TPRs	Trypco1→ Trypsin+VMAP-M8+VMAP-C→ MoxR→ vWA+SWACOS+TPRs*→	1403	Micromonospora echinofusca	GCA_900091445.1	actinobacteria
SCG36816.1	vWA+Trypsin+HDxxH+VMAP-M0+VMAP-C	Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+Trypsin+HDxxH+VMAP-M0+VMAP-C*→ ?→ ‖← ?← ?‖?→ DUF397→	1064	Micromonospora humi	GCA_900090105.1	actinobacteria
SCG40329.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ‖← METALLOPROTEASE+TPRs	1315	Micromonospora humi	GCA_900090105.1	actinobacteria
SCK15830.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→	1138	Streptomyces sp. SceaMP-e96	GCA_900090095.1	actinobacteria
SCK31273.1	vWA+TPRs	← TCAD15‖Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ TIR+APATPase+TPRs→	1129	Streptomyces sp. SceaMP-e96	GCA_900090095.1	actinobacteria
SCK31299.1	vWA+TPRs	← TCAD15‖Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1018	Streptomyces sp. WMMB 322	GCA_900090145.1	actinobacteria
SCK33554.1	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+wHTH+TPRs+cNMP_cyclase*→	1277	Streptomyces	GCA_900090165.1	actinobacteria
SCK52956.1	vWA+wHTH+TPRs+APATPase+wHTH+TPRs	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+wHTH+TPRs+APATPase+wHTH+TPRs*→ ?→ ?→ ‖← AB_hydrolase	1607	Streptomyces sp. SceaMP-e96	GCA_900090095.1	actinobacteria
SCL25845.1	vWA+Calcineurin-like+NACHT	Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+Calcineurin-like+NACHT*→	1535	Micromonospora inyonensis	GCA_900091415.1	actinobacteria
SCL28499.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ‖← METALLOPROTEASE+TPRs← FXSXX-COOH-like	1353	Micromonospora nigra	GCA_900091585.1	actinobacteria
SCL86372.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ AB_hydrolase→	1445	Streptomyces sp. DpondAA-F4	GCA_900095575.1	actinobacteria
SCY50757.1	vWA+TPRs	← TCAD15‖Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1157	Streptomyces sp. 136MFCol5.1	GCA_900101975.1	actinobacteria
SDA57601.1	vWA+Calcineurin-like+APATPase+SFII-helicase	AB_hydrolase→ CASPASE+VMAP-M4+VMAP-C→ MoxR→ vWA+Calcineurin-like+APATPase+SFII-helicase*→	1397	Janthinobacterium sp. 551a	GCA_900103675.1	betaproteobacteria
SDE27042.1	vWA+SFII-helicase+Trypsin+cNMP_cyclase	AB_hydrolase→ CASPASE+VMAP-M2+VMAP-C→ MoxR→ vWA+SFII-helicase+Trypsin+cNMP_cyclase*→	1461	Streptomyces emeiensis	GCA_900101585.1	actinobacteria
SDF68672.1	vWA+APATPase+wHTH+TPRs	cNMP_cyclase+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ‖← METALLOPROTEASE+TPRs← FXSXX-COOH-like	1458	Lechevalieria fradiae	GCA_900100955.1	actinobacteria
SDG68818.1	vWA+STAND_NTPase+Trypsin+CASPASE+S1COLD	AB_hydrolase→ CASPASE+VMAP-M0+VMAP-C→ MoxR→ vWA+STAND_NTPase+Trypsin+CASPASE+S1COLD*→	1349	Streptomyces jietaisiensis	GCA_900102095.1	actinobacteria
SDK59304.1	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD*→	1689	Streptomyces indicus	GCA_900100315.1	actinobacteria
SDL96695.1	vWA+TPRs	← TCAD15‖Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1111	Streptomyces wuyuanensis	GCA_900103455.1	actinobacteria
SDM15376.1	vWA+APATPase+wHTH+TPRs	← cNMP_binding+HTH_Crp_2‖cNMP_cyclase+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ‖← METALLOPROTEASE+TPRs← FXSXX-COOH-like‖?→ ?→ TIR+TPRs→	1411	Lentzea violacea	GCA_900100275.1	actinobacteria
SDM66838.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ vWA+APATPase+wHTH+TPRs*→ ‖← METALLOPROTEASE+TPRs← FXSXX-COOH-like← Trypsin+EAD2← Trypco2‖FXSXX-COOH-like→ METALLOPROTEASE+TPRs→	1318	Streptomyces sp. cf386	GCA_900103585.1	actinobacteria
SDN22428.1	vWA+APATPase+wHTH+TPRs	PNP_UDP_1+EAD2→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ‖← METALLOPROTEASE+TPRs← FXSXX-COOH-like	1504	Streptomyces guanduensis	GCA_900103985.1	actinobacteria
SDN24910.1	vWA+Pkinase+FtsK+TPRs	ADP_ribosyl_GH→ Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+FtsK+TPRs*→ NUDIX→ SIR2→	1325	Streptomyces wuyuanensis	GCA_900103455.1	actinobacteria
SDQ92256.1	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD	Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD*→	1558	Streptomyces sp. cf386	GCA_900103585.1	actinobacteria
SDR23156.1	vWA+TPRs	← TCAD15‖Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ TIR+APATPase+TPRs→	1134	Streptomyces sp. KS_16	GCA_900102245.1	actinobacteria
SDT07870.1	vWA+APATPase+SWACOS+wHTH+TPRs+Beta-rich-tail	Trypco1→ Trypsin+EAD2→ EAD2+VMAP-M10+VMAP-C→ MoxR→ vWA+APATPase+SWACOS+wHTH+TPRs+Beta-rich-tail*→	1562	Streptomyces sp. TLI_053	GCA_900105395.1	actinobacteria
SDT36692.1	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+wHTH+TPRs+cNMP_cyclase*→	1352	Streptomyces sp. 2114.2	GCA_900104935.1	actinobacteria
SDT74622.1	vWA+TPRs	← TCAD15‖Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→ Trypco1→	1144	Streptomyces sp. 2114.2	GCA_900104935.1	actinobacteria
SDU45427.1	vWA+APATPase+wHTH+TPRs	cNMP_cyclase+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ‖← METALLOPROTEASE+TPRs← FXSXX-COOH-like← cNMP_binding+HTH_Crp_2	1449	Amycolatopsis keratiniphila	GCA_900105855.1	actinobacteria
SDX38190.1	vWA+FGS-fold_domain+FGS-fold_domain+FGS-fold_domain	AB_hydrolase→ CASPASE+VMAP-M4+VMAP-C→ MoxR→ vWA+FGS-fold_domain+FGS-fold_domain+FGS-fold_domain*→	1552	Thiocapsa roseopersicina	GCA_900106925.1	gammaproteobacteria
SDY41558.1	vWA+APATPase+wHTH+TPRs	← cNMP_binding+HTH_Crp_2‖cNMP_cyclase+EAD2→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ‖← METALLOPROTEASE+TPRs	1388	Amycolatopsis xylanica	GCA_900107045.1	actinobacteria
SDY89948.1	vWA+APATPase+wHTH+Pkinase	CASPASE+VMAP-M2+VMAP-C→ MoxR→ vWA+APATPase+wHTH+Pkinase*→	1024	Amycolatopsis xylanica	GCA_900107045.1	actinobacteria
SEB55912.1	vWA+TPRs	← TCAD15‖Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ TIR+APATPase+TPRs→	1134	Streptomyces sp. 2224.1	GCA_900105915.1	actinobacteria
SEB60365.1	vWA_protein	AB_hydrolase→ CASPASE+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA_protein*→ vWA+TIR+FxsC_Cter→	306	Streptomyces sp. PAN_FS17	GCA_900105465.1	actinobacteria
SEB64482.1	vWA+CASPASE+NACHT+PIN	Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+CASPASE+NACHT+PIN*→	1157	Streptomyces sp. 2131.1	GCA_900105515.1	actinobacteria
SEB86929.1	vWA+TPRs	AB_hydrolase→ CASPASE+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→	1003	Streptomyces melanosporofaciens	GCA_900105695.1	actinobacteria
SEC39357.1	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD	Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD*→	1578	Streptomyces sp. PAN_FS17	GCA_900105465.1	actinobacteria
SEC48111.1	vWA+APATPase+wHTH	HTH+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH*→	1170	Amycolatopsis tolypomycina	GCA_900105945.1	actinobacteria
SEC51035.1	vWA+TPRs	← TCAD15‖Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1044	Streptomyces sp. TLI_105	GCA_900105415.1	actinobacteria
SEC56283.1	vWA+TPRs	← TCAD15‖Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1155	Streptomyces sp. 2131.1	GCA_900105515.1	actinobacteria
SEC79446.1	vWA+Pkinase+ZNR+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	SIR2→ ‖← ?← ?‖Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ZNR+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→ Porphobil_deam+Porphobil_deamC→	1501	Streptomyces melanosporofaciens	GCA_900105695.1	actinobacteria

acc	architecture	operon	len	species	gca	taxend
SEC83562.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← Na_H_Exchanger||AB_hydrolase→ CASPASE+EAD2→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→	1512	Streptomyces sp. 1222.5	GCA_900105245.1	actinobacteria
SEC83886.1	vWA+wHTH+cNMP_cyclase+Band7+HAD	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+wHTH+cNMP_cyclase+Band7+HAD*→	1271	Streptomyces sp. 1222.5	GCA_900105245.1	actinobacteria
SEC94800.1	vWA+wHTH+cNMP_cyclase+Band7+HAD	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+wHTH+cNMP_cyclase+Band7+HAD*→	1268	Streptomyces sp. 2231.1	GCA_900105605.1	actinobacteria
SEC95242.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← Na_H_Exchanger||AB_hydrolase→ CASPASE+EAD2→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→	1512	Streptomyces sp. 2231.1	GCA_900105605.1	actinobacteria
SED06705.1	vWA+APATPase+wHTH+TPRs	PNP_UDP_1+EAD2→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like	1452	Streptomyces melanosporofaciens	GCA_900105695.1	actinobacteria
SED37029.1	vWA+TIR+FxsC_Cter	AB_hydrolase→ CASPASE+VMAP-M2+VMAP-C→ MoxR→ vWA+TIR+FxsC_Cter*→	1001	Streptomyces griseus	GCA_900105705.1	actinobacteria
SED44913.1	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD	Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD*→	1578	Streptomyces sp. KS_5	GCA_900105275.1	actinobacteria
SED54965.1	vWA+APATPase+wHTH+TPRs	cNMP_cyclase+EAD2→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like	1341	Amycolatopsis tolypomycina	GCA_900105945.1	actinobacteria
SED97882.1	vWA+APATPase+wHTH+TPRs	Trypco2→ EAD2+VMAP-M0+VMAP-C→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like← Trypsin+EAD2	1309	Streptomyces misionensis	GCA_900104815.1	actinobacteria
SEE32562.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ TIR+APATPase+TPRs→	1134	Streptomyces sp. 2112.3	GCA_900105775.1	actinobacteria
SEE51089.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ TIR+APATPase+TPRs→	1146	Streptomyces sp. 2314.4	GCA_900105525.1	actinobacteria
SEE56281.1	vWA+TPRs	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→	1201	Streptomyces sp. 2314.4	GCA_900105525.1	actinobacteria
SEE67995.1	vWA+APATPase+wHTH+TPRs	vWA+APATPase+wHTH+TPRs*→ ?→ ||← ?← ?← S1COLD	1167	Streptomyces sp. KS_5	GCA_900105275.1	actinobacteria
SEF23786.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like	1401	Amycolatopsis pretoriensis	GCA_900107925.1	actinobacteria
SEF26728.1	vWA+APATPase+wHTH+TPRs	cNMP_cyclase+EAD2→ EAD2+VMAP-M0+VMAP-C→ vWA+APATPase+wHTH+TPRs→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like||EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like	1419	Amycolatopsis pretoriensis	GCA_900107925.1	actinobacteria
SEF26739.1	vWA+APATPase+wHTH+TPRs	cNMP_cyclase+EAD2→ EAD2+VMAP-M0+VMAP-C→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like||EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like	1320	Amycolatopsis pretoriensis	GCA_900107925.1	actinobacteria
SEF86779.1	vWA+TPRs	TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→ Trypco1→	1150	Streptomyces yanglinensis	GCA_900107965.1	actinobacteria
SEF89170.1	vWA+APATPase+wHTH+TPRs	PNP_UDP_1+EAD2→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like	1507	Streptomyces yanglinensis	GCA_900107965.1	actinobacteria
SEG16301.1	vWA+APATPase+wHTH+TPRs	Radical_SAM→ METALLOPROTEASE+TPRs→ ||← TIR+APATPase+TPRs||FXSXX-COOH-like→ ?→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ || METALLOPROTEASE+TPRs← Radical_SAM← FXSXX-COOH	1381	Actinomadura echinospora	GCA_900108175.1	actinobacteria
SEG54017.1	vWA+BetaPropeller+SWACOS+STAND_NTPase	Trypco1→ Trypsin+VMAP-M8+VMAP-C→ MoxR→ vWA+BetaPropeller+SWACOS+STAND_NTPase*→	1835	Actinomadura echinospora	GCA_900108175.1	actinobacteria
SEG88246.1	vWA+APATPase+wHTH+TPRs	Trypsin+EAD2→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like	1411	Nonomuraea solani	GCA_900108335.1	actinobacteria
SEG93346.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→	1119	Streptomyces yanglinensis	GCA_900107965.1	actinobacteria
SEN16512.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like← Trypsin+EAD2← Trypco2	1316	Streptomyces rubidus	GCA_900110255.1	actinobacteria
SEQ80125.1	vWA+APATPase+wHTH+TPRs	cNMP_binding+HTH_Crp_2||cNMP_cyclase+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like	1446	Lechevalieria xinjiangensis	GCA_900110955.1	actinobacteria
SER48031.1	vWA+APATPase+wHTH+TPRs	cNMP_binding+HTH_Crp_2||cNMP_cyclase+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like	1445	Lentzea albida	GCA_900111005.1	actinobacteria
SER87460.1	vWA+wHTH+cNMP_cyclase+Band7+HAD	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+wHTH+cNMP_cyclase+Band7+HAD*→	1328	Streptomyces sp. yr375	GCA_900110755.1	actinobacteria
SES32171.1	vWA+Trypsin+TCAD11+TPRs	CASPASE+VMAP-M2+VMAP-C→ MoxR→ vWA+Trypsin+TCAD11+TPRs*→	1417	Actinokineospora terrae	GCA_900111175.1	actinobacteria
SES36659.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→	1146	Streptomyces sp. yr375	GCA_900110755.1	actinobacteria
SES49412.1	vWA+APATPase+wHTH+TPRs	cNMP_binding+HTH_Crp_2||cNMP_cyclase+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like	1443	Lentzea flaviverrucosa	GCA_900110985.1	actinobacteria
SFE91364.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like	1265	Actinoplanes philippinensis	GCA_900113015.1	actinobacteria
SFF36468.1	vWA+TPRs	TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1157	Streptomyces alni	GCA_900112845.1	actinobacteria
SFF65888.1	vWA+SFII-helicase+Z1	AB_hydrolase→ CASPASE+VMAP-M2+VMAP-C→ VMAP-C(partial)→ MoxR→ vWA+SFII-helicase+Z1*→	1391	Streptomyces mirabilis	GCA_900112965.1	actinobacteria
SFM91649.1	vWA+METALLOPROTEASE+TCAD8	AB_hydrolase→ CASPASE+VMAP-M4+VMAP-C→ MoxR→ vWA+METALLOPROTEASE+TCAD8*→	1077	Rugamonas rubra	GCA_900114705.1	gammaproteobacteria
SFN86739.1	vWA+APATPase+wHTH+TPRs	Radical_SAM→ ||← TIR+APATPase+TPRs||?→ SWACOS→ ?→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← Radical_SAM← ?||cNMP_cyclase+EAD2→	1390	Actinomadura madurae	GCA_900115095.1	actinobacteria
SFO06617.1	vWA+APATPase+wHTH+TPRs	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+GGDEF+EAD2+VMAP-M0→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→	1414	Streptomyces sp. cf124	GCA_900114955.1	actinobacteria
SFO06655.1	vWA+APATPase+GGDEF+EAD2+VMAP-M0	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+GGDEF+EAD2+VMAP-M0*→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs→	1163	Streptomyces sp. cf124	GCA_900114955.1	actinobacteria
SFQ99524.1	vWA+APATPase+wHTH+TPRs	cNMP_binding+HTH_Crp_2||cNMP_cyclase+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like	1381	Lentzea waywayandensis	GCA_900115955.1	actinobacteria
SFR29853.1	vWA+CASPASE+NACHT+TPRs	AB_hydrolase→ BTLCP+VMAP-M2+VMAP-C→ MoxR→ vWA+CASPASE+NACHT+TPRs*→	1828	Lentzea waywayandensis	GCA_900115955.1	actinobacteria
SFS61774.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1157	Streptomyces sp. ok210	GCA_900116325.1	actinobacteria
SFS77547.1	vWA_protein	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA_protein*→ TIR+APATPase+TPRs→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like← TIR+EAD2	391	Saccharopolyspora flava	GCA_900116135.1	actinobacteria
SFS99759.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1110	Streptomyces harbinensis	GCA_900116145.1	actinobacteria
SFV19391.1	vWA+CASPASE+TPRs	AB_hydrolase→ CASPASE+VMAP-M4+VMAP-C→ MoxR→ vWA+CASPASE+TPRs*→	1254	Bradyrhizobium arachidis	GCA_900116675.1	alphaproteobacteria
SFW79240.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like	1400	Amycolatopsis australiensis	GCA_900119165.1	actinobacteria
SFX27404.1	vWA+TPRs	Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→ Trypco1→	1133	Streptomyces atratus	GCA_900119365.1	actinobacteria
SFY49287.1	vWA+APATPase+wHTH+TPRs	Trypco2→ tRNA→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like← Trypsin+EAD2	1309	Streptomyces sp. F-1	GCA_900079405.3	actinobacteria
SHH97075.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1124	Streptomyces sp. 3124.6	GCA_900129855.1	actinobacteria
SHI04221.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→	1130	Streptomyces sp. 3124.6	GCA_900129855.1	actinobacteria
SHI52217.1	vWA+SFII-helicase+Z1	AB_hydrolase→ CASPASE+VMAP-M2+VMAP-C→ MoxR→ vWA+SFII-helicase+Z1*→	1348	Streptomyces sp. 3124.6	GCA_900129855.1	actinobacteria

acc	architecture	operon	len	species	gca	taxend
SHK77186.1	vWA+TPRs	TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1112	Streptomyces paucisporeus	GCA_900142575.1	actinobacteria
SMD27174.1	vWA+APATPase+wHTH+TPRs	cNMP_cyclase+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs	1452	Kibdelosporangium aridum	GCA_900176515.1	actinobacteria
SME88395.1	vWA	TCAD9+Pkinase+NACHT+HEAT_repeats→ EAD2+VMAP-M0+VMAP-C→ vWA*→ MoxR→ vWA+APATPase+TPRs→	459	Streptomyces sp. Amel2xC10	GCA_900177255.1	actinobacteria
SOF02547.1	vWA+cNMP_binding+HTH_Crp_2+TerD	AB_hydrolase→ CASPASE+VMAP-M0+VMAP-C→ MoxR→ vWA+cNMP_binding+HTH_Crp_2+TerD*→	1494	Streptomyces sp. OV198	GCA_900230075.1	actinobacteria
WP_002735856.1	vWA+FGS-fold_domain	Trypco1→ Trypsin+VMAP-M1+VMAP-C→ MoxR→ vWA+FGS-fold_domain*→	884	Microcystis aeruginosa	GCA_000330925.1	cyanobacteria
WP_002740175.1	vWA+FGS-fold_domain	HTH+VMAP-M9+VMAP-C→ MoxR→ vWA+FGS-fold_domain*→ ||← ?||?→ ?→ PSE→ FGS-fold_domain→	962	Microcystis aeruginosa	GCA_000330925.1	cyanobacteria
WP_002743980.1	vWA+FGS-fold_domain	HTH+VMAP-M9+VMAP-C→ MoxR→ vWA+FGS-fold_domain*→	955	Microcystis aeruginosa	GCA_000332585.1	cyanobacteria
WP_002750294.1	vWA+FGS-fold_domain	Trypco1→ Trypsin+VMAP-M1+VMAP-C→ MoxR→ vWA+FGS-fold_domain*→ ?→ PSE→ ||← PSE||PSE→ FGS-fold_domain→	928	Microcystis aeruginosa	GCA_000307995.2	cyanobacteria
WP_002752611.1	vWA+FGS-fold_domain	AB_hydrolase→ CASPASE+VMAP-M14+VMAP-C→ MoxR→ vWA+FGS-fold_domain*→	842	Microcystis aeruginosa	GCA_000307995.2	cyanobacteria
WP_002755866.1	vWA+FGS-fold_domain	HTH+VMAP-M9+VMAP-C→ MoxR→ vWA+FGS-fold_domain*→ ?→ FGS-fold_domain→	962	Microcystis aeruginosa	GCA_000307995.2	cyanobacteria
WP_002756922.1	vWA+FGS-fold_domain	AB_hydrolase→ CASPASE+EAD2→ EAD2+VMAP-M11+VMAP-C→ MoxR→ vWA+FGS-fold_domain*→	705	Microcystis aeruginosa	GCA_000312165.1	cyanobacteria
WP_002757190.1	vWA+FGS-fold_domain	HTH+VMAP-M9+VMAP-C→ MoxR→ vWA+FGS-fold_domain*→ ?→ ?→ ?→ PSE→ FGS-fold_domain→	962	Microcystis aeruginosa	GCA_000312165.1	cyanobacteria
WP_002762808.1	vWA+FGS-fold_domain	AB_hydrolase→ CASPASE+VMAP-M14+VMAP-C→ MoxR→ vWA+FGS-fold_domain*→	842	Microcystis aeruginosa	GCA_000312165.1	cyanobacteria
WP_002771100.1	vWA+FGS-fold_domain	CASPASE+VMAP-M14+VMAP-C→ MoxR→ vWA+FGS-fold_domain*→	841	Microcystis aeruginosa	GCA_000312185.1	cyanobacteria
WP_002775631.1	vWA+FGS-fold_domain	AB_hydrolase→ CASPASE+VMAP-M14+VMAP-C→ MoxR→ vWA+FGS-fold_domain*→	842	Microcystis aeruginosa	GCA_000312205.1	cyanobacteria
WP_002782653.1	vWA+FGS-fold_domain	AB_hydrolase→ CASPASE+VMAP-M14+VMAP-C→ MoxR→ vWA+FGS-fold_domain*→	843	Microcystis aeruginosa	GCA_000312725.1	cyanobacteria
WP_002783570.1	vWA+FGS-fold_domain	vWA+FGS-fold_domain*→	838	Microcystis aeruginosa	GCA_000312725.1	cyanobacteria
WP_002786766.1	vWA+FGS-fold_domain	HTH+VMAP-M9+VMAP-C→ MoxR→ vWA+FGS-fold_domain*→	964	Microcystis aeruginosa	GCA_000312225.1	cyanobacteria
WP_002787893.1	vWA+FGS-fold_domain	AB_hydrolase→ CASPASE+VMAP-M14+VMAP-C→ MoxR→ vWA+FGS-fold_domain*→	848	Microcystis aeruginosa	GCA_000312225.1	cyanobacteria
WP_002788676.1	vWA+FGS-fold_domain	Trypsin+VMAP-M1+VMAP-C→ MoxR→ vWA+FGS-fold_domain*→ FGS-fold_domain→	883	Microcystis aeruginosa	GCA_000312225.1	cyanobacteria
WP_002791729.1	vWA+FGS-fold_domain	Trypsin+VMAP-M1+VMAP-C→ MoxR→ vWA+FGS-fold_domain*→	885	Microcystis aeruginosa	GCA_000312245.1	cyanobacteria
WP_002792348.1	vWA+FGS-fold_domain	AB_hydrolase→ PSE→ MoxR→ vWA+FGS-fold_domain*→	842	Microcystis aeruginosa	GCA_000312245.1	cyanobacteria
WP_002795442.1	vWA+FGS-fold_domain	CASPASE+EAD2→ EAD2+VMAP-M11+VMAP-C→ MoxR→ vWA+FGS-fold_domain*→	916	Microcystis aeruginosa	GCA_000312265.1	cyanobacteria
WP_003103440.1	vWA+APATPase+wHTH+TPRs	cNMP_cyclase+EAD2→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs	1475	Amycolatopsis vancoresmycina	GCA_000388135.1	actinobacteria
WP_003961788.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ ?→ vWA+TPRs*→	1091	Streptomyces clavuligerus	GCA_000163875.1	actinobacteria
WP_003963216.1	vWA+wHTH+TPRs+wHTH+TPRs+APATPase+wHTH+TPRs	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+wHTH+TPRs+wHTH+TPRs+APATPase+wHTH+TPRs*→	1828	Streptomyces clavuligerus	GCA_000163875.1	actinobacteria
WP_003969340.1	vWA+TPRs+TIR+FxsC_Cter(partial)	AB_hydrolase→ CASPASE+VMAP-M2+VMAP-C→ MoxR→ vWA+TPRs+TIR+FxsC_Cter(partial)*→	1499	Streptomyces sp. ACT-1	GCA_000177175.2	actinobacteria
WP_003973698.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→ Trypco1→	1096	Streptomyces	GCA_000158935.1	actinobacteria
WP_003987317.1	vWA+wHTH+TPRs+wHTH+TPRs+APATPase+wHTH+TPRs	vWA+wHTH+TPRs+wHTH+TPRs+APATPase+wHTH+TPRs*→	1342	Streptomyces rimosus	GCA_000331185.1	actinobacteria
WP_004001495.1	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD*→	1415	Streptomyces viridochromogenes	GCA_000332625.1	actinobacteria
WP_004003790.1	vWA+APATPase+wHTH+TPRs	Trypsin+EAD2→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like	1449	Streptomyces viridochromogenes	GCA_000332625.1	actinobacteria
WP_004162655.1	vWA+FGS-fold_domain	Trypco1→ Trypsin+VMAP-M1+VMAP-C→ MoxR→ vWA+FGS-fold_domain*→	871	Microcystis aeruginosa	GCA_000312265.1	cyanobacteria
WP_004162811.1	vWA+FGS-fold_domain	HTH+VMAP-M9+VMAP-C→ MoxR→ vWA+FGS-fold_domain*→ ?→ ?→ FGS-fold_domain→	962	Microcystis aeruginosa	GCA_000312265.1	cyanobacteria
WP_004268279.1	vWA+FGS-fold_domain	HTH+VMAP-M9+VMAP-C→ MoxR→ vWA+FGS-fold_domain*→ PSE→ FGS-fold_domain→	962	Microcystis aeruginosa	GCA_000312285.1	cyanobacteria
WP_004269016.1	vWA+FGS-fold_domain	AB_hydrolase→ CASPASE+VMAP-M14+VMAP-C→ MoxR→ vWA+FGS-fold_domain*→	842	Microcystis aeruginosa	GCA_000312285.1	cyanobacteria
WP_005157860.1	vWA+APATPase+wHTH+TPRs	cNMP_cyclase+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like← cNMP_binding+HTH_Crp_2	1466	Amycolatopsis azurea	GCA_000340415.1	actinobacteria
WP_005308092.1	vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats	VMAP-C→ MoxR→ vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats*→	1306	Streptomyces pristinaespiralis	GCA_001278075.1	actinobacteria
WP_006100461.1	vWA+FGS-fold_domain	EAD9+EAD1+VMAP-C→ ?→ MoxR→ ||← ?||?→ ?→ vWA+FGS-fold_domain*→ FGS-fold_domain→ ||← ?← ?||FGS-fold_domain→ FGS-fold_domain→ ?→ FGS-fold_domain→	894	Coleofasciculus chthonoplastes	GCA_000155555.1	cyanobacteria
WP_006346673.1	vWA+TPRs	vWA+TPRs*→	959	Streptomyces tsukubensis	GCA_000297155.2	actinobacteria
WP_006514987.1	vWA+Cas_csx3	FGS-fold_domain→ ||← ?||PNP_UDP_1+VMAP-M1+VMAP-C→ MoxR→ vWA+Cas_csx3*→	729	Leptolyngbya sp. PCC 7375	GCA_000316115.1	cyanobacteria
WP_006541138.1	vWA+APATPase+wHTH+TPRs	EAD2+EAD1→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs	1577	Frankia sp. EUN1f	GCA_000177675.1	actinobacteria
WP_006541355.1	vWA+APATPase+wHTH+TPRs	vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like	1270	Frankia sp. EUN1f	GCA_000177675.1	actinobacteria
WP_006602968.1	vWA+TPRs	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ ?→ PSE→ vWA+TPRs*→ ||← AB_hydrolase	1207	Streptomyces auratus	GCA_000280865.1	actinobacteria
WP_006603150.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ TIR+APATPase+TPRs→	1147	Streptomyces auratus	GCA_000280865.1	actinobacteria
WP_006626227.1	vWA+TPRs	VMAP-C_protein→ MoxR→ vWA+TPRs*→	770	Arthrospira platensis	GCA_000307915.1	cyanobacteria
WP_006670063.1	vWA+TPRs+CASPASE	VMAP-C_protein→ MoxR→ vWA+TPRs+CASPASE*→	1436	Arthrospira maxima	GCA_000173555.1	cyanobacteria
WP_007445178.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← Na_H_Exchanger	1547	Streptomyces coelicoflavus	GCA_000241835.2	actinobacteria
WP_007447796.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ Radical_SAM→ TIR+APATPase+TPRs→	1002	Streptomyces sp. W007	GCA_000239075.2	actinobacteria

acc	architecture	operon	len	species	gca	taxend
WP_007516491.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs→ ‖← METALLOPROTEASE+TPRs‖EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ‖← METALLOPROTEASE+TPRs	1518	Frankia sp. CN3	GCF_000235425.2	actinobacteria
WP_007822168.1	vWA+TPRs	TCAD15‖Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→ Trypco1→	1303	Streptomyces sp. Tu6071	GCA_000213055.1	actinobacteria
WP_008050073.1	vWA+TPRs+CASPASE	VMAP-C_protein→ MoxR→ vWA+TPRs+CASPASE*→	2054	Arthrospira sp. PCC 8005	GCA_000176895.2	cyanobacteria
WP_008185551.1	vWA+FGS-fold_domain	AB_hydrolase→ CASPASE+VMAP-M14+VMAP-C→ MoxR→ vWA+FGS-fold_domain*→ FGS-fold_domain→ four_helix_bundle_protein→ FGS-fold_domain→ four_helix_bundle_protein→	873	Moorea producens	GCA_000211815.1	cyanobacteria
WP_008196903.1	vWA+FGS-fold_domain	AB_hydrolase→ CASPASE+VMAP-M14+VMAP-C→ MoxR→ vWA+FGS-fold_domain*→	841	Microcystis sp. T1-4	GCA_000297435.1	cyanobacteria
WP_008307738.1	vWA+FGS-fold_domain	FGS-fold_domain→ ‖← ?‖?→ ?→ PNP_UDP_1+VMAP-M1+VMAP-C→ MoxR→ vWA+FGS-fold_domain*→ ‖← PSE‖?→ ‖← ?‖?→ FGS-fold_domain→ FGS-fold_domain→	984	Leptolyngbya sp. PCC 6406	GCF_000332095.2	cyanobacteria
WP_009149137.1	vWA+TPRs+CASPASE	EAD1+Trypsin→ EAD1+VMAP-M1+Calcineurin-like→ EAD1+VMAP-M1+VMAP-C→ MoxR→ vWA+TPRs+CASPASE*→	1817	Moorea producens	GCA_000211815.1	cyanobacteria
WP_009714190.1	vWA+Pkinase+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	SIR2→ ‖← ?← ?← ?← PSE‖Trypco1→ PSE→ MoxR→ vWA+Pkinase+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→ Porphobil_deam+Porphobil_deamC→	1213	Streptomyces himastatinicus	GCA_000158915.1	actinobacteria
WP_009784648.1	vWA+CASPASE	vWA+CASPASE*→	1193	Lyngbya sp. PCC 8106	GCA_000169095.1	cyanobacteria
WP_009997502.1	vWA+TPRs	TCAD15‖Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→	1155	Streptomyces clavuligerus	-	actinobacteria
WP_010033823.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ‖← Na_H_Exchanger‖AB_hydrolase→ CASPASE+EAD2→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→	1517	Streptomyces chartreusis	GCA_900236475.1	actinobacteria
WP_010042268.1	vWA+cNMP_cyclase+Band7+HAD	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+cNMP_cyclase+Band7+HAD*→	1083	Streptomyces chartreusis	GCA_900236475.1	actinobacteria
WP_010271951.1	vWA+TPRs	TCAD15‖Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→ Trypco1→	1303	Streptomyces sp. SA3_actG	GCA_900091815.1	actinobacteria
WP_010310059.1	vWA+TPRs	S1COLD→ PSE→ ?→ PSE→ ‖← ?‖?→ Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ Voltage_CLC→ FXSXX-COOH-like→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1149	Saccharopolyspora spinosa	GCA_002846475.1	actinobacteria
WP_010353495.1	vWA+TIR+FxsC_Cter(partial)	AB_hydrolase→ CASPASE+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+TIR+FxsC_Cter(partial)*→	809	Streptomyces acidiscabies	GCF_000242715.1	actinobacteria
WP_010353577.1	vWA+TPRs	TCAD15‖PSE→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1197	Streptomyces acidiscabies	-	actinobacteria
WP_010354765.1	vWA+Pkinase+wHTH+cNMP_cyclase+Band7+HAD	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+wHTH+cNMP_cyclase+Band7+HAD*→	1366	Streptomyces acidiscabies	GCF_000242715.1	actinobacteria
WP_010356078.1	vWA+Pkinase+TPRs	Trypco2→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+TPRs*→	1028	Streptomyces acidiscabies	GCA_001485105.1	actinobacteria
WP_010470739.1	vWA+APATPase+wHTH+TPRs+cNMP_cyclase+NaeI	Trypco1→ AB_hydrolase→ CASPASE+VMAP-M2+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs+cNMP_cyclase+NaeI*→	1708	Streptomyces somaliensis	GCF_000258595.1	actinobacteria
WP_010642339.1	vWA+TPRs	TCAD15‖Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ PSE→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1137	Streptomyces sp. S4	-	actinobacteria
WP_010983774.1	vWA+APATPase+wHTH+TPRs+cNMP_cyclase+NaeI	AB_hydrolase→ CASPASE+VMAP-M2+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs+cNMP_cyclase+NaeI*→	1667	Streptomyces avermitilis	GCA_000009765.2	actinobacteria
WP_011028360.1	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+wHTH+TPRs+cNMP_cyclase*→	1349	Streptomyces coelicolor	GCF_000203835.1	actinobacteria
WP_011030142.1	vWA+TPRs	TCAD15‖Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→ Trypco1→	1096	Streptomyces coelicolor	GCF_000203835.1	actinobacteria
WP_011601499.1	vWA+APATPase+wHTH+TPRs	EAD2→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ‖← METALLOPROTEASE+TPRs	1346	Frankia alni	GCA_000058485.1	actinobacteria
WP_011611368.1	vWA+FGS-fold_domain	Trypco1→ Trypsin+VMAP-M1+VMAP-C→ MoxR→ vWA+FGS-fold_domain*→ four_helix_bundle_protein→ PSE→ FGS-fold_domain→	877	Trichodesmium erythraeum	GCA_000014265.1	cyanobacteria
WP_011611683.1	vWA+FGS-fold_domain	EAD7+VMAP-M1+VMAP-C→ MoxR→ ?→ ?→ vWA+FGS-fold_domain*→ FGS-fold_domain→	892	Trichodesmium erythraeum	GCA_000014265.1	cyanobacteria
WP_012167133.1	vWA+VMAP-C+FGS-fold_domain	FGS-fold_domain→ ‖← ?‖PNP_UDP_1+VMAP-M1+VMAP-C→ MoxR→ vWA+VMAP-C+FGS-fold_domain*→ FGS-fold_domain→ ‖← PSE‖FGS-fold_domain→	1201	Acaryochloris marina	GCA_000018105.1	cyanobacteria
WP_012266972.1	vWA+FGS-fold_domain	HTH+VMAP-M9+VMAP-C→ VMAP-C(partial)→ MoxR→ vWA+FGS-fold_domain*→ ?→ ?→ ?→ FGS-fold_domain→	961	Microcystis aeruginosa	GCA_000010625.1	cyanobacteria
WP_012267113.1	vWA+FGS-fold_domain	Trypco1→ ‖← ?‖Trypsin+VMAP-M1+VMAP-C→ PSE→ ?→ vWA+FGS-fold_domain*→	871	Microcystis aeruginosa	GCA_000010625.1	cyanobacteria
WP_012377981.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→ ‖← ?← ?← PSE‖?→ ‖← ?← PSE← ?← Trypco1	1070	Streptomyces griseus	GCA_000010605.1	actinobacteria
WP_012381064.1	vWA+TPRs+TIR+FxsC_Cter(partial)	AB_hydrolase→ CASPASE+VMAP-M2+VMAP-C→ MoxR→ vWA+TPRs+TIR+FxsC_Cter(partial)*→	1512	Streptomyces griseus	GCA_000010605.1	actinobacteria
WP_012784685.1	vWA+TPRs	Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ ?→ Radical_SAM→	822	Catenulispora acidiphila	GCA_000024025.1	actinobacteria
WP_013155599.1	vWA+APATPase+wHTH+TPRs	Trypsin+VMAP-M0+VMAP-C→ vWA+APATPase+wHTH+TPRs*→ ‖← DUF397‖Trypco1→	1261	Nocardiopsis dassonvillei	GCA_000092985.1	actinobacteria
WP_013229639.1	vWA+APATPase+wHTH+TPRs	cNMP_cyclase+EAD2→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ‖← METALLOPROTEASE+TPRs← FXSXX-COOH-like	1226	Amycolatopsis mediterranei	GCA_000196835.1	actinobacteria
WP_013424069.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ EAD2+EAD1→	1387	Frankia inefficax	GCA_000166135.1	actinobacteria
WP_014043988.1	vWA+SFII-helicase+Z1	AB_hydrolase→ CASPASE+VMAP-M2+VMAP-C→ MoxR→ vWA+SFII-helicase+Z1*→	1390	Streptomyces	GCA_000177195.2	actinobacteria
WP_014049540.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ AB_hydrolase→ CASPASE+EAD2→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→	1445	Streptomyces	GCA_000177195.2	actinobacteria
WP_014055711.1	vWA+Pkinase+ZNR+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	ADP_ribosyl_GH→ SIR2→ ‖← ?← ?‖Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ZNR+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→ Porphobil_deam+Porphobil_deamC→	1619	Streptomyces violaceusniger	GCA_000147815.3	actinobacteria
WP_014056867.1	vWA+APATPase+wHTH+TPRs	PNP_UDP_1+EAD2→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ‖← METALLOPROTEASE+TPRs	1452	Streptomyces violaceusniger	GCA_000147815.3	actinobacteria
WP_014133537.1	vWA+CASPASE+TCAD14+PIN+CCCH(ZNR)+FHA	Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+CASPASE+TCAD14+PIN+CCCH(ZNR)+FHA*→	1228	Kitasatospora setae	GCA_000269985.1	actinobacteria
WP_014142316.1	vWA+TPRs	AB_hydrolase→ CASPASE+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→	1153	Streptomyces cattleya	GCA_000240165.1	actinobacteria
WP_014144833.1	vWA+TPRs	TCAD15‖Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ TIR+APATPase+TPRs→	1087	Streptomyces cattleya	GCA_000240165.1	actinobacteria
WP_014145553.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→	1098	Streptomyces cattleya	GCA_000240165.1	actinobacteria
WP_014174718.1	vWA_protein	PNP_UDP_1+EAD2→ ?→ vWA*→ ?→ ?→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs→ ‖← METALLOPROTEASE+TPRs	258	Streptomyces bingchenggensis	GCA_000092385.1	actinobacteria
WP_014174725.1	vWA+APATPase+wHTH+TPRs	PNP_UDP_1+EAD2→ ?→ vWA→ ?→ ?→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ‖← METALLOPROTEASE+TPRs	1460	Streptomyces bingchenggensis	GCA_000092385.1	actinobacteria
WP_014175451.1	vWA+Pkinase+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→ Porphobil_deam+Porphobil_deamC→	1410	Streptomyces bingchenggensis	GCA_000092385.1	actinobacteria
WP_014275764.1	vWA+TPRs+CASPASE	VMAP-C_protein→ MoxR→ vWA+TPRs+CASPASE*→	1693	Arthrospira platensis	GCA_000210375.1	cyanobacteria
WP_014672525.1	vWA+Pkinase+cNMP_cyclase+Band7+HAD	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+cNMP_cyclase+Band7+HAD*→	1308	Streptomyces hygroscopicus	GCA_000245355.1	actinobacteria
WP_014674945.1	vWA+TPRs	TCAD15→ Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1157	Streptomyces hygroscopicus	GCA_000245355.1	actinobacteria

acc	architecture	operon	len	species	gca	taxend
WP_015036147.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1090	Streptomyces venezuelae	GCA_001886595.1	actinobacteria
WP_015038303.1	vWA+wHTH+TPRs+wHTH+TPRs+APATPase+wHTH+TPRs	Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+wHTH+TPRs+wHTH+TPRs+APATPase+wHTH+TPRs*→	1802	Streptomyces venezuelae	GCA_001886595.1	actinobacteria
WP_015079684.1	vWA+FGS-fold_domain	vWA+FGS-fold_domain*→	731	Anabaena sp. 90	GCA_000312705.1	cyanobacteria
WP_015081254.1	vWA+TPRs	CASPASE← ?||?→ ?→ EAD10+VMAP-M1+VMAP-C→ MoxR→ vWA+TPRs*→	725	Anabaena sp. 90	GCA_000312705.1	cyanobacteria
WP_015083216.1	vWA	vWA*→	603	Anabaena sp. 90	GCA_000312705.1	cyanobacteria
WP_015119023.1	vWA+FGS-fold_domain	EAD1+Trypsin→ EAD1+VMAP-M1+VMAP-C→ MoxR→ vWA+FGS-fold_domain*→ FGS-fold_domain→	886	Rivularia sp. PCC 7116	GCA_000316665.1	cyanobacteria
WP_015135700.1	vWA+GAF+FGS-fold_domain	FGS-fold_domain→ ||← RVT_1← four_helix_bundle_protein||FGS-fold_domain→ PSE→ Trypsin+VMAP-M1+VMAP-C→ MoxR→ vWA+GAF+FGS-fold_domain*→	1106	Leptolyngbya sp. PCC 7376	GCA_000316605.1	cyanobacteria
WP_015197943.1	vWA+MNS+CASPASE+MNS	MoxR← EAD10+VMAP-M1+VMAP-C← CASPASE← ?||EAD10+VMAP-M1+VMAP-C→ MoxR→ vWA+MNS+CASPASE+MNS*→	1286	Calothrix parietina	GCA_000317435.1	cyanobacteria
WP_015620661.1	vWA+TCAD13+NaeI+TPRs	AB_hydrolase→ CASPASE+VMAP-M2+VMAP-C→ MoxR→ vWA+TCAD13+NaeI+TPRs*→	1332	Actinoplanes sp. N902-109	GCA_000389965.1	actinobacteria
WP_015655512.1	vWA+EAD2+VMAP-M0+VMAP-C	Trypco1→ Trypsin+VMAP-M7+VMAP-C→ MoxR→ vWA+EAD2+VMAP-M0+VMAP-C*→	1007	Streptomyces davawensis	GCA_000349325.1	actinobacteria
WP_015655648.1	vWA+STAND_NTPase+Trypsin+CASPASE+S1COLD	AB_hydrolase→ CASPASE+VMAP-M0+VMAP-C→ MoxR→ vWA+STAND_NTPase+Trypsin+CASPASE+S1COLD*→	1319	Streptomyces davawensis	GCA_000349325.1	actinobacteria
WP_015660488.1	vWA+APATPase+wHTH+TPRs	AB_hydrolase→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← CASPASE+EAD2	1416	Streptomyces davawensis	GCA_000349325.1	actinobacteria
WP_015660598.1	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD*→	1583	Streptomyces davawensis	GCA_000349325.1	actinobacteria
WP_015792498.1	vWA+TPRs+CASPASE	AB_hydrolase→ CASPASE+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs+CASPASE*→	1199	Catenulispora acidiphila	GCA_000024025.1	actinobacteria
WP_016188158.1	vWA+APATPase+wHTH+TPRs	vWA+APATPase+wHTH+TPRs*→ ||← DUF397||Trypco1→	1422	Thermobifida fusca	GCA_000401915.1	actinobacteria
WP_016334896.1	vWA+GCV_H+HTH+cNMP_cyclase+cNMP_cyclase+TIR+CASPASE	AB_hydrolase→ CASPASE+VMAP-M0+VMAP-C→ MoxR→ vWA+GCV_H+HTH+cNMP_cyclase+cNMP_cyclase+TIR+CASPASE*→	1568	Amycolatopsis orientalis	GCA_000400635.2	actinobacteria
WP_016435421.1	vWA+cNMP_cyclase+Band7+HAD	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+cNMP_cyclase+Band7+HAD*→	1093	Streptomyces sp. HGB0020	GCA_000411315.1	actinobacteria
WP_016469758.1	vWA+TPRs	TCAD15→ ?→ ?→ Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1054	Streptomyces	GCA_000411495.1	actinobacteria
WP_016515783.1	vWA+FGS-fold_domain	MoxR→ vWA(partial)→ vWA+FGS-fold_domain*→	838	Microcystis aeruginosa	GCA_000412595.1	cyanobacteria
WP_016516064.1	vWA+FGS-fold_domain	HTH+VMAP-M9+VMAP-C→ MoxR→ vWA+FGS-fold_domain*→	961	Microcystis aeruginosa	GCA_000412595.1	cyanobacteria
WP_016642618.1	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+HAD	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ ||← ?||vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+HAD*→	1140	Streptomyces aurantiacus	GCA_000414115.1	actinobacteria
WP_016907460.1	vWA+TPRs	Trypco1||Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1054	Streptomyces xiaopingdaonensis	GCF_000262345.1	actinobacteria
WP_017530615.1	vWA+BetaPropeller+TCAD10+REC	AB_hydrolase→ CASPASE+VMAP-M16+VMAP-C→ MoxR→ vWA+BetaPropeller+TCAD10+REC*→	1202	Pseudomonas fluorescens	GCF_000308175.1	gammaproteobacteria
WP_017562502.1	vWA+APATPase+wHTH+TPRs	Trypsin+VMAP-M0+VMAP-C→ vWA+APATPase+wHTH+TPRs*→ ||← DUF397||Trypco1→	1259	Nocardiopsis synnemataformans	GCF_000340945.1	actinobacteria
WP_017563873.1	vWA+APATPase+wHTH+TPRs	Trypsin+EAD2→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← DUF397	1516	Nocardiopsis synnemataformans	GCF_000340945.1	actinobacteria
WP_017571137.1	vWA+APATPase+wHTH+TPRs	Trypsin+EAD2→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← DUF397	1494	Nocardiopsis halotolerans	GCF_000341065.1	actinobacteria
WP_017577293.1	vWA+APATPase+wHTH+TPRs	Trypsin+VMAP-M0+VMAP-C→ vWA+APATPase+wHTH+TPRs*→ ||← DUF397||Trypco1→	1283	Nocardiopsis kunsanensis	GCF_000340965.1	actinobacteria
WP_017587752.1	vWA+APATPase+wHTH+TPRs	Trypsin+EAD2→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← DUF397	1518	Nocardiopsis ganjiahuensis	GCF_000341085.1	actinobacteria
WP_017591222.1	vWA+APATPase+wHTH+TPRs	Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← DUF397||Trypco1→	1508	Nocardiopsis potens	GCF_000341105.1	actinobacteria
WP_017595227.1	vWA+APATPase+wHTH+TPRs	Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← DUF397	1532	Nocardiopsis potens	GCF_000341105.1	actinobacteria
WP_017600471.1	vWA+APATPase+wHTH+TPRs	vWA+APATPase+wHTH+TPRs*→ ||← DUF397||Trypco1→	1252	Nocardiopsis lucentensis	GCF_000341125.1	actinobacteria
WP_017607480.1	vWA+APATPase+wHTH+TPRs	Trypsin+VMAP-M0+VMAP-C→ vWA+APATPase+wHTH+TPRs*→ ||← DUF397||Trypco1→	1282	Nocardiopsis xinjiangensis	GCF_000341145.1	actinobacteria
WP_017615244.1	vWA+APATPase+wHTH+TPRs	Trypsin+VMAP-M0+VMAP-C→ vWA+APATPase+wHTH+TPRs*→ ||← DUF397||Trypco1→	1276	Nocardiopsis salina	GCF_000341025.1	actinobacteria
WP_017622184.1	vWA+APATPase+wHTH+TPRs	Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← DUF397||Trypco1→	1528	Nocardiopsis chromatogenes	GCF_000341185.1	actinobacteria
WP_017661634.1	vWA+FGS-fold_domain	-	871	Geitlerinema sp. PCC 7105	-	cyanobacteria
WP_017742480.1	vWA+FGS-fold_domain	EAD1+VMAP-M1+VMAP-C→ MoxR→ vWA+FGS-fold_domain*→ four_helix_bundle_protein→ RVT_1→	871	Scytonema hofmannii	GCA_000346485.2	cyanobacteria
WP_017742621.1	vWA+CASPASE+APATPase	low-complexity+VMAP-M26+VMAP-C→ MoxR→ vWA+CASPASE+APATPase*→	1326	Scytonema hofmannii	GCA_000346485.2	cyanobacteria
WP_017746610.1	vWA_protein	vWA_protein*→	259	Scytonema hofmannii	GCA_000346485.2	cyanobacteria
WP_017748256.1	vWA+FGS-fold_domain	TCAD3+EAD1+EAD9→ EAD9+EAD1+VMAP-C→ MoxR→ vWA+FGS-fold_domain*→ FGS-fold_domain→ four_helix_bundle_protein→ RVT_1→	882	Scytonema hofmannii	GCA_000346485.2	cyanobacteria
WP_018087270.1	vWA+wHTH+TPRs+APATPase+wHTH+TPRs	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+wHTH+TPRs+APATPase+wHTH+TPRs*→ ?→ ?→ ||← AB_hydrolase	1612	Streptomyces sp. FxanaC1	GCF_000375625.1	actinobacteria
WP_018087461.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ TIR+APATPase+TPRs→	1132	Streptomyces sp. FxanaC1	-	actinobacteria
WP_018102708.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→ Trypco1→	1139	Streptomyces	GCF_000375725.1	actinobacteria
WP_018383820.1	vWA+APATPase+wHTH+TPRs	AB_hydrolase→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← CASPASE+EAD2	1526	Streptomyces vitaminophilus	GCA_001445835.1	actinobacteria
WP_018470761.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1137	Streptomyces sp. LaPpAH-202	GCA_003688775.1	actinobacteria
WP_018535458.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ AB_hydrolase→ CASPASE+EAD2→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→	1440	Streptomyces sp. HmicA12	GCF_000373565.1	actinobacteria
WP_018543767.1	vWA+APATPase+wHTH+TPRs	Trypsin+EAD2→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like||Trypco1→	1537	Streptomyces sp. LaPpAH-108	GCF_000373625.1	actinobacteria
WP_018558006.1	vWA+APATPase+wHTH+TPRs	Trypco1→ Trypsin+EAD2→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like	1483	Streptomyces sp. BoleA5	GCF_000373665.1	actinobacteria
WP_018835112.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ TIR+APATPase+TPRs→	1072	Streptomyces sp. CNQ766	GCF_000377105.1	actinobacteria
WP_018853257.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ TIR+APATPase+TPRs→	1072	Streptomyces sp. CNY243	GCF_000377165.1	actinobacteria
WP_018893565.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1137	Streptomyces sp. CNY228	GCF_000377545.1	actinobacteria
WP_018955297.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ AB_hydrolase→ CASPASE+EAD2→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→	1484	Streptomyces sp. CNB091	GCF_000377965.1	actinobacteria

acc	architecture	operon	len	species	gca	taxend
WP_019325899.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← Na_H_Exchanger	1548	Streptomyces sp. TOR3209	GCA_003984925.1	actinobacteria
WP_019354554.1	vWA+TPRs	Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1069	Streptomyces sp. AA1529	GCF_000280905.1	actinobacteria
WP_019433358.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→	1110	Streptomyces sp. AA0539	GCF_000297635.1	actinobacteria
WP_019496021.1	vWA+Glyco_trans_4_4+Glycos_transf_1	EAD1+VMAP-M23+VMAP-C→ MoxR→ vWA+Glyco_trans_4_4+Glycos_transf_1*→	977	Calothrix sp. PCC 7103	GCF_000331305.1	cyanobacteria
WP_019496294.1	vWA+FGS-fold_domain	EAD9+VMAP-M1+VMAP-C→ MoxR→ vWA+FGS-fold_domain*→ FGS-fold_domain→ EAD1+APATPase+TPRs→	875	Calothrix sp. PCC 7103	GCF_000331305.1	cyanobacteria
WP_019496819.1	vWA+MNS+CASPASE+MNS	VMAP-M1+VMAP-C→ MoxR→ vWA+MNS+CASPASE+MNS*→	1293	Calothrix sp. PCC 7103	GCF_000331305.1	cyanobacteria
WP_019545070.1	vWA+TPRs	TCAD15← ?||?→ ||← Trypco1||Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1054	Streptomyces sulphureus	GCF_000381025.1	actinobacteria
WP_019607628.1	vWA+APATPase+wHTH+TPRs	Trypsin+EAD2→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← DUF397	1509	Nocardiopsis sp. CNS-639	GCF_000381685.1	actinobacteria
WP_019608801.1	vWA+APATPase+wHTH+TPRs	Trypsin+VMAP-M0+VMAP-C→ vWA+APATPase+wHTH+TPRs*→ ||← DUF397||Trypco1→	1261	Nocardiopsis sp. CNS-639	GCF_000381685.1	actinobacteria
WP_019889387.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ Radical_SAM→ TIR+APATPase+TPRs→	1062	Streptomyces purpureus	GCF_000384175.1	actinobacteria
WP_020126655.1	vWA+APATPase+wHTH+TPRs	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+GGDEF+EAD2+EAD2+VMAP-M0→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→	1428	Streptomyces sp. 303MFCol5.2	-	actinobacteria
WP_020275244.1	vWA+cNMP_cyclase+Band7	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ ?→ vWA+cNMP_cyclase+Band7*→	851	Streptomyces afghaniensis	GCA_000415505.1	actinobacteria
WP_020277090.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→	1107	Streptomyces afghaniensis	GCA_000415505.1	actinobacteria
WP_020507876.1	vWA+FGS-fold_domain+FGS-fold_domain+PilP+FGS-fold_domain	CASPASE+VMAP-M27+VMAP-C→ MoxR→ vWA+FGS-fold_domain+FGS-fold_domain+PilP+FGS-fold_domain*→	1617	Lamprocystis purpurea	GCF_000379525.1	gammaproteobacteria
WP_020634031.1	vWA+APATPase+wHTH+TPRs	cNMP_cyclase+VMAP-M0+VMAP-C→ PSE→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like← cNMP_binding+HTH_Crp_2	1471	Amycolatopsis alba	GCA_002234385.1	actinobacteria
WP_020641866.1	vWA+APATPase+wHTH+TPRs	Trypco1← ?||EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs	1394	Amycolatopsis balhimycina	GCF_000384295.1	actinobacteria
WP_021593015.1	vWA+APATPase+wHTH+TPRs	Radical_SAM→ ||← TIR+APATPase+TPRs||SWACOS→ ?→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← Radical_SAM← ?||cNMP_cyclase+EAD2→ ||← ?||cNMP_binding+HTH_Crp_2→	1392	Actinomadura madurae	GCF_000468475.2	actinobacteria
WP_023065259.1	vWA+FGS-fold_domain	Trypco1→ Trypsin+VMAP-M1+VMAP-C→ MoxR→ vWA+FGS-fold_domain*→ ||← ?||FGS-fold_domain→	868	Lyngbya aestuarii	GCA_000478195.2	cyanobacteria
WP_023072613.1	vWA+FGS-fold_domain	FGS-fold_domain→ ||← ?||PNP_UDP_1+VMAP-M1+VMAP-C→ MoxR→ vWA+FGS-fold_domain*→ FGS-fold_domain→	879	Leptolyngbya sp. Heron Island J	GCA_000482245.1	cyanobacteria
WP_023538706.1	vWA+TPRs	TCAD15||PSE→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	982	Streptomyces niveus	GCA_000497425.1	actinobacteria
WP_023546824.1	vWA+TPRs	TCAD15→ Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ PSE→ PSE→ TIR+APATPase+TPRs→	1092	Streptomyces roseochromogenus	GCA_000497445.1	actinobacteria
WP_023590986.1	vWA+APATPase+wHTH+TPRs+cNMP_cyclase+NaeI	Trypco1→ ?→ ?→ AB_hydrolase→ CASPASE+VMAP-M2+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs+cNMP_cyclase+NaeI*→	1704	Streptomyces thermolilacinus	GCA_000478605.2	actinobacteria
WP_024075602.1	vWA+BetaPropeller+TCAD10+REC	AB_hydrolase→ CASPASE+VMAP-M16+VMAP-C→ MoxR→ vWA+BetaPropeller+TCAD10+REC*→	1202	Pseudomonas	GCA_000508205.1	gammaproteobacteria
WP_024491665.1	vWA+TPRs	AB_hydrolase→ CASPASE+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→	1191	Streptomyces sp. AW19M42	GCF_000470535.1	actinobacteria
WP_024758050.1	vWA+APATPase+wHTH+TPRs	Trypsin+EAD2→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs	1550	Streptomyces exfoliatus	GCF_000518045.1	actinobacteria
WP_024761808.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1073	Streptomyces exfoliatus	-	actinobacteria
WP_024934114.1	vWA+FtsK+FtsK+FtsK	Trypco1→ Trypsin+VMAP-M8+VMAP-C→ MoxR→ vWA+FtsK+FtsK+FtsK*→	1506	Actinomadura madurae	GCF_000468475.2	actinobacteria
WP_024968775.1	vWA+FGS-fold_domain	MoxR→ vWA+FGS-fold_domain*→	884	Microcystis aeruginosa	GCF_000599945.1	cyanobacteria
WP_024969247.1	vWA+FGS-fold_domain	vWA+FGS-fold_domain*→	876	Microcystis aeruginosa	GCF_000599945.1	cyanobacteria
WP_024970302.1	vWA+FGS-fold_domain	AB_hydrolase→ CASPASE+VMAP-M14+VMAP-C→ MoxR→ vWA+FGS-fold_domain*→	842	Microcystis aeruginosa	GCF_000599945.1	cyanobacteria
WP_026065859.1	vWA+TPRs	Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH-like→	874	Actinoalloteichus spitiensis	GCF_000239155.1	actinobacteria
WP_026118556.1	vWA	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA*→ Trypco1→	546	Nocardiopsis salina	GCF_000341025.1	actinobacteria
WP_026122567.1	vWA+APATPase+wHTH+TPRs	Trypsin+VMAP-M0+VMAP-C→ vWA+APATPase+wHTH+TPRs*→ ||← DUF397||Trypco1→	1269	Nocardiopsis halotolerans	GCF_000341065.1	actinobacteria
WP_026124370.1	vWA+APATPase+wHTH+TPRs	Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← DUF397||Trypco1→	1504	Nocardiopsis baichengensis	GCF_000341205.1	actinobacteria
WP_026178210.1	vWA+APATPase+Trypsin+TIR+FxsC_Cter(partial)	TIR+EAD2→ EAD2+VMAP-M10+VMAP-C→ MoxR→ vWA+APATPase+Trypsin+TIR+FxsC_Cter(partial)*→	1265	Streptomyces hokutonensis	GCF_000376565.1	actinobacteria
WP_026206227.1	vWA+CASPASE	AB_hydrolase→ CASPASE+VMAP-M2+VMAP-C→ MoxR→ vWA+CASPASE*→	923	Actinoplanes globisporus	GCF_000379645.1	actinobacteria
WP_026211906.1	vWA+TPRs+CASPASE	Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs+CASPASE*→	1257	Longispora albida	GCF_000379825.1	actinobacteria
WP_026217851.1	vWA+BetaPropeller	CASPASE+VMAP-M19→ VMAP-C→ MoxR→ vWA+BetaPropeller*→	924	Streptomyces scabrisporus	GCF_000372745.1	actinobacteria
WP_026249297.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→ Trypco1→	1137	Streptomyces sp. ATexAB-D23	GCF_000373645.1	actinobacteria
WP_026276898.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ TIR+APATPase+TPRs→	1072	Streptomyces sp. CNS335	GCF_000377125.1	actinobacteria
WP_026401298.1	vWA+APATPase+wHTH+TPRs	Radical_SAM→ METALLOPROTEASE+TPRs→ ||← TIR+APATPase+TPRs||?→ ?→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||FXSXX-COOH-like||cNMP_cyclase+EAD2→	1399	Actinomadura rifamycini	GCF_000425065.1	actinobacteria
WP_026401380.1	vWA+FtsK+FtsK+cNMP_cyclase+FtsK	Trypco1→ Trypsin+VMAP-M8+VMAP-C→ MoxR→ vWA+FtsK+FtsK+cNMP_cyclase+FtsK*→	1694	Actinomadura rifamycini	GCF_000425065.1	actinobacteria
WP_026418515.1	vWA+TPRs	Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH-like→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	874	Actinoalloteichus cyanogriseus	GCA_002895405.1	actinobacteria
WP_026423710.1	vWA+Trypsin+TCAD11	CASPASE+VMAP-M2+VMAP-C→ MoxR→ vWA+Trypsin+TCAD11*→	907	Actinokineospora inagensis	GCF_000482865.1	actinobacteria
WP_026468136.1	vWA+APATPase+wHTH	vWA+APATPase+wHTH*→	859	Amycolatopsis balhimycina	GCA_003947255.1	actinobacteria
WP_026468526.1	vWA+APATPase+wHTH+TPRs	vWA+APATPase+wHTH+TPRs→ ||← METALLOPROTEASE+TPRs||cNMP_cyclase+EAD2→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||METALLOPROTEASE+TPRs	1428	Amycolatopsis balhimycina	GCA_003947255.1	actinobacteria
WP_026468531.1	vWA+APATPase+wHTH+TPRs	-	1231	Amycolatopsis balhimycina	-	actinobacteria

acc	architecture	operon	len	species	gca	taxend
WP_027140710.1	vWA+APATPase+wHTH+TPRs	-	1281	Frankia sp. CN3	-	actinobacteria
WP_027344130.1	vWA+Trypsin+APATPase+wHTH+TPRs	Trypco1→ Trypsin+VMAP-M8+VMAP-C→ MoxR→ vWA+Trypsin+APATPase+wHTH+TPRs*→	1497	Hamadaea tsunoensis	GCF_000428945.1	actinobacteria
WP_027562298.1	vWA+CASPASE+TPRs	AB_hydrolase→ CASPASE+VMAP-M4+VMAP-C→ MoxR→ vWA+CASPASE+TPRs*→	1256	Bradyrhizobium	GCF_000472685.1	alphaproteobacteria
WP_027742287.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ TIR+APATPase+TPRs→	1072	Streptomyces sp. CNT371	GCF_000514995.1	actinobacteria
WP_027753922.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ TIR+APATPase+TPRs→	1105	Streptomyces sp. CNH099	GCF_000514715.1	actinobacteria
WP_027759022.1	vWA+TPRs	Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1069	Streptomyces sp. CNT318	GCF_000424765.1	actinobacteria
WP_027765362.1	vWA+TPRs	AB_hydrolase→ CASPASE+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→	1182	Streptomyces sp. CNS606	GCF_000426325.1	actinobacteria
WP_027766480.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ TIR+APATPase+TPRs→	1072	Streptomyces sp. CNQ865	GCF_000424805.1	actinobacteria
WP_027772933.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ TIR+APATPase+TPRs→	1073	Streptomyces sp. CNQ329	GCF_000482585.1	actinobacteria
WP_028442480.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ AB_hydrolase→ CASPASE+EAD2→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→	1457	Streptomyces sp. DpondAA-B6	GCA_900091745.1	actinobacteria
WP_028806360.1	vWA+cNMP_cyclase+Band7+HAD	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+cNMP_cyclase+Band7+HAD*→	1217	Streptomyces sp. 303MFCol5.2	GCF_000383635.1	actinobacteria
WP_028806989.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1123	Streptomyces sp. 303MFCol5.2	GCF_000383635.1	actinobacteria
WP_028807049.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	DUF397→ ||← ?||Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→	1117	Streptomyces sp. 303MFCol5.2	GCF_000383635.1	actinobacteria
WP_028808563.1	vWA+TPRs	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→	880	Streptomyces canus	GCF_000383615.1	actinobacteria
WP_028811696.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1059	Streptomyces flavidovirens	GCF_000429085.1	actinobacteria
WP_030017200.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ TIR+APATPase+TPRs→	1102	Streptomyces monomycini	GCF_000715845.1	actinobacteria
WP_030018283.1	vWA+wHTH+TPRs+wHTH	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+wHTH+TPRs+wHTH*→ ?→ ||← AB_hydrolase	1089	Streptomyces monomycini	-	actinobacteria
WP_030076156.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ AB_hydrolase→ CASPASE+EAD2→ PSE→ METALLOPROTEASE+TPRs→	1480	Streptomyces baarnensis	GCF_000716025.1	actinobacteria
WP_030165950.1	vWA+APATPase+wHTH+TPRs	Trypsin+EAD2→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like	1461	Streptomyces sp. NRRL S-813	GCF_000718945.1	actinobacteria
WP_030179051.1	vWA+wHTH+TPRs+wHTH+TPRs+APATPase+wHTH+TPRs	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+wHTH+TPRs+wHTH+TPRs+APATPase+wHTH+TPRs*→ ||← AB_hydrolase	1732	Streptomyces	GCA_000707945.1	actinobacteria
WP_030182699.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ TIR+APATPase+TPRs→	1102	Streptomyces	GCA_001270665.1	actinobacteria
WP_030190028.1	vWA+TPRs	TCAD15→ Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1097	Streptomyces violaceorubidus	GCF_000717995.1	actinobacteria
WP_030203313.1	vWA+Trypsin+cNMP_cyclase+TPRs	AB_hydrolase→ CASPASE+VMAP-M0+VMAP-C→ MoxR→ vWA+Trypsin+cNMP_cyclase+TPRs*→	1279	Streptomyces sp. NRRL S-87	GCF_000719335.1	actinobacteria
WP_030212926.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→	1423	Streptomyces sp. NRRL WC-3626	GCF_000718785.1	actinobacteria
WP_030244400.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← Na_H_Exchanger||AB_hydrolase→ CASPASE+EAD2→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→	1519	Streptomyces sp. NRRL S-455	GCF_000717875.1	actinobacteria
WP_030306272.1	vWA+TPRs	MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1137	Streptomyces	GCA_001509565.1	actinobacteria
WP_030328546.1	vWA+APATPase+wHTH+TPRs	CASPASE+TPRs→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← Radical_SAM← FXSXX-COOH-like	1417	Micromonospora parva	GCF_000718515.1	actinobacteria
WP_030355655.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1131	Streptomyces scopuliridis	GCA_003073355.1	actinobacteria
WP_030373066.1	vWA+wHTH+TPRs+wHTH+TPRs+APATPase+wHTH+TPRs	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+wHTH+TPRs+wHTH+TPRs+APATPase+wHTH+TPRs*→ ||← AB_hydrolase	1750	Streptomyces rimosus	GCF_000717815.1	actinobacteria
WP_030375332.1	vWA+TPRs	FXSXX-COOH-like||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ TIR+APATPase+TPRs→	1102	Streptomyces rimosus	GCF_000717815.1	actinobacteria
WP_030389769.1	vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats	AB_hydrolase→ CASPASE+VMAP-M0+VMAP-C→ MoxR→ vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats*→	1196	Streptomyces sp. NRRL S-241	GCF_000717925.1	actinobacteria
WP_030393995.1	vWA+APATPase+SWACOS+wHTH+TPRs+Beta-rich-tail	Trypsin+EAD2→ EAD2+VMAP-M10+VMAP-C→ MoxR→ vWA+APATPase+SWACOS+wHTH+TPRs+Beta-rich-tail*→	1580	Streptomyces purpeofuscus	GCF_000718025.1	actinobacteria
WP_030464470.1	vWA+CASPASE+TCAD14+PIN+CCCH(ZNR)+FHA	MoxR→ vWA+CASPASE+TCAD14+PIN+CCCH(ZNR)+FHA*→	1330	Kitasatospora sp. NRRL B-11411	GCF_000721345.1	actinobacteria
WP_030470827.1	vWA+APATPase+wHTH+TPRs	cNMP_cyclase+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like||TIR+APATPase+TPRs→ ||← DUF397	1157	Lechevalieria aerocolonigenes	GCF_000719205.1	actinobacteria
WP_030553426.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1076	Streptomyces exfoliatus	GCF_000725545.1	actinobacteria
WP_030574529.1	vWA+TPRs	TCAD15→ Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1068	Streptomyces sclerotialus	-	actinobacteria
WP_030592893.1	vWA+wHTH+TPRs+wHTH+TPRs+APATPase+wHTH+TPRs	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+wHTH+TPRs+wHTH+TPRs+APATPase+wHTH+TPRs*→ ||← AB_hydrolase	1732	Streptomyces	GCA_001270585.1	actinobacteria
WP_030604157.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ TIR+APATPase+TPRs→	1102	Streptomyces	GCA_001270585.1	actinobacteria
WP_030623484.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ AB_hydrolase→ CASPASE+EAD2→ PSE→ METALLOPROTEASE+TPRs→	1478	Streptomyces albus	GCF_000720915.1	actinobacteria
WP_030628104.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ TIR+APATPase+TPRs→	1102	Streptomyces	GCF_000716455.1	actinobacteria
WP_030630372.1	vWA+wHTH+TPRs+wHTH+TPRs+APATPase+wHTH+TPRs	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+wHTH+TPRs+wHTH+TPRs+APATPase+wHTH+TPRs*→ ||← AB_hydrolase	1750	Streptomyces rimosus	GCF_000720595.1	actinobacteria
WP_030632509.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ AB_hydrolase→ CASPASE+EAD2→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→	1457	Streptomyces	GCF_000720535.1	actinobacteria
WP_030647823.1	vWA+wHTH+TPRs+wHTH+TPRs+APATPase+wHTH+TPRs	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+wHTH+TPRs+wHTH+TPRs+APATPase+wHTH+TPRs*→ ||← AB_hydrolase	1734	Streptomyces rimosus	GCF_000718675.1	actinobacteria
WP_030652329.1	vWA+Pkinase+cNMP_cyclase+Band7+HAD	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+cNMP_cyclase+Band7+HAD*→	1313	Streptomyces	GCF_000716535.1	actinobacteria
WP_030654968.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ TIR+APATPase+TPRs→	1102	Streptomyces rimosus	GCF_000718675.1	actinobacteria
WP_030656871.1	vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats	AB_hydrolase→ CASPASE+VMAP-M0+VMAP-C→ MoxR→ vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats*→	1198	Streptomyces	GCF_000718705.1	actinobacteria
WP_030659385.1	vWA+CASPASE+TCAD12	AB_hydrolase→ CASPASE+VMAP-M2+VMAP-C→ MoxR→ vWA+CASPASE+TCAD12*→	1107	Streptomyces	-	actinobacteria
WP_030660077.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→ ?→ NUDIX→	1127	Streptomyces rimosus	GCF_000720725.1	actinobacteria

acc	architecture	operon	len	species	gca	taxend
WP_030663654.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ?→ ‖← Na_H_Exchanger‖AB_hydrolase→ CASPASE+EAD2→ FXSXX-COOH-like→	1542	Streptomyces cellulosae	GCF_000721105.1	actinobacteria
WP_030667973.1	vWA+wHTH+TPRs+wHTH+TPRs+APATPase+wHTH+TPRs	vWA+wHTH+TPRs+wHTH+TPRs+APATPase+wHTH+TPRs*→ ‖← AB_hydrolase	1616	Streptomyces rimosus	-	actinobacteria
WP_030672371.1	vWA+TPRs	TCAD15‖Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ TIR+APATPase+TPRs→	1102	Streptomyces rimosus	GCF_000720725.1	actinobacteria
WP_030695576.1	vWA+TPRs	TCAD15‖Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ ‖← ?‖Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1138	Streptomyces griseus	GCF_000719495.1	actinobacteria
WP_030705577.1	vWA_protein	AB_hydrolase→ CASPASE+VMAP-M2+VMAP-C→ MoxR→ vWA_protein*→ TIR+FxsC_Cter→	535	Streptomyces griseus	GCF_000717795.1	actinobacteria
WP_030711849.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ AB_hydrolase→ CASPASE+EAD2→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→	1463	Streptomyces griseus	GCF_000719355.1	actinobacteria
WP_030715041.1	vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats	AB_hydrolase→ CASPASE+VMAP-M0+VMAP-C→ MoxR→ vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats*→	1196	Streptomyces sp. NRRL S-237	GCF_000718935.1	actinobacteria
WP_030715500.1	vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats	AB_hydrolase→ CASPASE+VMAP-M0+VMAP-C→ MoxR→ vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats*→	1217	Streptomyces sp. NRRL F-2580	GCF_000720115.1	actinobacteria
WP_030754069.1	vWA+TPRs	TCAD15‖Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ ?→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1146	Streptomyces sp. NRRL F-5135	GCF_000719775.1	actinobacteria
WP_030765391.1	vWA+TPRs	TCAD15‖Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1137	Streptomyces griseus	GCF_000719435.1	actinobacteria
WP_030766032.1	vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats	AB_hydrolase→ CASPASE+VMAP-M0+VMAP-C→ MoxR→ vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats*→	1192	Streptomyces sp. NRRL F-2664	GCF_000719345.1	actinobacteria
WP_030766469.1	vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats	AB_hydrolase→ CASPASE+VMAP-M0+VMAP-C→ MoxR→ vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats*→	1198	Streptomyces	GCF_000720795.1	actinobacteria
WP_030799596.1	vWA+wHTH+TPRs+wHTH+TPRs	Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+wHTH+TPRs+wHTH+TPRs*→ ‖← AB_hydrolase‖?→ ‖← PSE‖?→ ‖← ?← PSE‖?→ ?→ ‖← DUF397	1377	Streptomyces sp. NRRL S-337	-	actinobacteria
WP_030816755.1	vWA+TPRs	Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1096	Streptomyces sp. NRRL F-2799	GCF_000719895.1	actinobacteria
WP_030821754.1	vWA+CASPASE+TCAD12	AB_hydrolase→ CASPASE+VMAP-M2+VMAP-C→ MoxR→ vWA+CASPASE+TCAD12*→	1107	Streptomyces	GCA_000966965.1	actinobacteria
WP_030825272.1	vWA+APATPase+wHTH+TPRs	PNP_UDP_1+EAD2→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ‖← METALLOPROTEASE+TPRs	1468	Streptomyces hygroscopicus	GCF_000721535.1	actinobacteria
WP_030831121.1	vWA+APATPase+wHTH+TPRs	Trypsin+EAD2→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ‖← METALLOPROTEASE+TPRs← Radical_SAM← FXSXX-COOH‖Voltage_CLC→	1517	Streptomyces	GCA_001279005.1	actinobacteria
WP_030836701.1	vWA+cNMP_cyclase+Band7+HAD	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+cNMP_cyclase+Band7+HAD*→	1089	Streptomyces sp. NRRL S-475	GCF_000720215.1	actinobacteria
WP_030853861.1	vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats	AB_hydrolase→ CASPASE+VMAP-M0+VMAP-C→ MoxR→ vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats*→	1193	Streptomyces sp. NRRL F-4474	GCF_000719855.1	actinobacteria
WP_030857533.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ‖← Na_H_Exchanger← ?‖METALLOPROTEASE+TPRs→	1537	Streptomyces sp. NRRL S-37	GCF_000721605.1	actinobacteria
WP_030863838.1	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+wHTH+TPRs+cNMP_cyclase*→	1352	Streptomyces violaceoruber	GCF_000717845.1	actinobacteria
WP_030873012.1	vWA+TPRs	TCAD15‖Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→ Trypco1→	1096	Streptomyces violaceoruber	GCF_000717845.1	actinobacteria
WP_030892008.1	vWA+TPRs	TCAD15→ ?→ ?→ PSE→ ?→ MoxR→ vWA+Trypsin+HDxxH+VMAP-M0+VMAP-C→ PSE→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1189	Streptomyces sp. NRRL F-5053	GCF_000721445.1	actinobacteria
WP_030895433.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ‖← Na_H_Exchanger‖AB_hydrolase→ CASPASE+EAD2→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→	1519	Streptomyces sp. NRRL S-474	GCF_000722015.1	actinobacteria
WP_030898785.1	vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats	AB_hydrolase→ CASPASE+VMAP-M0+VMAP-C→ MoxR→ vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats*→	1198	Streptomyces virginiae	GCF_000720455.1	actinobacteria
WP_030899222.1	vWA+CASPASE+TCAD12	AB_hydrolase→ CASPASE+VMAP-M2+VMAP-C→ MoxR→ vWA+CASPASE+TCAD12*→	1107	Streptomyces virginiae	-	actinobacteria
WP_030899562.1	vWA+TPRs	TCAD15‖Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1136	Streptomyces sp. NRRL F-5126	GCF_000721265.1	actinobacteria
WP_030940437.1	vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats+HAD	AB_hydrolase→ CASPASE+VMAP-M0+VMAP-C→ MoxR→ vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats+HAD*→	1589	Streptomyces violaceoruber	GCF_000720805.1	actinobacteria
WP_030944915.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→	1542	Streptomyces violaceoruber	GCF_000720805.1	actinobacteria
WP_030949105.1	vWA+APATPase+wHTH+TPRs	vWA+APATPase+wHTH+TPRs*→ KAP_NTPase→	877	Streptomyces sp. NRRL S-646	GCF_000720765.1	actinobacteria
WP_030969877.1	vWA+TPRs	TCAD15‖Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1143	Streptomyces sp. NRRL S-1824	-	actinobacteria
WP_030981804.1	vWA+TPRs	TCAD15‖Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ TIR+APATPase+TPRs→	1124	Streptomyces sp. NRRL S-1813	GCF_000719605.1	actinobacteria
WP_030993624.1	vWA+Pkinase+cNMP_cyclase+Band7+HAD	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+cNMP_cyclase+Band7+HAD*→	1314	Streptomyces sp. NRRL WC-3744	GCF_000717895.1	actinobacteria
WP_030995021.1	vWA+TPRs	TCAD15‖Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→ Trypco1→	1265	Streptomyces sp. NRRL F-5630	GCF_000719475.1	actinobacteria
WP_031015549.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ‖← Na_H_Exchanger‖AB_hydrolase→ CASPASE+EAD2→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→	1548	Streptomyces sp. NRRL WC-3795	GCF_000720675.1	actinobacteria
WP_031025253.1	vWA+Pkinase+cNMP_cyclase+Band7+HAD	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+cNMP_cyclase+Band7+HAD*→	1313	Streptomyces sp. NRRL WC-3725	GCF_000720295.1	actinobacteria
WP_031039674.1	vWA+TPRs	TCAD15‖Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1194	Streptomyces olivaceus	-	actinobacteria
WP_031044453.1	vWA+TPRs	TCAD15‖Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→ Trypco1→	1099	Streptomyces sp. NRRL F-5650	GCF_000721365.1	actinobacteria
WP_031085536.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ PSE→ PSE→ CASPASE+EAD2→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→	1451	Streptomyces sp. NRRL WC-3549	GCF_000721935.1	actinobacteria
WP_031096228.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ AB_hydrolase→ CASPASE+EAD2→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→	1443	Streptomyces	GCF_000722185.1	actinobacteria

acc	architecture	operon	len	species	gca	taxend
WP_031152033.1	vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats	AB_hydrolase→ CASPASE+VMAP-M0+VMAP-C→ MoxR→ vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats*→	1196	Streptomyces erythrochromogenes	GCF_000725555.1	actinobacteria
WP_031153630.1	vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats	AB_hydrolase→ CASPASE+VMAP-M0+VMAP-C→ MoxR→ vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats*→	1258	Streptomyces xanthophaeus	GCF_000725725.1	actinobacteria
WP_031177221.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1137	Streptomyces sp. NRRL B-3253	GCF_000725635.1	actinobacteria
WP_031181175.1	vWA+TPRs	TCAD15||PSE→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1096	Streptomyces seoulensis	GCA_004328625.1	actinobacteria
WP_031184764.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→ Trypco1→	1098	Streptomyces sp. NRRL F-5635	GCF_000725645.1	actinobacteria
WP_031522422.1	vWA+TPRs	TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1114	Streptomyces sp. NRRL F-5123	-	actinobacteria
WP_032771199.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ PSE→ CASPASE+EAD2→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→	1463	Streptomyces filamentosus	GCF_000156695.2	actinobacteria
WP_032780816.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→	1140	Streptomyces sp. CcalMP-8W	GCF_000373305.1	actinobacteria
WP_032798208.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ PSE→ PSE→ CASPASE+EAD2→ FXSXX-COOH-like→	1463	Streptomyces filamentosus	GCF_000156455.1	actinobacteria
WP_033034317.1	vWA+wHTH+TPRs+wHTH+TPRs+APATPase+wHTH+TPRs	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+wHTH+TPRs+wHTH+TPRs+APATPase+wHTH+TPRs*→ ||← AB_hydrolase	1732	Streptomyces rimosus	GCF_000716515.1	actinobacteria
WP_033209913.1	vWA+TPRs	TCAD15||PSE→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→	1055	Streptomyces bikiniensis	-	actinobacteria
WP_033218020.1	vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats	AB_hydrolase→ CASPASE+VMAP-M0+VMAP-C→ MoxR→ vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats*→	1192	Streptomyces virginiae	-	actinobacteria
WP_033238117.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1137	Streptomyces griseus	GCF_000717375.1	actinobacteria
WP_033266673.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ TIR+APATPase+TPRs→	1136	Streptomyces lydicus	GCF_000717345.1	actinobacteria
WP_033267593.1	vWA	EAD2+VMAP-M0+VMAP-C→ vWA*→	491	Streptomyces lydicus	GCF_001984445.1	actinobacteria
WP_033303679.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ AB_hydrolase→ CASPASE+EAD2→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→	1442	Streptomyces atroolivaceus	GCF_000717025.1	actinobacteria
WP_033306176.1	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD*→	1423	Streptomyces iakyrus	GCF_000717055.1	actinobacteria
WP_033433374.1	vWA+APATPase+wHTH+TPRs	vWA+APATPase+wHTH+TPRs→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like||?→ ||← ?||EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ || METALLOPROTEASE+TPRs	1343	Saccharothrix syringae	GCF_000716755.1	actinobacteria
WP_033433400.1	vWA+APATPase+wHTH+TPRs	-	1397	Saccharothrix syringae	-	actinobacteria
WP_033435813.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← TCAD15	1224	Saccharothrix syringae	GCF_000716755.1	actinobacteria
WP_033951030.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1135	Streptomyces sp. CNQ431	GCF_000797385.1	actinobacteria
WP_034272253.1	vWA+APATPase+wHTH+TPRs	PNP_UDP_1+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs||METALLOPROTEASE+TPRs→ ||← PNP_UDP_1+EAD2 EAD2+VMAP-M0+APATPase+TPRs	1393	Actinospica robiniae	GCF_000504285.1	actinobacteria
WP_035845007.1	vWA+APATPase+BetaPropeller+cNMP_cyclase+NaeI	Trypco1→ Trypsin+EAD2→ EAD2+VMAP-M10+VMAP-C→ MoxR→ vWA+APATPase+BetaPropeller+cNMP_cyclase+NaeI*→	1519	Kitasatospora azatica	GCF_000744785.1	actinobacteria
WP_035869417.1	vWA_protein	AB_hydrolase→ CASPASE+VMAP-M2+VMAP-C→ MoxR→ vWA_protein*→	521	Kitasatospora cheerisanensis	GCA_000696185.1	actinobacteria
WP_036013968.1	vWA+APATPase+wHTH+TPRs	cNMP_binding+HTH_Crp_2||cNMP_cyclase+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs FXSXX-COOH-like||TIR+TPRs→	1412	Lentzea albidocapillata	GCA_900176525.1	actinobacteria
WP_036266990.1	vWA_protein	EAD1+VMAP-M1+VMAP-C→ MoxR→ MoxR→ vWA_protein*→ vWA(partial)→ FGS-fold_domain→ FGS-fold_domain→	433	Mastigocoleus testarum	GCA_001456025.1	cyanobacteria
WP_037064623.1	vWA+APATPase+wHTH+TPRs	-	1224	Pseudonocardia acaciae	-	actinobacteria
WP_037614039.1	vWA+TPRs	TCAD15→ ?→ ?→ Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1054	Streptomyces albus	GCA_004768505.1	actinobacteria
WP_037620923.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1104	Streptomyces aureus	GCF_000725495.1	actinobacteria
WP_037623874.1	vWA+DO-GTPase2	AB_hydrolase→ CASPASE+VMAP-M18+VMAP-C→ MoxR→ vWA+DO-GTPase2*→	971	Streptomyces aureus	GCF_000725495.1	actinobacteria
WP_037655222.1	vWA+Pkinase+cNMP_cyclase+Band7+HAD	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+cNMP_cyclase+Band7+HAD*→	1320	Streptomyces griseofuscus	GCF_000718315.1	actinobacteria
WP_037669722.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ PSE→ vWA+APATPase+wHTH+TPRs*→	1191	Streptomyces afghaniensis	GCF_000415505.1	actinobacteria
WP_037672148.1	vWA+cNMP_cyclase+Band7+HAD	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+cNMP_cyclase+Band7+HAD*→	1108	Streptomyces griseus	GCF_000720255.1	actinobacteria
WP_037673438.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1039	Streptomyces globisporus	-	actinobacteria
WP_037685307.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1112	Streptomyces durhamensis	-	actinobacteria
WP_037689151.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1150	Streptomyces atratus	GCF_000745675.1	actinobacteria
WP_037691437.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ AB_hydrolase→ CASPASE+EAD2→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→	1440	Streptomyces atratus	GCF_000745675.1	actinobacteria
WP_037703811.1	vWA_protein	vWA_protein*→	251	Streptomyces scabiei	GCA_000738695.1	actinobacteria
WP_037722884.1	vWA	TCAD9+Pkinase+NACHT+HEAT_repeats→ EAD2+VMAP-M0+VMAP-C→ vWA*→ MoxR→ vWA+APATPase+TPRs→	481	Streptomyces scabiei	GCA_000738715.1	actinobacteria
WP_037743264.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← Na_H_Exchanger||AB_hydrolase→ CASPASE+EAD2→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→	1519	Streptomyces mirabilis	GCF_000746395.1	actinobacteria
WP_037751402.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ TIR+APATPase+TPRs→	1071	Streptomyces sp. CNQ-525	GCF_000701285.1	actinobacteria
WP_037761316.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→	1003	Streptomyces sp. FXJ7.023	GCF_000404005.1	actinobacteria
WP_037767255.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ AB_hydrolase→ CASPASE+EAD2→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→	1497	Streptomyces olindensis	GCA_000696115.1	actinobacteria
WP_037783701.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1089	Streptomyces sp. HGB0020	-	actinobacteria
WP_037787089.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1135	Streptomyces sp. GBA 94-10	GCF_000495635.1	actinobacteria

acc	architecture	operon	len	species	gca	taxend
WP_037798431.1	vWA+APATPase+wHTH+TPRs	cNMP_binding+HTH_Crp_2← ?||EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← Na_H_Exchanger||AB_hydrolase→ CASPASE+EAD2→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→	1525	Streptomyces sp. Mg1	GCA_000412265.2	actinobacteria
WP_037821823.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1120	Streptomyces sp. NRRL B-24720	-	actinobacteria
WP_037824673.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→ Trypco1→	1098	Streptomyces	GCF_000719665.1	actinobacteria
WP_037832270.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→ Trypco1→	1098	Streptomyces sp. NRRL S-1831	GCF_000721335.1	actinobacteria
WP_037839805.1	vWA+TPRs	TCAD15||PSE→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ TIR+APATPase+TPRs→	1226	Streptomyces sp. NRRL S-337	GCF_000720175.1	actinobacteria
WP_037842882.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1137	Streptomyces sp. NRRL F-6628	GCF_000721455.1	actinobacteria
WP_037880970.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ AB_hydrolase→ CASPASE+EAD2→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→	1457	Streptomyces sp. NTK 937	GCA_000698495.1	actinobacteria
WP_037895842.1	vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats	AB_hydrolase→ CASPASE+VMAP-M0+VMAP-C→ MoxR→ vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats*→	1258	Streptomyces xanthophaeus	GCF_000725805.1	actinobacteria
WP_037930286.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← Na_H_Exchanger||FXSXX-COOH-like→ METALLOPROTEASE+TPRs→	1517	Streptomyces toyocaensis	GCA_000725125.1	actinobacteria
WP_037952430.1	vWA+APATPase+wHTH+TPRs	PNP_UDP_1+EAD2→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like	1455	Streptomyces sp. PRh5	GCA_000590515.1	actinobacteria
WP_037969441.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1135	Streptomyces sp. PVA 94-07	GCF_000495755.1	actinobacteria
WP_038524289.1	vWA+APATPase+wHTH+TPRs	-	1197	Amycolatopsis japonica	-	actinobacteria
WP_038534869.1	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+wHTH+TPRs+cNMP_cyclase*→	1349	Streptomyces	GCA_000739105.1	actinobacteria
WP_039651442.1	vWA+TPRs	TCAD15→ ?→ Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1136	Streptomyces	GCA_000802245.2	actinobacteria
WP_039727590.1	vWA+FGS-fold_domain	Trypco1→ Trypsin+VMAP-M1+VMAP-C→ MoxR→ vWA+FGS-fold_domain*→ ?→ FGS-fold_domain→	893	Lyngbya confervoides	GCA_004212215.1	cyanobacteria
WP_039795711.1	vWA+APATPase+wHTH+TPRs	-	1202	Amycolatopsis alba	-	actinobacteria
WP_039896832.1	vWA+FGS-fold_domain	-	883	Lyngbya sp. PCC 8106	-	cyanobacteria
WP_039923843.1	vWA+APATPase+wHTH+TPRs	-	1199	Amycolatopsis decaplanina	-	actinobacteria
WP_039936444.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like	1451	Streptomyces himastatinicus	GCF_000158915.1	actinobacteria
WP_039938052.1	vWA+APATPase+wHTH+TPRs	vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← Radical_SAM← FXSXX-COOH||?→ ?→ ||← Trypco1	1131	Streptomyces himastatinicus	GCF_000158915.1	actinobacteria
WP_040793520.1	vWA+TPRs	Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ Voltage_CLC→ METALLOPROTEASE→ TIR+APATPase+wHTH+TPRs→	794	Nocardia paucivorans	GCF_000308675.1	actinobacteria
WP_040841206.1	vWA+TPRs	Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ Voltage_CLC→ METALLOPROTEASE→ TIR+APATPase+wHTH+TPRs→	794	Nocardia brevicatena	GCF_000308495.1	actinobacteria
WP_041256884.1	vWA+APATPase+wHTH+TPRs	-	1324	Frankia sp. EAN1pec	-	actinobacteria
WP_041316524.1	vWA+APATPase+wHTH+TPRs	-	1280	Saccharothrix espanaensis	-	actinobacteria
WP_041318577.1	vWA+APATPase+wHTH+TPRs	-	1434	Saccharothrix espanaensis	-	actinobacteria
WP_041439415.1	vWA+APATPase+wHTH+TPRs	-	1272	Thermomonospora curvata	-	actinobacteria
WP_041826591.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1137	Streptomyces albus	GCA_003182435.1	actinobacteria
WP_041992912.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← Na_H_Exchanger||AB_hydrolase→ CASPASE+EAD2→ FXSXX-COOH-like→	1445	Streptomyces sp. AcH 505	GCA_000818175.1	actinobacteria
WP_042152731.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→	1136	Streptomyces sp. NBRC 110027	GCA_000829715.2	actinobacteria
WP_042196291.1	vWA+EAD2+VMAP-M0+VMAP-C	AB_hydrolase→ CASPASE+VMAP-M2+VMAP-C→ MoxR→ vWA+EAD2+VMAP-M0+VMAP-C*→	1031	Kibdelosporangium sp. MJ126-NF4	GCA_000826545.1	actinobacteria
WP_042456080.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1053	Streptacidiphilus jiangxiensis	GCA_900109465.1	actinobacteria
WP_042829953.1	vWA+wHTH+TPRs+wHTH+TPRs+APATPase+wHTH+TPRs	Trypco1→ PSE→ MoxR→ vWA+wHTH+TPRs+wHTH+TPRs+APATPase+wHTH+TPRs*→ ||← AB_hydrolase	1732	Streptomyces rimosus	GCA_000707965.1	actinobacteria
WP_043177770.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1114	Streptomyces sp. NRRL F-2890	GCF_000719915.1	actinobacteria
WP_043270727.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→	1153	Streptomyces sp. CT34	GCF_000805335.1	actinobacteria
WP_043437220.1	vWA+APATPase+wHTH+TPRs	Trypsin+EAD2→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← Radical_SAM← FXSXX-COOH||Voltage_CLC→ ||← Trypco1	1493	Streptomyces nodosus	GCF_000819545.1	actinobacteria
WP_043464408.1	vWA+APATPase+SWACOS+wHTH+TPRs+Beta-rich-tail	Trypsin+EAD2→ EAD2+VMAP-M10+VMAP-C→ MoxR→ ||← ?||vWA+APATPase+SWACOS+wHTH+TPRs+Beta-rich-tail*→	1327	Kitasatospora sp. MBT66	GCF_000710405.2	actinobacteria
WP_043498196.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like	1466	Streptomyces glaucescens	GCA_000761215.1	actinobacteria
WP_043678220.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ AB_hydrolase→ CASPASE+EAD2→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→	1475	Streptomyces xylophagus	GCF_000716435.1	actinobacteria
WP_043777243.1	vWA+APATPase+wHTH+TPRs	cNMP_cyclase+EAD2→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like	1201	Amycolatopsis rifamycinica	GCA_000695625.1	actinobacteria
WP_043978690.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ TIR+APATPase+TPRs→	1102	Streptomyces rimosus	GCA_000707945.1	actinobacteria
WP_043996830.1	vWA+FGS-fold_domain	HTH+VMAP-M9+VMAP-C→ MoxR→ ?→ vWA+FGS-fold_domain*→ ?→ PSE→ FGS-fold_domain→	839	Microcystis aeruginosa	GCF_000312185.1	cyanobacteria
WP_044367918.1	vWA+APATPase+wHTH+TPRs	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→	1346	Streptomyces natalensis	GCA_000935125.1	actinobacteria
WP_044370540.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ AB_hydrolase→ CASPASE+EAD2→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→	1463	Streptomyces griseus	GCA_003147545.1	actinobacteria
WP_044567980.1	vWA+APATPase+wHTH+TPRs	PNP_UDP_1+EAD2→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs	1454	Streptomyces iranensis	GCA_000938975.1	actinobacteria
WP_044575624.1	vWA+TPRs	AB_hydrolase→ CASPASE+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→	1166	Streptomyces iranensis	GCA_000938975.1	actinobacteria
WP_045051690.1	vWA+REC+TCAD8	AB_hydrolase→ CASPASE+VMAP-M4+VMAP-C→ MoxR→ vWA+REC+TCAD8*→	1336	Chromobacterium violaceum	GCA_000952105.1	betaproteobacteria
WP_045304982.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→	1125	Saccharothrix sp. ST-888	GCA_000955975.1	actinobacteria
WP_046085906.1	vWA+APATPase+wHTH+TPRs	PNP_UDP_1+EAD2→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs	1454	Streptomyces antioxidans	-	actinobacteria

acc	architecture	operon	len	species	gca	taxend
WP_046086747.1	vWA+TPRs	AB_hydrolase→ CASPASE+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→	1177	Streptomyces antioxidans	-	actinobacteria
WP_046114163.1	vWA+BetaPropeller+REC	AB_hydrolase→ CASPASE+VMAP-M0+VMAP-C→ MoxR→ vWA+BetaPropeller+REC*→	1536	Aquincola tertiaricarbonis	GCF_000969605.1	betaproteobacteria
WP_046321251.1	vWA+TPRs+CASPASE	VMAP-C_protein→ MoxR→ vWA+TPRs+CASPASE*→	2052	Arthrospira sp. TJSD091	GCF_003060805.1	cyanobacteria
WP_046471648.1	vWA+APATPase+wHTH+TPRs	Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← DUF397||Trypco1→	1516	Allosalinactinospora lopnorensis	GCF_000981225.1	actinobacteria
WP_046507861.1	vWA+TPRs	vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1010	Streptomyces sp. NRRL B-24891	GCF_000981895.1	actinobacteria
WP_046591908.1	vWA+TPRs	vWA+CASPASE+NACHT+PIN← MoxR← Trypsin+HDxxH+VMAP-M0+VMAP-C← Trypco1||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ TIR+APATPase+TPRs→	1116	Streptomyces mangrovisoli	GCA_000974985.2	actinobacteria
WP_046724800.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1114	Streptomyces xiamenensis	GCA_000993785.2	actinobacteria
WP_046729107.1	vWA+APATPase+wHTH+TPRs	Trypsin+EAD2+VMAP-M0+VMAP-C→ vWA+APATPase+wHTH+TPRs*→ KAP_NTPase→	803	Streptomyces humi	GCF_001005085.2	actinobacteria
WP_046779758.1	vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats	AB_hydrolase→ CASPASE+VMAP-M0+VMAP-C→ MoxR→ vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats*→	1198	Streptomyces yangpuensis	GCF_001005295.1	actinobacteria
WP_047020366.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ TIR+APATPase+TPRs→	1072	Streptomyces sp. CNQ-509	GCA_001011035.1	actinobacteria
WP_047141005.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→	1138	Streptomyces sp. KE1	GCA_001014595.1	actinobacteria
WP_047155762.1	vWA+FGS-fold_domain	-	878	Trichodesmium erythraeum	-	cyanobacteria
WP_047155868.1	vWA_protein	-	567	Trichodesmium erythraeum	-	cyanobacteria
WP_047467284.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1138	Streptomyces sp. M10	GCF_000800535.1	actinobacteria
WP_047861214.1	vWA+SLOG	EAD1+VMAP-M1+VMAP-C→ vWA+SLOG*→	1012	Archangium gephyra	GCF_001027285.1	deltaproteobacteria
WP_048244483.1	vWA+APATPase+wHTH	AB_hydrolase→ CASPASE+VMAP-M4+VMAP-C→ MoxR→ vWA+APATPase+wHTH*→	1373	Burkholderia cepacia	GCA_001039005.1	betaproteobacteria
WP_048584307.1	vWA+APATPase+wHTH+TPRs	Trypco2→ EAD2+VMAP-M0+VMAP-C→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like← Trypsin+EAD2	1301	Streptomyces viridochromogenes	GCF_001047325.1	actinobacteria
WP_048586084.1	vWA+TPRs	TCAD15→ Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ Radical_SAM→ TIR+APATPase+TPRs→	1089	Streptomyces viridochromogenes	GCF_001047325.1	actinobacteria
WP_048832216.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1096	Streptomyces varsoviensis	GCF_000718635.1	actinobacteria
WP_049580601.1	vWA+TPRs	vWA+TPRs*→ FXSXX-COOH→	938	Streptomyces sp. SBT349	GCF_001083795.1	actinobacteria
WP_049716945.1	vWA+TPRs	TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1159	Streptomyces caatingaensis	GCA_001187435.1	actinobacteria
WP_049770996.1	vWA	FGS-fold_domain← ?← ?← ?||?→ VMAP-M1+VMAP-C→ MoxR→ vWA*→ ||← zf-IS66+DDE_Tnp_IS66← TIR+EAD9← PSE← Trypsin← Trypco1	640	Cyanothece sp. PCC 7425	GCF_000022045.1	cyanobacteria
WP_049977087.1	vWA+TPRs	TCAD15← ?||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1137	Streptomyces wadayamensis	GCA_000698945.1	actinobacteria
WP_050025079.1	vWA+AP-GTPase+COR+EAD1+Trypsin	VMAP-M22+VMAP-C→ MoxR→ vWA+AP-GTPase+COR+EAD1+Trypsin*→	1458	Verrucomicrobium sp. BvORR034	GCF_000739635.1	verrucomicrobia
WP_050358421.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→	1245	Streptomyces europaeiscabiei	GCF_001189025.1	actinobacteria
WP_050360439.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ Radical_SAM→ TIR+APATPase+TPRs→	936	Streptomyces europaeiscabiei	GCF_001189025.1	actinobacteria
WP_050361396.1	vWA+TPRs	AB_hydrolase→ CASPASE+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→	1170	Streptomyces europaeiscabiei	GCF_001189025.1	actinobacteria
WP_050371750.1	vWA+Pkinase+TPRs	Trypco2→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+TPRs*→	1028	Streptomyces acidiscabies	GCF_001189015.1	actinobacteria
WP_050373512.1	vWA+Pkinase+wHTH+cNMP_cyclase+Band7+HAD	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+wHTH+cNMP_cyclase+Band7+HAD*→	1190	Streptomyces acidiscabies	GCF_001189015.1	actinobacteria
WP_050500594.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→ ?→ NUDIX→	1128	Streptomyces rimosus	GCF_000720595.1	actinobacteria
WP_050503919.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→ ?→ NUDIX→	1127	Streptomyces rimosus	GCF_000718675.1	actinobacteria
WP_050505663.1	vWA+Pkinase+TPRs	Trypco2→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+TPRs*→	1129	Streptomyces albus	GCF_000716945.1	actinobacteria
WP_050507882.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→ ?→ NUDIX→	1127	Streptomyces	GCF_000716455.1	actinobacteria
WP_050509157.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ TIR+APATPase+TPRs→	1102	Streptomyces rimosus	GCF_000716515.1	actinobacteria
WP_050512457.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→ ?→ NUDIX→	1127	Streptomyces rimosus	GCF_000717815.1	actinobacteria
WP_050987396.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→	1108	Streptomyces acidiscabies	GCF_000242715.1	actinobacteria
WP_050990728.1	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+wHTH+TPRs+cNMP_cyclase*→	1270	Streptomyces sp. TOR3209	GCF_000259895.1	actinobacteria
WP_051034042.1	vWA+TPRs	Trypco2→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ AB_hydrolase→	1420	Streptomyces sp. SS	GCF_000302615.1	actinobacteria
WP_051034131.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← Na_H_Exchanger||AB_hydrolase→ CASPASE+EAD2→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→	1552	Streptomyces sp. SS	GCF_000302615.1	actinobacteria
WP_051042918.1	vWA	Trypsin+EAD2→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA*→ Trypco1→	548	Nocardiopsis xinjiangensis	GCF_000341145.1	actinobacteria
WP_051087510.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→	1055	Streptomyces vitaminophilus	GCA_001445835.1	actinobacteria
WP_051093954.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	-	1179	Streptomyces sp. MspMP-M5	-	actinobacteria
WP_051095183.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→	1116	Streptomyces sp. LaPpAH-108	GCF_000373625.1	actinobacteria
WP_051101697.1	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7*→	1343	Streptomyces sp. FxanaD5	GCF_000373465.1	actinobacteria
WP_051102942.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→	1114	Streptomyces sp. CNY243	GCF_000377165.1	actinobacteria
WP_051103089.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→	1114	Streptomyces sp. CNQ766	-	actinobacteria

acc	architecture	operon	len	species	gca	taxend
WP_051105858.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→	1110	Streptomyces hokutonensis	GCF_000376565.1	actinobacteria
WP_051107757.1	vWA+cNMP_cyclase+cNMP_cyclase+FtsK+TPRs	Trypco1→ Trypsin+VMAP-M8+VMAP-C→ MoxR→ vWA+cNMP_cyclase+cNMP_cyclase+FtsK+TPRs*→ ?→ ?→ ‖← DUF397← DUF397	1751	Actinomadura atramentaria	GCF_000381885.1	actinobacteria
WP_051113540.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ vWA+APATPase+wHTH+TPRs*→ ‖← METALLOPROTEASE+TPRs← FXSXX-COOH-like← Trypsin+EAD2‖METALLOPROTEASE+TPRs→	1290	Streptomyces davawensis	GCF_000349325.1	actinobacteria
WP_051114495.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→	1114	Streptomyces sp. CNS335	GCF_000377125.1	actinobacteria
WP_051114526.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→	1077	Streptomyces sp. CNB091	GCF_000377965.1	actinobacteria
WP_051127194.1	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+EAD2+Band7+HAD	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+EAD2+Band7+HAD*→	1459	Streptomyces sp. HmicA12	GCF_000373565.1	actinobacteria
WP_051138277.1	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7*→	1313	Streptomyces canus	-	actinobacteria
WP_051159397.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→	1150	Streptomyces sp. FXJ7.023	GCF_000404005.1	actinobacteria
WP_051159736.1	vWA+TPRs	AB_hydrolase→ CASPASE+EAD2+VMAP-M0+VMAP-C→ MoxR→ ‖← ?‖vWA+TPRs*→ ‖← DUF397	1059	Streptomyces sp. FXJ7.023	GCF_000404005.1	actinobacteria
WP_051262220.1	vWA+TPRs	TCAD15→ ?→ ‖← ?‖Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1043	Streptomyces sp. CNH287	GCF_000424825.1	actinobacteria
WP_051312162.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→	1114	Streptomyces sp. CNQ865	GCF_000424805.1	actinobacteria
WP_051370568.1	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD*→ ?→ ?→ ?→ Radical_SAM→ Antibiotic_NAT→ TIR+FxsC_Cter→	1618	Streptomyces sp. 142MFCol3.1	GCF_000424945.1	actinobacteria
WP_051370807.1	vWA+TPRs	TCAD15‖Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1096	Streptomyces sp. 142MFCol3.1	GCF_000424945.1	actinobacteria
WP_051387006.1	vWA+TPRs	MoxR→ vWA+TPRs*→	1096	Streptomyces sp. AW19M42	-	actinobacteria
WP_051433611.1	vWA+Pkinase+TPRs	Trypco2→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+TPRs*→	1134	Streptomyces niveus	GCF_000497425.1	actinobacteria
WP_051572814.1	vWA+CASPASE+TCAD13	AB_hydrolase→ CASPASE+VMAP-M2+VMAP-C→ MoxR→ vWA+CASPASE+TCAD13*→	1093	Streptomyces sp. PRh5	GCA_000590515.1	actinobacteria
WP_051647873.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	NUDIX→ Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→ SIR2→	1003	Streptomyces fradiae	GCA_001756925.1	actinobacteria
WP_051652644.1	vWA_protein	Trypsin+EAD2+VMAP-M0+VMAP-C→ PSE→ vWA_protein*→ BetaPropeller→	350	Kitasatospora cheerisanensis	GCF_000696185.1	actinobacteria
WP_051674211.1	vWA+TPRs	TCAD15‖Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1105	Streptomyces sp. URHA0041	GCF_000701325.1	actinobacteria
WP_051695577.1	vWA+TPRs	TCAD15‖Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ PSE→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1079	Streptomyces sp. NRRL S-244	GCF_000717915.1	actinobacteria
WP_051695727.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→	1092	Streptomyces sp. NRRL S-244	GCF_000717915.1	actinobacteria
WP_051700487.1	vWA+TPRs	TCAD15‖Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→	1104	Streptomyces sp. NRRL F-4474	GCF_000719855.1	actinobacteria
WP_051715921.1	vWA+TPRs	TCAD15‖Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ Radical_SAM→ TIR+APATPase+TPRs→	1106	Streptomyces sp. NRRL S-475	GCF_000720215.1	actinobacteria
WP_051716612.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ‖← Na_H_Exchanger‖AB_hydrolase→ CASPASE+EAD2→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→	1487	Streptomyces sp. NRRL F-5727	GCF_000719555.1	actinobacteria
WP_051716748.1	vWA+TPRs	Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1003	Streptomyces megasporus	GCF_000718985.1	actinobacteria
WP_051731479.1	vWA+TPRs	TCAD15‖Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ TIR+APATPase+TPRs→	1102	Streptomyces rimosus	GCA_000707925.1	actinobacteria
WP_051738500.1	vWA+TPRs	TCAD15‖Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ TIR+APATPase+TPRs→	1102	Streptomyces rimosus	GCA_000707965.1	actinobacteria
WP_051740295.1	vWA+CASPASE+TCAD6+cNMP_cyclase+Antibiotic_NAT	AB_hydrolase→ CASPASE+VMAP-M2+VMAP-C→ MoxR→ vWA+CASPASE+TCAD6+cNMP_cyclase+Antibiotic_NAT*→	1375	Kitasatospora sp. MBT66	GCF_000710405.2	actinobacteria
WP_051744676.1	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD	Trypco1→ PSE→ MoxR→ vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD*→	1574	Streptomyces yerevanensis	GCF_000716805.1	actinobacteria
WP_051744857.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ vWA+APATPase+wHTH+TPRs*→ ‖← METALLOPROTEASE+TPRs← Trypsin+EAD2← Trypco2← ?‖?→ DUF397→	1317	Streptomyces yerevanensis	-	actinobacteria
WP_051756012.1	vWA+CASPASE+TCAD6+cNMP_cyclase+Antibiotic_NAT	AB_hydrolase→ ?→ ‖← ?‖MoxR→ vWA+CASPASE+TCAD6+cNMP_cyclase+Antibiotic_NAT*→	1381	Streptomyces purpeofuscus	GCF_000718025.1	actinobacteria
WP_051761502.1	vWA+TIR+FxsC_Cter	Trypco1→ Trypsin+VMAP-M8+VMAP-C→ MoxR→ vWA+TIR+FxsC_Cter*→	939	Microbispora rosea	GCF_000718475.1	actinobacteria
WP_051763106.1	vWA+TPRs	TCAD15‖Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1083	Streptomyces virginiae	GCF_000716685.1	actinobacteria
WP_051766461.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ‖← METALLOPROTEASE+TPRs← FXSXX-COOH-like‖?→ ‖← ?‖EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs→	1409	Saccharothrix syringae	GCF_000716755.1	actinobacteria
WP_051770902.1	vWA+APATPase+SWACOS+wHTH+TPRs+Beta-rich-tail	Trypco1→ Trypsin+EAD2→ EAD2+VMAP-M10+VMAP-C→ MoxR→ vWA+APATPase+SWACOS+wHTH+TPRs+Beta-rich-tail*→	1569	Streptomyces sp. NRRL F-6131	GCF_000719695.1	actinobacteria
WP_051772444.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ vWA+APATPase+wHTH+TPRs*→ ‖← METALLOPROTEASE+TPRs← cNMP_cyclase+EAD2	1242	Saccharothrix sp. NRRL B-16314	GCF_000716595.1	actinobacteria
WP_051772626.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ?→ ‖← METALLOPROTEASE+TPRs	1445	Saccharothrix sp. NRRL B-16314	GCF_000716595.1	actinobacteria
WP_051774580.1	vWA+TPRs	TCAD15‖Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1082	Streptomyces sp. NRRL S-237	GCF_000718935.1	actinobacteria
WP_051777157.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→	1111	Streptomyces violaceorubidus	GCF_000717995.1	actinobacteria
WP_051777805.1	vWA+CASPASE+TCAD14+PIN+CCCH(ZNR)+FHA	Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+CASPASE+TCAD14+PIN+CCCH(ZNR)+FHA*→	1267	Kitasatospora phosalacinea	GCF_000717185.1	actinobacteria
WP_051778639.1	vWA+Coiled-coil+TIR+FxsC_Cter(partial)	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Coiled-coil+TIR+FxsC_Cter(partial)*→	815	Kitasatospora phosalacinea	GCF_000717185.1	actinobacteria
WP_051779191.1	vWA+TPRs	TCAD15‖Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ ?→ Radical_SAM→	1132	Streptomyces sp. NRRL S-241	GCF_000717925.1	actinobacteria
WP_051781725.1	vWA+TPRs	TCAD15‖Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1083	Streptomyces	GCF_000720795.1	actinobacteria
WP_051783241.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→	1116	Streptomyces	GCF_001417675.1	actinobacteria
WP_051785085.1	vWA+TPRs	TCAD15‖Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1120	Streptomyces virginiae	GCF_000720455.1	actinobacteria
WP_051787118.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ‖← Na_H_Exchanger‖AB_hydrolase→ CASPASE+EAD2→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→	1500	Streptomyces	GCF_000716445.1	actinobacteria
WP_051787936.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→	1470	Microtetraspora glauca	-	actinobacteria
WP_051790540.1	vWA+Pkinase+wHTH+TPRs	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+wHTH+TPRs*→	1081	Streptomyces sp. NRRL S-1022	GCF_000720135.1	actinobacteria

acc	architecture	operon	len	species	gca	taxend
WP_051796644.1	vWA+APATPase+wHTH+TPRs	-	1187	Rhodococcus rhodnii	-	actinobacteria
WP_051796738.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1111	Streptomyces sp. NRRL S-87	-	actinobacteria
WP_051797194.1	vWA+APATPase+wHTH+TPRs	METALLOPROTEASE+TPRs→ EAD2+VMAP-M0+VMAP-C→ vWA+APATPase+wHTH+TPRs*→	1241	Catenuloplanes japonicus	GCF_000717135.1	actinobacteria
WP_051804663.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← Na_H_Exchanger||AB_hydrolase→ CASPASE+EAD2→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→	1476	Streptomyces griseus	GCF_000718525.1	actinobacteria
WP_051805087.1	vWA+TPRs	TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1075	Streptomyces sp. NRRL F-2747	GCF_000720145.1	actinobacteria
WP_051807270.1	vWA+APATPase+wHTH+TPRs	PNP_UDP_1+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs	1428	Actinoplanes subtropicus	GCF_000721705.1	actinobacteria
WP_051807479.1	vWA+TPRs	TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→	1122	Streptomyces sp. NRRL F-2664	GCF_000719345.1	actinobacteria
WP_051810361.1	vWA+TPRs	vWA+TPRs*→ FXSXX-COOH→	1134	Streptomyces sp. NRRL S-378	-	actinobacteria
WP_051810959.1	vWA+Pkinase+FtsK+TPRs	ADP_ribosyl_GH→ Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ PSE→ PSE→ vWA+Pkinase+FtsK+TPRs*→ NUDIX→	1401	Streptomyces	GCF_000716675.1	actinobacteria
WP_051811665.1	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+HAD	MoxR→ vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+HAD*→	1496	Streptomyces	GCF_000716675.1	actinobacteria
WP_051814235.1	vWA+APATPase+wHTH+TPRs	Trypsin+EAD2→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← Trypco1	1374	Streptomyces iakyrus	-	actinobacteria
WP_051820561.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1085	Streptomyces flavochromogenes	GCF_000717595.1	actinobacteria
WP_051820772.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→	1104	Streptomyces flavochromogenes	GCF_000717595.1	actinobacteria
WP_051823228.1	vWA+wHTH+TPRs+wHTH+TPRs	Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+wHTH+TPRs+wHTH+TPRs*→ ||← AB_hydrolase||?→ ||← ?||?→ ||← PSE← ?← DUF397	1364	Streptomyces sp. NRRL S-1448	-	actinobacteria
WP_051828049.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→	1132	Streptomyces bicolor	GCF_000725465.1	actinobacteria
WP_051830823.1	vWA+SWACOS+wHTH	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+SWACOS+wHTH*→	1279	Streptomyces violens	GCF_000717745.1	actinobacteria
WP_051831367.1	vWA+TPRs	TCAD15← ?||Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→ TIR+APATPase+TPRs→	1093	Streptomyces violens	GCF_000717745.1	actinobacteria
WP_051831996.1	vWA+TPRs	TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1081	Streptomyces katrae	GCF_000717655.1	actinobacteria
WP_051833218.1	vWA+TIR+APATPase+Trypsin+HDxxH+VMAP-M0+VMAP-C	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TIR+APATPase+Trypsin+HDxxH+VMAP-M0+VMAP-C*→	1434	Streptomyces sp. NRRL S-646	GCF_000720765.1	actinobacteria
WP_051836728.1	vWA+TPRs	TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1148	Streptomyces sp. NRRL F-2580	GCF_000720115.1	actinobacteria
WP_051837519.1	vWA+TIR+FxsC_Cter	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ vWA+TIR+FxsC_Cter*→	809	Streptomyces sp. NRRL WC-3742	GCF_000720635.1	actinobacteria
WP_051840310.1	vWA+TPRs	TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1117	Streptomyces lavendulae	GCA_002803845.1	actinobacteria
WP_051842349.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← Na_H_Exchanger||AB_hydrolase→ CASPASE+EAD2→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→	1495	Streptomyces sp. NRRL F-5193	GCF_000721515.1	actinobacteria
WP_051842718.1	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD*→	1659	Streptomyces	-	actinobacteria
WP_051846592.1	vWA+Trypsin+HDxxH+VMAP-M0+VMAP-C	TCAD15→ ?→ ?→ PSE→ ?→ MoxR→ vWA+Trypsin+HDxxH+VMAP-M0+VMAP-C*→ PSE→ MoxR→ vWA+TPRs→ FXSXX-COOH→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1251	Streptomyces sp. NRRL F-5053	GCF_000721445.1	actinobacteria
WP_051847209.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	Trypco1→ PSE→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→	1174	Streptomyces sp. NRRL F-5053	GCF_000721445.1	actinobacteria
WP_051850261.1	vWA+APATPase+wHTH+TPRs	Trypco2→ EAD2+VMAP-M0+VMAP-C→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← Trypsin+EAD2← HTH_31	1321	Streptomyces griseofuscus	GCF_000718315.1	actinobacteria
WP_051850820.1	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+wHTH+TPRs+cNMP_cyclase*→	1272	Streptomyces sp. NRRL WC-3795	GCF_000720675.1	actinobacteria
WP_051850937.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→	1113	Streptomyces sp. NRRL WC-3795	GCF_000720675.1	actinobacteria
WP_051851738.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→	1116	Streptomyces sp. NRRL F-5650	GCF_000721365.1	actinobacteria
WP_051854418.1	vWA+APATPase+wHTH+TPRs	Trypco1→ Trypsin+VMAP-M8+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→	1472	Streptomyces sp. NRRL B-1347	GCF_000720325.1	actinobacteria
WP_051854856.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	DUF397→ ||← ?||Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→	1129	Streptomyces sp. NRRL B-1347	GCF_000720325.1	actinobacteria
WP_051855892.1	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+HAD	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+HAD*→	1325	Streptomyces sp. NRRL B-1347	GCF_000720325.1	actinobacteria
WP_051857016.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→	1174	Streptomyces sp. NRRL S-1868	GCF_000721305.1	actinobacteria
WP_051857985.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→	1109	Streptomyces toyocaensis	GCF_000725125.1	actinobacteria
WP_051858348.1	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD*→	1632	Streptomyces toyocaensis	GCA_000725125.1	actinobacteria
WP_051859650.1	vWA+TPRs	TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1214	Streptomyces xanthophaeus	GCF_000725725.1	actinobacteria
WP_051861419.1	vWA+TPRs	TCAD15||PSE→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→ TIR+APATPase+TPRs→	1092	Streptomyces ochraceiscleroticus	-	actinobacteria
WP_051862305.1	vWA+SWACOS+wHTH	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+SWACOS+wHTH*→	1268	Streptomyces ochraceiscleroticus	GCF_000720485.1	actinobacteria
WP_051865813.1	vWA+APATPase+wHTH+TPRs	Trypco2→ ?→ EAD2+VMAP-M0+VMAP-C→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← Trypsin+EAD2	1330	Streptomyces griseus	GCF_000720255.1	actinobacteria
WP_051872174.1	vWA+TPRs	TCAD15||PSE→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→ TIR+APATPase+TPRs→	1096	Streptomyces sclerotialus	-	actinobacteria
WP_051885844.1	vWA+TPRs	AB_hydrolase→ CASPASE+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→	1335	Streptomyces hygroscopicus	GCF_000721535.1	actinobacteria
WP_051893194.1	vWA+TPRs	TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ ?→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1113	Streptomyces erythrochromogenes	GCF_000725555.1	actinobacteria

acc	architecture	operon	len	species	gca	taxend
WP_051902870.1	vWA+TPRs	TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1308	Streptomyces xanthophaeus	GCF_000725805.1	actinobacteria
WP_051905926.1	vWA+REase+cNMP_cyclase+CASPASE	SIR2→ ?→ ||← ?||AB_hydrolase→ CASPASE+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+REase+cNMP_cyclase+CASPASE*→	1176	Streptomyces	GCF_000725785.1	actinobacteria
WP_051926349.1	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD*→	1613	Streptomyces durhamensis	GCF_000725475.1	actinobacteria
WP_051927217.1	vWA+Pkinase+TIR+APATPase+wHTH+TPRs	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+TIR+APATPase+wHTH+TPRs*→	1512	Streptomyces durhamensis	GCF_000725475.1	actinobacteria
WP_051958240.1	vWA+PNP_UDP_1+APATPase+wHTH+TPRs	AB_hydrolase→ CASPASE+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+PNP_UDP_1+APATPase+wHTH+TPRs*→	1506	Streptomyces mirabilis	GCF_000745715.1	actinobacteria
WP_052030314.1	vWA+TPRs	TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1104	Streptomyces sp. PCS3-D2	GCF_000612545.1	actinobacteria
WP_052146298.1	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+wHTH+TPRs+cNMP_cyclase*→ ?→ ?→ ||← ?||Radical_SAM→ Antibiotic_NAT→ TIR+FxsC_Cter→	979	Streptomyces galbus	GCF_000772895.1	actinobacteria
WP_052164025.1	vWA+CASPASE(partial)	AB_hydrolase→ CASPASE+EAD2→ VMAP-M0+VMAP-C→ MoxR→ vWA+CASPASE(partial)*→	791	Actinoplanes utahensis	GCF_000785985.1	actinobacteria
WP_052164720.1	vWA+cNMP_cyclase+HTH+HTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+cNMP_cyclase+HTH+HTH+TPRs*→	1283	Actinoplanes utahensis	GCF_000785985.1	actinobacteria
WP_052183279.1	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7*→	1343	Streptomyces sp. UNC401CLCol	GCF_000686765.1	actinobacteria
WP_052261118.1	vWA+BetaPropeller+TCAD10+REC	AB_hydrolase→ CASPASE+VMAP-M16+VMAP-C→ MoxR→ vWA+BetaPropeller+TCAD10+REC*→	1211	Pseudomonas sp. C5pp	GCF_000814065.1	gammaproteobacteria
WP_052310350.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→	997	Streptomyces viridochromogenes	GCF_000158955.1	actinobacteria
WP_052330862.1	vWA+FGS-fold_domain	-	888	Rivularia sp. PCC 7116	-	cyanobacteria
WP_052360456.1	vWA+TIR+BetaPropeller	EAD2+VMAP-M0+VMAP-C→ MoxR→ ?→ vWA+TIR+BetaPropeller*→ ?→ ?→ ||← cNMP_cyclase+EAD2||cNMP_binding+HTH_Crp_2→ ?→ SIR2→	1194	Kutzneria albida	GCF_000525635.1	actinobacteria
WP_052390345.1	vWA+CASPASE+TIR+FxsC_Cter(partial)	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+CASPASE+TIR+FxsC_Cter(partial)*→	1010	Streptomyces sp. NRRL B-24484	-	actinobacteria
WP_052390618.1	vWA+TPRs	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→	881	Streptomyces sp. NRRL B-24484	GCF_000717715.1	actinobacteria
WP_052398034.1	vWA+APATPase+wHTH+BetaPropeller	Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+BetaPropeller*→	1462	Streptomyces sp. NRRL F-5123	GCF_000721495.1	actinobacteria
WP_052410846.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→	1150	Streptomyces olivaceus	GCF_000721235.1	actinobacteria
WP_052411496.1	vWA+NACHT+CASPASE+BetaPropeller	Trypco1→ MoxR→ vWA+NACHT+CASPASE+BetaPropeller*→	1448	Streptomyces sp. NRRL S-118	GCF_000716335.1	actinobacteria
WP_052411905.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→	974	Streptomyces sp. NRRL S-118	GCF_000716335.1	actinobacteria
WP_052413856.1	vWA+TIR+APATPase+Trypsin+HDxxH+VMAP-M0+VMAP-C	TCAD15||PSE→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TIR+APATPase+Trypsin+HDxxH+VMAP-M0+VMAP-C*→	1343	Streptomyces glaucescens	GCA_000761215.1	actinobacteria
WP_052424449.1	vWA+Pkinase+STAND_NTPase+STAND_NTPase	Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+STAND_NTPase+STAND_NTPase*→	1335	Streptomyces fulvoviolaceus	GCF_000718165.1	actinobacteria
WP_052479908.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← Trypsin+EAD2← Trypco2||METALLOPROTEASE+TPRs→	1318	Streptomyces sp. NBRC 110035	GCF_000829695.1	actinobacteria
WP_052499299.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1038	Streptomyces vietnamensis	GCF_000830005.1	actinobacteria
WP_052499534.1	vWA+REase+SWACOS+TPRs+cNMP_cyclase	AB_hydrolase→ CASPASE+VMAP-M2+VMAP-C→ MoxR→ vWA+REase+SWACOS+TPRs+cNMP_cyclase*→	1715	Streptomyces vietnamensis	GCF_000830005.1	actinobacteria
WP_052518892.1	vWA+SLOG+EAD1+TIR	EAD1+Trypsin→ EAD1+VMAP-M1+VMAP-C→ MoxR→ vWA+SLOG+EAD1+TIR*→	1400	Archangium violaceum	GCA_000733295.1	deltaproteobacteria
WP_052579849.1	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD	Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD*→ ||← ?||?→ ?→ ?→ ?→ ||← ?||PSE→ TIR+FxsC_Cter→	1648	Actinosporangium sp. NRRL B-3428	-	actinobacteria
WP_052658798.1	vWA+TPRs	AB_hydrolase→ CASPASE+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→	1168	Streptomyces sp. MNU77	GCA_000935135.2	actinobacteria
WP_052680467.1	vWA+Pkinase+TPRs	Trypco2→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+TPRs*→	1155	Streptomyces sp. NRRL F-4428	GCF_000956015.1	actinobacteria
WP_052680669.1	vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats	AB_hydrolase→ CASPASE+VMAP-M0+VMAP-C→ MoxR→ vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats*→	1199	Streptomyces sp. NRRL F-4428	GCF_000956015.1	actinobacteria
WP_052680675.1	vWA+TPRs	TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→	1093	Streptomyces sp. NRRL F-4428	-	actinobacteria
WP_052682031.1	vWA+CASPASE+TIR+FxsC_Cter(partial)	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+CASPASE+TIR+FxsC_Cter(partial)*→	1000	Saccharothrix sp. ST-888	GCF_000955975.1	actinobacteria
WP_052687083.1	vWA+APATPase+wHTH+TPRs	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← AB_hydrolase	1324	Streptomyces lydicus	GCA_000952035.2	actinobacteria
WP_052687086.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ TIR+APATPase+TPRs→	1106	Streptomyces lydicus	GCA_000952035.2	actinobacteria
WP_052701300.1	vWA+ZNR+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	SIR2→ ||← ?← ?||Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+ZNR+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→ Porphobil_deam+Porphobil_deamC→	1201	Streptomyces iranensis	GCA_000938975.1	actinobacteria
WP_052709503.1	vWA+APATPase+SWACOS+wHTH+TPRs+Beta-rich-tail	Trypsin+EAD2→ EAD2+VMAP-M10+VMAP-C→ MoxR→ vWA+APATPase+SWACOS+wHTH+TPRs+Beta-rich-tail*→	1558	Streptomyces sp. NRRL S-495	GCF_000966955.1	actinobacteria
WP_052709964.1	vWA+APATPase+wHTH+TPRs	AB_hydrolase→ CASPASE+VMAP-M4+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→	1575	Azospirillum thiophilum	GCF_001305595.1	alphaproteobacteria
WP_052714800.1	vWA+TPRs	TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→	1120	Streptomyces	GCF_000720235.1	actinobacteria
WP_052718810.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ TIR+APATPase+TPRs→	1130	Streptomyces sp. NBRC 110027	GCF_000829715.2	actinobacteria
WP_052720904.1	vWA+SWACOS+TPRs	Trypco1→ Trypsin+VMAP-M8+VMAP-C→ MoxR→ vWA+SWACOS+TPRs*→	1320	Actinoplanes rectilineatus	GCF_000962825.1	actinobacteria
WP_052721099.1	vWA+APATPase+wHTH+TPRs	TIR+EAD2→ METALLOPROTEASE+TPRs→ EAD2+VMAP-M0+VMAP-C→ vWA+APATPase+wHTH+TPRs*→	1274	Actinoplanes rectilineatus	GCF_000962825.1	actinobacteria
WP_052731472.1	vWA+TIR+APATPase+Trypsin+HDxxH+VMAP-M0+VMAP-C	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TIR+APATPase+Trypsin+HDxxH+VMAP-M0+VMAP-C*→	1422	Streptomyces sp. MBT28	GCF_000972435.1	actinobacteria
WP_052743202.1	vWA+CASPASE+NACHT+PIN	vWA+TPRs← MoxR← Trypsin+HDxxH+VMAP-M0+VMAP-C← Trypco1||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+CASPASE+NACHT+PIN*→	1151	Streptomyces mangrovisoli	GCA_000974985.2	actinobacteria
WP_052745063.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like← CASPASE+EAD2	1295	Micromonospora sp. HK10	GCF_000982955.1	actinobacteria
WP_052745900.1	vWA+APATPase+wHTH+TPRs	Trypco1||Trypsin+EAD2→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← DUF397	1497	Allosalinactinospora lopnorensis	GCF_000981225.1	actinobacteria
WP_052757695.1	vWA+TPRs	TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ PSE→ PSE→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1132	Streptomyces yangpuensis	GCF_001005295.1	actinobacteria

acc	architecture	operon	len	species	gca	taxend
WP_052771536.1	vWA+APATPase+wHTH+TPRs	MoxR→ vWA+APATPase+wHTH+TPRs*→	1041	Streptomyces scabiei	GCF_001005405.1	actinobacteria
WP_052840000.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← PSE||AB_hydrolase→ CASPASE+EAD2→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→	1556	Streptomyces aureofaciens	-	actinobacteria
WP_052842417.1	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+wHTH+TPRs+cNMP_cyclase*→	1345	Streptomyces aureofaciens	-	actinobacteria
WP_052845518.1	vWA+TPRs	vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ TIR+APATPase+TPRs→ FXSXX-COOH→ Radical_SAM→	982	Streptomyces sp. NRRL S-31	GCF_000718775.1	actinobacteria
WP_052848444.1	vWA+TPRs	TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1100	Streptomyces avicenniae	-	actinobacteria
WP_052856488.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ TIR+APATPase+TPRs→	1126	Streptomyces celluloflavus	GCF_000720995.1	actinobacteria
WP_052867817.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→ Trypco1→	1110	Streptomyces niger	GCF_000718305.1	actinobacteria
WP_052868496.1	vWA+SWACOS+wHTH	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+SWACOS+wHTH*→	1275	Streptomyces niger	GCF_000718305.1	actinobacteria
WP_052871930.1	vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats	AB_hydrolase→ CASPASE+VMAP-M0+VMAP-C→ MoxR→ vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats*→	1199	Streptomyces sp. NRRL F-4335	-	actinobacteria
WP_052873786.1	vWA+TPRs	TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ PSE→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1138	Streptomyces sp. NRRL F-4335	-	actinobacteria
WP_053048758.1	vWA+Pkinase+ZNR+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ZNR+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→ Porphobil_deam+Porphobil_deamC→	1341	Streptomyces antioxidans	-	actinobacteria
WP_053055495.1	vWA+APATPase+wHTH+TPRs	Trypco2→ EAD2+VMAP-M0+VMAP-C→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like← Trypsin+EAD2	1323	Streptomyces malaysiense	GCF_000980885.2	actinobacteria
WP_053065798.1	vWA+TPRs	TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1076	Streptomyces sp. Mg1	GCF_000412265.2	actinobacteria
WP_053066357.1	vWA+CASPASE+SLOG+TPRs	EAD1+VMAP-M1+VMAP-C→ MoxR→ vWA+CASPASE+SLOG+TPRs*→	1460	Archangium gephyra	GCA_001027285.1	deltaproteobacteria
WP_053080709.1	vWA+TPRs	TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ PSE→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1104	Streptomyces roseus	GCF_001044425.1	actinobacteria
WP_053138638.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← Na_H_Exchanger||AB_hydrolase→ CASPASE+EAD2→ FXSXX-COOH-like→ PSE→ METALLOPROTEASE+TPRs→	1562	Streptomyces ambofaciens	GCA_001267885.1	actinobacteria
WP_053167756.1	vWA+TPRs	TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1139	Streptomyces virginiae	GCF_001270565.1	actinobacteria
WP_053200553.1	vWA+APATPase+wHTH+TPRs	Trypco2→ EAD2+VMAP-M0+VMAP-C→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like← Trypsin+EAD2	1303	Streptomyces viridochromogenes	GCF_001270485.1	actinobacteria
WP_053211137.1	vWA+Pkinase+cNMP_cyclase+Band7+HAD	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+cNMP_cyclase+Band7+HAD*→	1308	Streptomyces antibioticus	GCA_001270635.1	actinobacteria
WP_053612266.1	vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats	AB_hydrolase→ CASPASE+VMAP-M0+VMAP-C→ MoxR→ vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats*→	1198	Streptomyces sp. XY533	GCA_001279845.1	actinobacteria
WP_053612976.1	vWA+CASPASE+TCAD12	AB_hydrolase→ CASPASE+VMAP-M2+VMAP-C→ MoxR→ vWA+CASPASE+TCAD12*→	1107	Streptomyces	GCA_001279445.1	actinobacteria
WP_053613993.1	vWA+TPRs	TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→	1114	Streptomyces	GCF_001279445.1	actinobacteria
WP_053625154.1	vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats	AB_hydrolase→ CASPASE+VMAP-M0+VMAP-C→ MoxR→ vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats*→	1198	Streptomyces	GCA_001279445.1	actinobacteria
WP_053627348.1	vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats	AB_hydrolase→ CASPASE+VMAP-M0+VMAP-C→ MoxR→ vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats*→	1198	Streptomyces sp. XY511	GCA_001279485.1	actinobacteria
WP_053627414.1	vWA+CASPASE+TCAD12	AB_hydrolase→ CASPASE+VMAP-M2+VMAP-C→ MoxR→ vWA+CASPASE+TCAD12*→	1107	Streptomyces sp. XY511	GCA_001279485.1	actinobacteria
WP_053628752.1	vWA+TPRs	TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→	1114	Streptomyces sp. XY511	GCF_001279485.1	actinobacteria
WP_053629375.1	vWA+CASPASE+TCAD12	AB_hydrolase→ CASPASE+VMAP-M2+VMAP-C→ MoxR→ vWA+CASPASE+TCAD12*→	1107	Streptomyces sp. H021	GCA_001279495.1	actinobacteria
WP_053629734.1	vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats	AB_hydrolase→ CASPASE+VMAP-M0+VMAP-C→ MoxR→ vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats*→	1198	Streptomyces sp. H021	GCA_001279495.1	actinobacteria
WP_053630092.1	vWA+TPRs	TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1120	Streptomyces sp. H021	GCF_001279495.1	actinobacteria
WP_053633026.1	vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats	AB_hydrolase→ CASPASE+VMAP-M0+VMAP-C→ MoxR→ vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats*→	1198	Streptomyces	GCA_001279685.1	actinobacteria
WP_053633406.1	vWA+TPRs	TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→	1120	Streptomyces	GCF_001279855.1	actinobacteria
WP_053633441.1	vWA+CASPASE+TCAD12	AB_hydrolase→ CASPASE+VMAP-M2+VMAP-C→ MoxR→ vWA+CASPASE+TCAD12*→	1107	Streptomyces	GCA_001279855.1	actinobacteria
WP_053635218.1	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD*→	1659	Streptomyces sp. XY152	GCF_001279455.1	actinobacteria
WP_053637571.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→ Trypco1→	1098	Streptomyces sp. NRRL F-4707	GCF_001279605.1	actinobacteria
WP_053640772.1	vWA+TPRs	vWA+TPRs*→ FXSXX-COOH→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	884	Streptomyces sp. NRRL F-6492	GCF_001280125.1	actinobacteria
WP_053647130.1	vWA+APATPase+SWACOS+wHTH+TPRs+Beta-rich-tail	vWA+APATPase+SWACOS+wHTH+TPRs+Beta-rich-tail*→	1497	Streptomyces sp. XY431	GCF_001279805.1	actinobacteria
WP_053651319.1	vWA+TPRs	AB_hydrolase→ CASPASE+EAD2+VMAP-C→ MoxR→ vWA+TPRs*→	2139	Streptomyces sp. XY431	GCF_001279805.1	actinobacteria
WP_053653628.1	vWA+APATPase+wHTH+TPRs	CASPASE+TPRs→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← Radical_SAM← FXSXX-COOH-like	1417	Micromonospora sp. NRRL B-16802	GCA_001279555.1	actinobacteria
WP_053655870.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs	1268	Micromonospora sp. NRRL B-16802	GCF_001279555.1	actinobacteria
WP_053659581.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→	1112	Streptomyces sp. MMG1121	GCF_001280015.1	actinobacteria
WP_053661282.1	vWA+TPRs	TCAD15→ Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1089	Streptomyces sp. MMG1121	GCA_001280015.1	actinobacteria

acc	architecture	operon	len	species	gca	taxend
WP_053662415.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→ Trypco1→ PSE→ ?→ CASPASE→	1098	Streptomyces sp. NRRL F-7442	GCF_001279615.1	actinobacteria
WP_053662834.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→	1116	Streptomyces sp. NRRL F-7442	GCF_001279615.1	actinobacteria
WP_053669153.1	vWA+TPRs	TCAD15||PSE→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1058	Streptomyces sp. NRRL F-6491	GCF_001280095.1	actinobacteria
WP_053676461.1	vWA+TPRs	TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1056	Streptomyces sp. WM4235	-	actinobacteria
WP_053679072.1	vWA+TPRs	TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→	1120	Streptomyces sp. XY66	GCF_001279905.1	actinobacteria
WP_053679427.1	vWA+CASPASE+TCAD12	AB_hydrolase→ CASPASE+VMAP-M2+VMAP-C→ MoxR→ vWA+CASPASE+TCAD12*→	1107	Streptomyces sp. XY66	GCA_001279905.1	actinobacteria
WP_053681301.1	vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats	AB_hydrolase→ CASPASE+VMAP-M0+VMAP-C→ MoxR→ vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats*→	1198	Streptomyces sp. XY66	GCA_001279905.1	actinobacteria
WP_053683716.1	vWA+CASPASE+TCAD12	AB_hydrolase→ CASPASE+VMAP-M2+VMAP-C→ MoxR→ vWA+CASPASE+TCAD12*→	1111	Streptomyces sp. XY593	GCA_001279885.1	actinobacteria
WP_053685064.1	vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats	AB_hydrolase→ CASPASE+VMAP-M0+VMAP-C→ MoxR→ vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats*→	1198	Streptomyces sp. XY593	GCA_001279885.1	actinobacteria
WP_053685938.1	vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats	AB_hydrolase→ CASPASE+VMAP-M0+VMAP-C→ MoxR→ vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats*→	1198	Streptomyces sp. IGB124	GCA_001279935.1	actinobacteria
WP_053686250.1	vWA+TPRs	TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→	1120	Streptomyces sp. IGB124	GCF_001279935.1	actinobacteria
WP_053687101.1	vWA+CASPASE+TCAD12	AB_hydrolase→ CASPASE+VMAP-M2+VMAP-C→ MoxR→ vWA+CASPASE+TCAD12*→	1107	Streptomyces sp. IGB124	-	actinobacteria
WP_053691781.1	vWA+TPRs	TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1075	Streptomyces sp. WM6372	-	actinobacteria
WP_053697007.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ TIR+APATPase+TPRs→ TIR+APATPase+TPRs→	1111	Streptomyces sp. NRRL F-5755	GCF_001279365.1	actinobacteria
WP_053703978.1	vWA+TPRs	TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→	1137	Streptomyces sp. WM6368	GCF_001279625.1	actinobacteria
WP_053704399.1	vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats	AB_hydrolase→ CASPASE+VMAP-M0+VMAP-C→ MoxR→ vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats*→	1196	Streptomyces sp. WM6368	GCA_001279625.1	actinobacteria
WP_053705991.1	vWA+TPRs	TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→	1120	Streptomyces sp. WM6373	GCF_001279685.1	actinobacteria
WP_053712681.1	vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats	AB_hydrolase→ CASPASE+VMAP-M0+VMAP-C→ MoxR→ vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats*→	1198	Streptomyces sp. XY413	GCA_001279765.1	actinobacteria
WP_053713048.1	vWA+CASPASE+TCAD12	AB_hydrolase→ CASPASE+VMAP-M2+VMAP-C→ MoxR→ vWA+CASPASE+TCAD12*→	1107	Streptomyces sp. XY413	GCA_001279765.1	actinobacteria
WP_053713228.1	vWA+TPRs	TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→	1120	Streptomyces sp. XY413	GCF_001279765.1	actinobacteria
WP_053736427.1	vWA+CASPASE+APATPase+TPRs	AB_hydrolase→ BTLCP+VMAP-M2+VMAP-C→ MoxR→ vWA+CASPASE+APATPase+TPRs*→	1091	Nocardia sp. NRRL S-836	GCA_001279525.1	actinobacteria
WP_053741039.1	vWA+TPRs	MoxR→ vWA+TPRs*→ Radical_SAM→ TIR+APATPase+TPRs→ Radical_SAM→ ?→ STAND_NTPase→ vWA→ TIR+APATPase+TPRs→	1088	Streptomyces sp. NRRL WC-3618	GCF_001280005.1	actinobacteria
WP_053759729.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like← Trypsin+EAD2← Trypco2||METALLOPROTEASE+TPRs→	1290	Streptomyces sp. AS58	GCF_001279985.1	actinobacteria
WP_053784648.1	vWA+TPRs	TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1081	Streptomyces sp. XY332	GCF_001280885.1	actinobacteria
WP_053800883.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ TIR+APATPase+TPRs→	1102	Streptomyces rimosus	GCF_001279345.1	actinobacteria
WP_053922005.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ TIR+APATPase+TPRs→	1105	Streptomyces chattanoogensis	GCF_001294335.1	actinobacteria
WP_053930842.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ AB_hydrolase→ CASPASE+EAD2→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→	1443	Streptomyces sp. NRRL S-4	GCA_001294345.1	actinobacteria
WP_054099049.1	vWA+TPRs	-	1127	Streptomyces sp. NRRL WC-3753	-	actinobacteria
WP_054102283.1	vWA+APATPase+wHTH+TPRs	-	1547	Streptomyces sp. NRRL WC-3753	-	actinobacteria
WP_054214454.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	NUDIX→ Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→ SIR2→	1131	Actinobacteria bacterium OK074	GCF_001298575.1	actinobacteria
WP_054220968.1	vWA+TPRs	TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1067	Actinobacteria bacterium OV450	GCA_001298555.1	actinobacteria
WP_054230306.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	ADP_ribosyl_GH→ NUDIX→ Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→	1156	Actinobacteria bacterium OK006	GCA_001298565.1	actinobacteria
WP_054232446.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like← Trypsin+EAD2← Trypco2||METALLOPROTEASE+TPRs→	1296	Actinobacteria bacterium OK006	-	actinobacteria
WP_054236610.1	vWA+BetaPropeller	AB_hydrolase→ CASPASE+VMAP-M2+VMAP-C→ MoxR→ vWA+BetaPropeller*→	803	Actinobacteria bacterium OK006	GCF_001298565.1	actinobacteria
WP_054238173.1	vWA+cNMP_cyclase+Band7+HAD	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+cNMP_cyclase+Band7+HAD*→	1132	Actinobacteria bacterium OV320	-	actinobacteria
WP_054242429.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	DUF397→ Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→	1116	Actinobacteria bacterium OV320	GCA_001298545.1	actinobacteria

acc	architecture	operon	len	species	gca	taxend
WP_054242795.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1126	Actinobacteria bacterium OV320	GCF_001298545.1	actinobacteria
WP_054289253.1	vWA+SWACOS	AB_hydrolase→ CASPASE+VMAP-M2+VMAP-C→ MoxR→ vWA+SWACOS*→	1294	Kibdelosporangium phytohabitans	GCA_001302585.1	actinobacteria
WP_054294635.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs||EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs→ || METALLOPROTEASE+TPRs← FXSXX-COOH-like	1442	Kibdelosporangium phytohabitans	GCA_001302585.1	actinobacteria
WP_054568190.1	vWA+APATPase+wHTH+TPRs	EAD2+EAD1→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs	1592	Frankia sp. R43	GCA_001306465.1	actinobacteria
WP_055419746.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← Na_H_Exchanger||AB_hydrolase→ CASPASE+EAD2→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→	1544	Streptomyces pactum	GCA_002005225.1	actinobacteria
WP_055420298.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→	1015	Streptomyces pactum	GCA_002005225.1	actinobacteria
WP_055467560.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→ Trypco1→	1098	Streptomyces sp. NBRC 110030	GCF_001417675.1	actinobacteria
WP_055491167.1	vWA+APATPase+wHTH+TPRs	Trypsin+EAD2→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← Radical_SAM← FXSXX-COOH||Voltage_CLC→	1477	Streptomyces sp. TP-A0356	GCF_001417775.1	actinobacteria
WP_055491865.1	vWA+APATPase+wHTH+TPRs	Trypsin+VMAP-M6+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← Radical_SAM← FXSXX-COOH-like← Trypco1	1470	Streptomyces sp. TP-A0356	GCF_001417775.1	actinobacteria
WP_055499354.1	vWA+TPRs	vWA+TPRs*→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1015	Streptomyces flocculus	GCF_001418505.1	actinobacteria
WP_055512459.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→	1119	Streptomyces aurantiacus	GCF_001418335.1	actinobacteria
WP_055516094.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→ AB_hydrolase→ CASPASE+EAD2→	1441	Streptomyces aurantiacus	GCF_001418335.1	actinobacteria
WP_055518044.1	vWA+APATPase+wHTH+TPRs	Trypsin+EAD2→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs||Trypco1→	1490	Streptomyces aurantiacus	GCF_001418335.1	actinobacteria
WP_055550146.1	vWA+TPRs	AB_hydrolase→ CASPASE+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→	1160	Streptomyces sp. NBRC 110028	GCF_001417735.1	actinobacteria
WP_055551712.1	vWA+APATPase+wHTH+TPRs	PNP_UDP_1+EAD2→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs	1452	Streptomyces sp. NBRC 110028	GCF_001417735.1	actinobacteria
WP_055556059.1	vWA+Pkinase+FtsK+TPRs	vWA+Pkinase+FtsK+TPRs*→	1068	Streptomyces kanamyceticus	GCF_001418465.1	actinobacteria
WP_055569004.1	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+HAD	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+HAD*→	1205	Streptomyces atriruber	GCF_001418325.1	actinobacteria
WP_055602658.1	vWA+TPRs	vWA+TPRs*→ FXSXX-COOH→ METALLOPROTEASE+TPRs→	847	Streptomyces aureus	GCF_001418135.1	actinobacteria
WP_055613191.1	vWA+APATPase+wHTH+TPRs	Trypsin+EAD2→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like||Trypco1→	1494	Streptomyces phaeochromogenes	GCF_001418655.1	actinobacteria
WP_055618099.1	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD*→	1436	Streptomyces phaeochromogenes	GCF_001418655.1	actinobacteria
WP_055631399.1	vWA+REase+cNMP_cyclase+CASPASE	AB_hydrolase→ CASPASE+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+REase+cNMP_cyclase+CASPASE*→	1144	Streptomyces griseoruber	GCA_001514205.1	actinobacteria
WP_055643571.1	vWA+TPRs	AB_hydrolase→ CASPASE+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→	1193	Streptomyces venezuelae	GCA_001443625.1	actinobacteria
WP_055643712.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← Na_H_Exchanger||AB_hydrolase→ CASPASE+EAD2→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→	1526	Streptomyces venezuelae	GCA_001443625.1	actinobacteria
WP_055702450.1	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+HAD	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+HAD*→	1252	Streptomyces silaceus	-	actinobacteria
WP_055705732.1	vWA+APATPase+wHTH+TPRs	Trypco2→ EAD2+VMAP-M0+VMAP-C→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← Trypsin+EAD2	1284	Streptomyces puniciscabiei	GCF_001419685.1	actinobacteria
WP_055706346.1	vWA+DNA-primase-like_ZnR+S1+KH+KH	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+DNA-primase-like_ZnR+S1+KH+KH*→	1101	Streptomyces puniciscabiei	GCF_001419685.1	actinobacteria
WP_055715312.1	vWA+APATPase+wHTH+TPRs	Trypsin+EAD2+VMAP-M0+VMAP-C→ vWA+APATPase+wHTH+TPRs*→	850	Streptomyces torulosus	GCF_001419765.1	actinobacteria
WP_055750281.1	vWA+APATPase+wHTH+TPRs	EAD2→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like	1346	Frankia sp. AvcI1	GCF_001420875.1	actinobacteria
WP_056567333.1	vWA+TPRs	TCAD15||PSE→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1063	Streptomyces	GCA_001426405.1	actinobacteria
WP_056644000.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1070	Streptomyces sp. Root431	GCA_001426585.1	actinobacteria
WP_056701957.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→	1245	Streptomyces	GCA_001426325.1	actinobacteria
WP_056706812.1	vWA+TPRs	AB_hydrolase→ CASPASE+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→	1170	Streptomyces	GCA_001426325.1	actinobacteria
WP_056794874.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→	1135	Streptomyces	GCA_001426615.1	actinobacteria
WP_057232849.1	vWA+APATPase+BetaPropeller+Pkinase+wHTH+TPRs+wHTH+TPRs+FtsK	Trypco1→ Trypsin+EAD2→ EAD2+VMAP-M10+VMAP-C→ MoxR→ vWA+APATPase+BetaPropeller+Pkinase+wHTH+TPRs+wHTH+TPRs+FtsK*→	2079	Kitasatospora sp. Root107	GCA_001424875.1	actinobacteria
WP_057238953.1	vWA+CASPASE+TIR+FxsC_Cter(partial)	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+CASPASE+TIR+FxsC_Cter(partial)*→	841	Kitasatospora	GCA_001424875.1	actinobacteria
WP_057241032.1	vWA+APATPase+BetaPropeller+Pkinase+wHTH+TPRs+wHTH+TPRs+FtsK	Trypco1→ Trypsin+EAD2→ EAD2+VMAP-M10+VMAP-C→ MoxR→ vWA+APATPase+BetaPropeller+Pkinase+wHTH+TPRs+wHTH+TPRs+FtsK*→	2142	Kitasatospora sp. Root187	GCA_001429805.1	actinobacteria
WP_057578299.1	vWA	EAD2+VMAP-M0+VMAP-C→ vWA*→ ||← vWA+APATPase+wHTH+TPRs← MoxR← DUF397	383	Streptomyces sp. Root264	GCA_001428885.1	actinobacteria
WP_057578301.1	vWA+APATPase+wHTH+TPRs	DUF397→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← vWA← EAD2+VMAP-M0+VMAP-C	886	Streptomyces sp. Root264	GCF_001428885.1	actinobacteria
WP_057584733.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1102	Streptomyces sp. Root264	GCA_001428885.1	actinobacteria
WP_057599902.1	vWA+cNMP_cyclase+Band7+HAD	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+cNMP_cyclase+Band7+HAD*→	1137	Streptomyces sp. Root1310	GCA_001426425.1	actinobacteria
WP_057602960.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→	1114	Streptomyces sp. Root1310	GCA_001426425.1	actinobacteria
WP_057603580.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1118	Streptomyces sp. Root1310	GCA_001426425.1	actinobacteria
WP_057605974.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← Trypsin+EAD2||Trypco2→	1274	Streptomyces sp. Root1310	GCA_001426425.1	actinobacteria
WP_057662565.1	vWA+TPRs	AB_hydrolase→ CASPASE+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→	1170	Streptomyces anulatus	GCF_001434355.1	actinobacteria
WP_057664687.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→	1245	Streptomyces anulatus	GCF_001434355.1	actinobacteria

acc	architecture	operon	len	species	gca	taxend
WP_058080417.1	vWA+Pkinase+cNMP_cyclase+Band7+HAD	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+cNMP_cyclase+Band7+HAD*→	1308	Streptomyces hygroscopicus	GCA_001447075.1	actinobacteria
WP_058184023.1	vWA+CASPASE+FGS-fold_domain	CASPASE+AB_hydrolase→ CASPASE+VMAP-M28+VMAP-C→ MoxR→ vWA+CASPASE+FGS-fold_domain*→	1553	Mastigocoleus testarum	GCA_001456025.1	cyanobacteria
WP_058915122.1	vWA	EAD2+VMAP-M0+VMAP-C→ vWA*→	386	Streptomyces sp. 4F	GCA_001484705.1	actinobacteria
WP_058915198.1	vWA	EAD2+VMAP-M0+VMAP-C→ vWA*→	385	Streptomyces sp. 4F	GCA_001484705.1	actinobacteria
WP_058925471.1	vWA+cNMP_cyclase+Band7+HAD	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+cNMP_cyclase+Band7+HAD*→	1094	Streptomyces sp. CdTB01	GCA_001484565.1	actinobacteria
WP_058930817.1	vWA+BetaPropeller+CASPASE+STAND_NTPase	AB_hydrolase→ CASPASE+VMAP-M17+VMAP-C→ MoxR→ vWA+BetaPropeller+CASPASE+STAND_NTPase*→	1717	Pseudarthrobacter sulfonivorans	GCA_001484605.1	actinobacteria
WP_059012194.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ PSE→ ?→ ?→ TIR+APATPase+TPRs→	1108	Streptomyces specialis	GCF_001493375.1	actinobacteria
WP_059042125.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→	1110	Streptomyces acidiscabies	GCA_001485105.1	actinobacteria
WP_059047321.1	vWA+TPRs	vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1062	Streptomyces acidiscabies	GCF_001485105.1	actinobacteria
WP_059128852.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1126	Streptomyces sp. NRRL F-5122	GCA_001507435.1	actinobacteria
WP_059146065.1	vWA+APATPase+wHTH+TPRs	PNP_UDP_1+EAD2→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs	1452	Streptomyces	GCA_001509775.1	actinobacteria
WP_059146322.1	vWA+TPRs	AB_hydrolase→ CASPASE+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→	1165	Streptomyces violaceusniger	GCA_001509775.1	actinobacteria
WP_059252564.1	vWA+TPRs	TCAD15→ Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1220	Streptomyces reticuli	GCF_001511815.1	actinobacteria
WP_059261798.1	vWA+Pkinase+cNMP_cyclase+Band7+HAD	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+cNMP_cyclase+Band7+HAD*→	1311	Streptomyces corchorusii	GCA_001514055.1	actinobacteria
WP_059264232.1	vWA+TPRs	TCAD15→ Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1157	Streptomyces corchorusii	GCA_001514055.1	actinobacteria
WP_059362765.1	vWA+APATPase+wHTH+TPRs	cNMP_cyclase+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like||TIR+APATPase+TPRs→ ||← DUF397	1201	Lechevalieria aerocolonigenes	GCF_000974445.1	actinobacteria
WP_059417485.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→	1118	Streptomyces azureus	GCA_001270025.1	actinobacteria
WP_060176762.1	vWA+TPRs	TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1099	Streptomyces sp. IMTB 1903	GCF_001531145.1	actinobacteria
WP_060730269.1	vWA+wHTH+TPRs+wHTH+TPRs+APATPase+wHTH+TPRs	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+wHTH+TPRs+wHTH+TPRs+APATPase+wHTH+TPRs*→ ||← AB_hydrolase	1733	Streptomyces albus	GCA_001541145.1	actinobacteria
WP_060733247.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ TIR+APATPase+TPRs→	1102	Streptomyces albus	GCA_001541145.1	actinobacteria
WP_060879576.1	vWA+APATPase+wHTH+TPRs	MoxR→ vWA+APATPase+wHTH+TPRs*→	1041	Streptomyces scabiei	GCF_001550225.1	actinobacteria
WP_060888221.1	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+wHTH+TPRs+cNMP_cyclase*→	1019	Streptomyces	GCF_001550315.1	actinobacteria
WP_060888708.1	vWA	vWA*→	377	Streptomyces scabiei	GCF_001550215.1	actinobacteria
WP_060895935.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→	1032	Streptomyces diastatochromogenes	-	actinobacteria
WP_060907571.1	vWA+APATPase+wHTH+TPRs	MoxR→ vWA+APATPase+wHTH+TPRs*→	1029	Streptomyces scabiei	GCF_001572115.1	actinobacteria
WP_060944903.1	vWA+APATPase+wHTH+TPRs	vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs	1323	Streptomyces hygroscopicus	GCF_001553455.1	actinobacteria
WP_060947196.1	vWA+TPRs	vWA+TPRs*→	1061	Streptomyces hygroscopicus	GCF_001553455.1	actinobacteria
WP_060948653.1	vWA+APATPase+wHTH+TPRs	PNP_UDP_1+EAD2→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs	1462	Streptomyces hygroscopicus	GCF_001553435.1	actinobacteria
WP_060950690.1	vWA+TPRs	AB_hydrolase→ CASPASE+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→	1308	Streptomyces hygroscopicus	GCF_001553435.1	actinobacteria
WP_061080206.1	vWA+APATPase+wHTH	Trypsin+VMAP-M8+VMAP-C→ MoxR→ vWA+APATPase+wHTH*→	1065	Nocardiopsis dassonvillei	-	actinobacteria
WP_061081053.1	vWA+APATPase+wHTH+TPRs	Trypsin+EAD2→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← DUF397	1514	Nocardiopsis dassonvillei	-	actinobacteria
WP_061083272.1	vWA+APATPase+wHTH+TPRs	Trypsin+VMAP-M0+VMAP-C→ vWA+APATPase+wHTH+TPRs*→	1261	Nocardiopsis dassonvillei	-	actinobacteria
WP_061430554.1	vWA+FGS-fold_domain	AB_hydrolase→ CASPASE+VMAP-M14+VMAP-C→ MoxR→ vWA+FGS-fold_domain*→	842	Microcystis aeruginosa	GCA_001578075.1	cyanobacteria
WP_061432000.1	vWA+FGS-fold_domain	HTH+VMAP-M9+VMAP-C→ MoxR→ vWA+FGS-fold_domain*→ ?→ ?→ FGS-fold_domain→	961	Microcystis aeruginosa	GCA_001578075.1	cyanobacteria
WP_061432248.1	vWA+FGS-fold_domain	Trypco1→ Trypsin+VMAP-M1+VMAP-C→ MoxR→ vWA+FGS-fold_domain*→	870	Microcystis aeruginosa	GCA_001578075.1	cyanobacteria
WP_061441116.1	vWA	EAD2+VMAP-M0+VMAP-C→ vWA*→	505	Streptomyces sp. CCM_MD2014	GCA_000772045.1	actinobacteria
WP_061442995.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→	1116	Streptomyces sp. CCM_MD2014	GCF_000772045.1	actinobacteria
WP_061446900.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→ Trypco1→	1077	Streptomyces sp. CCM_MD2014	GCF_000772045.1	actinobacteria
WP_061783879.1	vWA+APATPase+wHTH+TPRs	Trypsin+EAD2→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← DUF397||Trypco1→	1479	Thermobifida fusca	GCF_001592045.1	actinobacteria
WP_061790674.1	vWA+DRHyd+TCAD8	AB_hydrolase→ CASPASE+VMAP-M20+VMAP-C→ MoxR→ vWA+DRHyd+TCAD8*→	1395	Herbaspirillum rubrisubalbicans	GCA_003719195.1	betaproteobacteria
WP_061927345.1	vWA+TPRs	TCAD15||PSE→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→ Trypco1→	1114	Streptomyces bungoensis	GCA_001514215.1	actinobacteria
WP_061981586.1	vWA+APATPase+wHTH+TPRs	cNMP_cyclase+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like← cNMP_binding+HTH_Crp_2	1217	Amycolatopsis regifaucium	GCA_001613935.1	actinobacteria
WP_062009594.1	vWA+TPRs	AB_hydrolase→ CASPASE+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→	1317	Streptomyces sporocinereus	GCF_001570645.1	actinobacteria
WP_062152500.1	vWA+APATPase+wHTH+TPRs	Trypsin+EAD2→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like	1449	Streptomyces curacoi	GCA_001513975.1	actinobacteria
WP_062192328.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← Trypsin+EAD2	1318	Streptomyces sp. AVP053U2	GCA_001469455.2	actinobacteria
WP_062206696.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ ?→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1094	Streptomyces sp. NBRC 109706	GCF_000974485.1	actinobacteria
WP_062640490.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	DUF397→ Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→	1100	Streptomyces sp. NBRC 110468	GCF_001184025.1	actinobacteria
WP_062642514.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→ Trypco1→	1110	Streptomyces sp. NBRC 110468	GCF_001184025.1	actinobacteria

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WP_062649304.1	vWA+cNMP_cyclase+Band7+HAD	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+cNMP_cyclase+Band7+HAD*→	1170	Streptomyces sp. NBRC 110468	-	actinobacteria
WP_062706177.1	vWA+TPRs	Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ Radical_SAM→ TIR+APATPase+TPRs→ ||← TCAD15	1094	Streptomyces regalis	GCA_001509475.1	actinobacteria
WP_062717917.1	vWA+TPRs	TCAD15→ Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ Radical_SAM→ TIR+APATPase+TPRs→	1087	Streptomyces caeruleatus	GCA_001514235.1	actinobacteria
WP_062720228.1	vWA+TIR+FxsC_Cter(partial)	AB_hydrolase→ CASPASE+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+TIR+FxsC_Cter(partial)*→	865	Streptomyces caeruleatus	GCA_001514235.1	actinobacteria
WP_062721860.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→	1122	Streptomyces caeruleatus	GCF_001514235.1	actinobacteria
WP_063274055.1	vWA+APATPase+wHTH+TPRs	cNMP_cyclase+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like← cNMP_binding+HTH_Crp_2	1197	Amycolatopsis keratiniphila	-	actinobacteria
WP_063483361.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← Na_H_Exchanger||AB_hydrolase→ CASPASE+EAD2→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→	1562	Streptomyces ambofaciens	GCA_001632865.1	actinobacteria
WP_063628645.1	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ PSE→ vWA+Pkinase+wHTH+TPRs+cNMP_cyclase*→	1038	Streptomyces lividans	GCF_000158935.1	actinobacteria
WP_063731010.1	vWA+Pkinase+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→ Porphobil_deam+Porphobil_deamC→	1197	Streptomyces sp. RTd22	GCF_001650215.1	actinobacteria
WP_063732781.1	vWA+BetaPropeller+CASPASE+APATPase+wHTH+TPRs+AB_hydrolase	EAD1+Trypsin→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+BetaPropeller+CASPASE+APATPase+wHTH+TPRs+AB_hydrolase*→	1525	Streptomyces sp. RTd22	GCF_001640565.1	actinobacteria
WP_063734284.1	vWA+TPRs	AB_hydrolase→ CASPASE+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→	1161	Streptomyces sp. RTd22	GCF_001650215.1	actinobacteria
WP_063736496.1	vWA+APATPase+wHTH+TPRs	PNP_UDP_1+EAD2→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs	1451	Streptomyces sp. RTd22	GCF_001650215.1	actinobacteria
WP_063736878.1	vWA+APATPase+wHTH+TPRs	vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← Radical_SAM← FXSXX-COOH||Voltage_CLC→ PSE→ ||← Trypco1	1444	Streptomyces sp. RTd22	GCF_001640565.1	actinobacteria
WP_063781306.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ TIR+APATPase+TPRs→	1121	Streptomyces decoyicus	GCA_001270575.1	actinobacteria
WP_063784888.1	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD*→	1705	Streptomyces viridochromogenes	GCF_001270495.1	actinobacteria
WP_063798505.1	vWA+APATPase+wHTH+TPRs	cNMP_binding+HTH_Crp_2||cNMP_cyclase+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like	1397	Nocardia sp. NRRL S-836	GCA_001279525.1	actinobacteria
WP_063820828.1	vWA+APATPase+wHTH+TPRs	-	1433	Frankia sp. QA3	-	actinobacteria
WP_063826594.1	vWA+APATPase+wHTH+TPRs	EAD2+EAD1→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs	1554	Frankia discariae	GCF_000373365.1	actinobacteria
WP_063870491.1	vWA+APATPase+wHTH+TPRs	EAD2+EAD1→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like	1199	Frankia sp. CpI1-P	-	actinobacteria
WP_064273537.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← Radical_SAM← FXSXX-COOH||Voltage_CLC→ ||← Trypco1	1475	Streptomyces sp. RTd22	GCF_001650215.1	actinobacteria
WP_064273706.1	vWA+BetaPropeller+CASPASE+NACHT	EAD1+Trypsin→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+BetaPropeller+CASPASE+NACHT*→	1398	Streptomyces sp. RTd22	-	actinobacteria
WP_064455400.1	vWA+APATPase+wHTH+TPRs	PNP_UDP_1+EAD2→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs	1460	Streptomyces sp. NBRC 109436	GCF_001652895.1	actinobacteria
WP_064456135.1	vWA+TPRs	CASPASE+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→	1174	Streptomyces sp. NBRC 109436	GCF_001652895.1	actinobacteria
WP_065477020.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ AB_hydrolase→ CASPASE+EAD2→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→	1487	Streptomyces sp. PTY087I2	GCA_001687325.1	actinobacteria
WP_065757097.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→	1155	Streptomyces clavuligerus	GCA_001693675.1	actinobacteria
WP_065913170.1	vWA+APATPase+wHTH+TPRs	cNMP_binding+HTH_Crp_2||cNMP_cyclase+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like	1418	Lentzea guizhouensis	GCA_001701025.1	actinobacteria
WP_065917436.1	vWA+CASPASE+NACHT+TPRs	AB_hydrolase→ BTLCP+VMAP-M2+VMAP-C→ MoxR→ vWA+CASPASE+NACHT+TPRs*→	1833	Lentzea guizhouensis	GCA_001701025.1	actinobacteria
WP_065959104.1	vWA+TPRs	AB_hydrolase→ CASPASE+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→	1166	Streptomyces sparsogenes	GCA_001969965.1	actinobacteria
WP_065965731.1	vWA+Pkinase+Pkinase	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+Pkinase*→ Porphobil_deam+Porphobil_deamC→	1144	Streptomyces sparsogenes	GCF_001704635.1	actinobacteria
WP_065966463.1	vWA+APATPase+wHTH+TPRs	PNP_UDP_1+EAD2→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs	1466	Streptomyces sparsogenes	GCF_001704635.1	actinobacteria
WP_066027130.1	vWA+TPRs	AB_hydrolase→ CASPASE+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→	1308	Streptomyces sporocinereus	GCF_001705785.1	actinobacteria
WP_066027899.1	vWA+APATPase+wHTH+TPRs	PNP_UDP_1+EAD2→ ||← ?||EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs	1462	Streptomyces sporocinereus	GCF_001705785.1	actinobacteria
WP_066926886.1	vWA+wHTH+TPRs+APATPase+wHTH+TPRs	Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ ?→ vWA+wHTH+TPRs+APATPase+wHTH+TPRs*→	1358	Streptomyces sp. NBRC 110611	GCF_001590865.1	actinobacteria
WP_067008717.1	vWA+APATPase+wHTH+TPRs	Trypco2→ EAD2+VMAP-M0+VMAP-C→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← Trypsin+EAD2	1257	Streptomyces cellostaticus	GCA_001513965.1	actinobacteria
WP_067010480.1	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD	DUF397→ ?→ ?→ ?→ Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD*→	1580	Streptomyces cellostaticus	GCA_001513965.1	actinobacteria
WP_067017920.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→	1135	Streptomyces sp. RV15	GCA_001514305.1	actinobacteria
WP_067024564.1	vWA+APATPase+Trypsin+TIR+FxsC_Cter(partial)	TIR+EAD2→ EAD2+VMAP-M10+VMAP-C→ MoxR→ vWA+APATPase+Trypsin+TIR+FxsC_Cter(partial)*→ ||← DUF397	1226	Streptomyces sp. RV15	GCA_001514305.1	actinobacteria
WP_067031497.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→	983	Streptomyces sp. RV15	GCA_001514305.1	actinobacteria
WP_067043278.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→	1116	Streptomyces sp. FXJ1.172	GCA_001636945.1	actinobacteria
WP_067055649.1	vWA+TPRs	TCAD15→ Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1163	Streptomyces sp. FXJ1.172	GCA_001636945.1	actinobacteria
WP_067075421.1	vWA+APATPase+wHTH+TPRs	PNP_UDP_1+EAD2→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs	1462	Streptomyces endus	GCF_001553475.1	actinobacteria
WP_067079480.1	vWA+TPRs	AB_hydrolase→ CASPASE+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→	1191	Streptomyces endus	GCF_001553475.1	actinobacteria
WP_067128388.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→	1106	Streptomyces yokosukanensis	GCF_001514035.1	actinobacteria
WP_067129121.1	vWA+TPRs	TCAD15→ Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1073	Streptomyces yokosukanensis	GCA_001514035.1	actinobacteria
WP_067166187.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	NUDIX→ Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→	1133	Streptomyces sp. ERV7	GCA_001653515.1	actinobacteria
WP_067167742.1	vWA+TPRs	vWA+TPRs*→ Radical_SAM→ TIR+APATPase+TPRs→	986	Streptomyces sp. ERV7	GCA_001653515.1	actinobacteria
WP_067237319.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1084	Streptomyces longwoodensis	GCA_001514125.1	actinobacteria
WP_067244441.1	vWA+REase+cNMP_cyclase+CASPASE	AB_hydrolase→ CASPASE+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+REase+cNMP_cyclase+CASPASE*→	1144	Streptomyces sp. DSM 15324	GCA_001514285.1	actinobacteria
WP_067362281.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	ADP_ribosyl_GH→ NUDIX→ Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→	1156	Streptomyces olivochromogenes	GCA_002335465.1	actinobacteria
WP_067395191.1	vWA+APATPase+wHTH+TPRs	Trypsin+EAD2→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like||Trypco1→	1596	Streptomyces sp. F-3	GCF_001653115.1	actinobacteria

acc	architecture	operon	len	species	gca	taxend
WP_067415632.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1137	Streptomyces sampsonii	GCF_001704195.1	actinobacteria
WP_067455624.1	vWA+FtsK+FtsK+FtsK	Trypsin+VMAP-M8+VMAP-C→ MoxR→ vWA+FtsK+FtsK+FtsK*→	1335	Actinomadura macra	GCF_001552215.1	actinobacteria
WP_067632860.1	vWA+FtsK+FtsK+CASPASE+FtsK	Trypco1→ Trypsin+VMAP-M8+VMAP-C→ MoxR→ vWA+FtsK+FtsK+CASPASE+FtsK*→	1695	Actinomadura latina	GCF_001552195.1	actinobacteria
WP_067637708.1	vWA+APATPase+wHTH+TPRs	Radical_SAM→ ||← TIR+APATPase+TPRs||SWACOS→ PSE→ ?→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← Radical_SAM← ?||cNMP_cyclase+EAD2→	1384	Actinomadura latina	GCF_001552195.1	actinobacteria
WP_067794950.1	vWA+FtsK+FtsK+FtsK	Trypco1→ Trypsin+VMAP-M8+VMAP-C→ MoxR→ vWA+FtsK+FtsK+FtsK*→	1515	Actinomadura formosensis	GCF_001552155.1	actinobacteria
WP_067817617.1	vWA+FtsK+FtsK+FtsK+FtsK+FtsK+FtsK	Trypsin+VMAP-M8+VMAP-C→ MoxR→ vWA+FtsK+FtsK+FtsK+FtsK+FtsK+FtsK*→	2289	Actinomadura kijaniata	GCF_001552175.1	actinobacteria
WP_067892555.1	vWA+APATPase+wHTH	Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH*→ ?→ ||← ?← ?← ?||?→ ?→ DUF397→	934	Actinomadura chibensis	GCF_001552135.1	actinobacteria
WP_067896613.1	vWA+APATPase+wHTH+TPRs	Radical_SAM→ METALLOPROTEASE+TPRs→ ||← TIR+APATPase+TPRs||FXSXX-COOH→ ?→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ cNMP_cyclase+EAD2→	1385	Actinomadura chibensis	GCF_001552135.1	actinobacteria
WP_067901341.1	vWA+Integrin_beta(vWA)	AB_hydrolase→ BTLCP+VMAP-M0+VMAP-C→ MoxR→ vWA+Integrin_beta(vWA)*→	1071	Actinomadura chibensis	GCF_001552135.1	actinobacteria
WP_067973520.1	vWA+APATPase+wHTH+TPRs	Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← DUF397	1532	Nocardiopsis trehalosi	GCF_001552555.1	actinobacteria
WP_068013580.1	vWA+TPRs	Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ Voltage_CLC→ METALLOPROTEASE→ TIR+APATPase+wHTH+TPRs→ Radical_SAM→	813	Nocardia mexicana	GCA_003350525.1	actinobacteria
WP_068753449.1	vWA+APATPase+wHTH+TPRs	Trypsin+EAD2→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← DUF397||Trypco1→	1477	Thermobifida cellulosilytica	GCA_001517975.1	actinobacteria
WP_068790131.1	vWA+FGS-fold_domain	VMAP-C→ MoxR→ vWA+FGS-fold_domain*→ FGS-fold_domain→	867	Phormidium willei	GCA_001637315.1	cyanobacteria
WP_069169727.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ AB_hydrolase→ CASPASE+EAD2→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→	1444	Streptomyces griseus	GCF_001715295.1	actinobacteria
WP_069466096.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← Trypsin+EAD2← Trypco2	1212	Streptomyces rubidus	GCF_001723065.1	actinobacteria
WP_069570250.1	vWA	EAD2+VMAP-M0+VMAP-C→ vWA*→	491	Streptomyces lydicus	GCA_001729485.1	actinobacteria
WP_069571998.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→	1147	Streptomyces lydicus	GCA_001729485.1	actinobacteria
WP_069622119.1	vWA+Pkinase	Trypco2→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase*→	890	Streptomyces niveus	GCF_001723075.1	actinobacteria
WP_069622478.1	vWA+TPRs	vWA+TPRs*→ FXSXX-COOH→ METALLOPROTEASE+TPRs→	806	Streptomyces niveus	GCF_001723075.1	actinobacteria
WP_069628672.1	vWA+Pkinase+TPRs	Trypco2→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+TPRs*→	1121	Streptomyces niveus	GCF_001723055.1	actinobacteria
WP_069737637.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→	1256	Streptomyces sp. EN27	GCF_001746315.1	actinobacteria
WP_069740765.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→	1256	Streptomyces sp. EN23	GCF_001746305.1	actinobacteria
WP_069761741.1	vWA+APATPase+wHTH+TPRs	Trypsin+EAD2→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like||Trypco1→	1469	Streptomyces sp. LUP47B	GCF_001746295.1	actinobacteria
WP_069782621.1	vWA+APATPase+wHTH+TPRs	Trypsin+EAD2→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like||Trypco1→	1534	Streptomyces punicescabiei	GCA_001735805.1	actinobacteria
WP_069860373.1	vWA+APATPase+wHTH+TPRs	PNP_UDP_1+EAD2→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like	1453	Streptomyces sp. SPMA113	GCF_001748165.1	actinobacteria
WP_069866024.1	vWA+TPRs	AB_hydrolase→ CASPASE+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→	1171	Streptomyces sp. SPMA113	GCF_001748165.1	actinobacteria
WP_069886105.1	vWA+Pkinase+FtsK+TPRs	ADP_ribosyl_GH→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+FtsK+TPRs*→ NUDIX→	1260	Streptomyces luteocolor	GCF_001748305.1	actinobacteria
WP_069886112.1	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+HAD	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+HAD*→	1252	Streptomyces luteocolor	-	actinobacteria
WP_069921916.1	vWA+TPRs	TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1208	Streptomyces subrutilus	GCA_001746425.1	actinobacteria
WP_069926978.1	vWA+TPRs	TCAD15||PSE→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1075	Streptomyces agglomeratus	GCA_001746465.1	actinobacteria
WP_069933003.1	vWA+TPRs	TCAD15||PSE→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1075	Streptomyces agglomeratus	GCA_001746415.1	actinobacteria
WP_069992837.1	vWA+TPRs	Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1069	Streptomyces	GCA_001751375.1	actinobacteria
WP_070025225.1	vWA+Pkinase+cNMP_cyclase+Band7+HAD	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+cNMP_cyclase+Band7+HAD*→	1268	Streptomyces sp. F-1	GCA_900079405.3	actinobacteria
WP_070202374.1	vWA+TIR+FxsC_Cter	AB_hydrolase→ CASPASE+VMAP-M2+VMAP-C→ MoxR→ vWA+TIR+FxsC_Cter*→	941	Streptomyces nanshensis	-	actinobacteria
WP_070202821.1	vWA(partial)+REase+STAND_NTPase+TPRs+cNMP_cyclase	CASPASE+VMAP-M2+VMAP-C→ MoxR→ PSE→ PSE→ vWA(partial)+REase+STAND_NTPase+TPRs+cNMP_cyclase*→	1317	Streptomyces nanshensis	GCA_001751305.1	actinobacteria
WP_070344004.1	vWA+TPRs	TCAD15||PSE→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1075	Streptomyces agglomeratus	GCA_001746485.1	actinobacteria
WP_070388963.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→	1081	Streptomyces pactum	GCA_001767375.1	actinobacteria
WP_070390415.1	vWA+TPRs	TCAD15||PSE→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ PSE→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1161	Streptomyces pactum	GCA_001767375.1	actinobacteria
WP_070391592.1	vWA+FGS-fold_domain	EAD1+Trypsin→ ||← ?||PSE→ EAD1+VMAP-M1+VMAP-C→ MoxR→ vWA+FGS-fold_domain*→	939	Moorea producens	GCA_001767235.1	cyanobacteria
WP_071102798.1	vWA+FGS-fold_domain	EAD1+Trypsin→ EAD1+VMAP-M1+Calcineurin-like→ EAD1+VMAP-M1+VMAP-C→ MoxR→ vWA+FGS-fold_domain*→	902	Moorea producens	GCA_001854205.1	cyanobacteria
WP_071106909.1	vWA+FGS-fold_domain	AB_hydrolase→ CASPASE+VMAP-M14+VMAP-C→ MoxR→ vWA+FGS-fold_domain*→ FGS-fold_domain→ four_helix_bundle_protein→	869	Moorea producens	GCA_001854205.1	cyanobacteria
WP_071330512.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1137	Streptomyces sampsonii	GCF_001865315.1	actinobacteria
WP_071336898.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1137	Streptomyces albidoflavus	GCF_001865795.1	actinobacteria
WP_071370429.1	vWA+cNMP_cyclase+Band7+HAD	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+cNMP_cyclase+Band7+HAD*→	1115	Streptomyces sp. MUSC 14	GCA_001866675.1	actinobacteria
WP_071376575.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1105	Streptomyces sp. MUSC 14	GCA_001866675.1	actinobacteria
WP_071381763.1	vWA+cNMP_cyclase+Band7+HAD	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+cNMP_cyclase+Band7+HAD*→	1122	Streptomyces sp. MUSC 1	GCA_001866665.1	actinobacteria
WP_071384258.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1105	Streptomyces sp. MUSC 1	GCA_001866665.1	actinobacteria
WP_071387451.1	vWA+Pkinase+cNMP_cyclase+Band7+HAD	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+cNMP_cyclase+Band7+HAD*→	1272	Streptomyces malaysiense	GCA_000980885.2	actinobacteria
WP_071515078.1	vWA+FGS-fold_domain	-	847	Geitlerinema sp. PCC 9228	-	cyanobacteria
WP_071623019.1	vWA+APATPase+wHTH+TPRs	Trypsin+VMAP-M0+VMAP-C→ vWA+APATPase+wHTH+TPRs*→ ||← DUF397||Trypco1→	1261	Nocardiopsis dassonvillei	GCA_001877055.1	actinobacteria
WP_072031082.1	vWA+APATPase+wHTH+TPRs	cNMP_cyclase+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like← cNMP_binding+HTH_Crp_2	1197	Amycolatopsis keratiniphila	GCA_001953855.1	actinobacteria

acc	architecture	operon	len	species	gca	taxend
WP_072319532.1	vWA+FGS-fold_domain	AB_hydrolase→ CASPASE+EAD2→ EAD2+VMAP-M11+VMAP-C→ MoxR→ vWA+FGS-fold_domain*→	701	Microcystis aeruginosa	GCF_001578075.1	cyanobacteria
WP_072926264.1	vWA+FGS-fold_domain	HTH+VMAP-M9+VMAP-C→ MoxR→ vWA+FGS-fold_domain*→	961	Microcystis aeruginosa	GCF_001895325.1	cyanobacteria
WP_072926889.1	vWA+FGS-fold_domain	AB_hydrolase→ CASPASE+VMAP-M14+VMAP-C→ MoxR→ vWA+FGS-fold_domain*→	842	Microcystis aeruginosa	GCF_001895325.1	cyanobacteria
WP_072927156.1	vWA+FGS-fold_domain	Trypco1→ Trypsin+VMAP-M1+VMAP-C→ MoxR→ vWA+FGS-fold_domain*→	883	Microcystis aeruginosa	GCF_001895325.1	cyanobacteria
WP_073223271.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→	1242	Streptomyces sp. NBRC 110465	GCF_001895105.1	actinobacteria
WP_073380260.1	vWA+APATPase+wHTH+TPRs	Trypsin+EAD2→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ‖← DUF397‖Trypco1→	1504	Nocardiopsis flavescens	GCA_900141985.1	actinobacteria
WP_073595266.1	vWA+FGS-fold_domain	-	864	Phormidium ambiguum	-	cyanobacteria
WP_073631276.1	vWA+FGS-fold_domain	Trypco2→ TCAD3+TCAD4+CASPASE+EAD1→ EAD1+VMAP-M1+VMAP-C→ MoxR→ vWA+FGS-fold_domain*→ FGS-fold_domain→	947	Scytonema sp. HK-05	GCA_002368235.1	cyanobacteria
WP_073631997.1	vWA+FGS-fold_domain	Trypco1→ Trypsin+EAD9→ EAD9+EAD1+VMAP-C→ MoxR→ vWA+FGS-fold_domain*→ ‖← ?‖FGS-fold_domain→	958	Scytonema sp. HK-05	GCA_002368235.1	cyanobacteria
WP_073700917.1	vWA+APATPase+wHTH+TPRs	Trypsin+VMAP-M0+VMAP-C→ vWA+APATPase+wHTH+TPRs*→ ‖← DUF397‖Trypco1→	1263	Nocardiopsis sp. TSRI0078	GCA_001905145.1	actinobacteria
WP_073717857.1	vWA+TPRs	TCAD15‖Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ Radical_SAM→ TIR+APATPase+TPRs→	1138	Streptomyces sp. TSRI0281	GCA_001905125.1	actinobacteria
WP_073719856.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ AB_hydrolase→ CASPASE+EAD2→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→	1440	Streptomyces sp. TSRI0281	GCA_001905125.1	actinobacteria
WP_073721464.1	vWA+wHTH+TPRs+wHTH+TPRs+APATPase+wHTH+TPRs	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+wHTH+TPRs+wHTH+TPRs+APATPase+wHTH+TPRs*→	1783	Streptomyces sp. TSRI0281	GCF_001905125.1	actinobacteria
WP_073722820.1	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+wHTH+TPRs+cNMP_cyclase*→	1311	Streptomyces sp. CB02414	GCA_001905385.1	actinobacteria
WP_073732208.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ‖← Na_H_Exchanger‖AB_hydrolase→ CASPASE+EAD2→ FXSXX-COOH-like→ PSE→ METALLOPROTEASE+TPRs→	1539	Streptomyces sp. CB02414	GCA_001905385.1	actinobacteria
WP_073735943.1	vWA+TPRs	AB_hydrolase→ CASPASE+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→	1183	Streptomyces sp. CB02488	-	actinobacteria
WP_073736958.1	vWA+TPRs	TCAD15‖Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→ Trypco1→	1163	Streptomyces sp. CB02488	GCA_001905365.1	actinobacteria
WP_073741611.1	vWA+TPRs	AB_hydrolase→ CASPASE+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→	1170	Streptomyces sp. CB02115	-	actinobacteria
WP_073742765.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ AB_hydrolase→ CASPASE+EAD2→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→	1484	Streptomyces sp. CB02115	GCF_001905645.1	actinobacteria
WP_073755836.1	vWA+wHTH+TPRs+wHTH+TPRs+APATPase+wHTH+TPRs	Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+wHTH+TPRs+wHTH+TPRs+APATPase+wHTH+TPRs*→	1790	Streptomyces sp. CB03234	GCF_001905885.1	actinobacteria
WP_073757570.1	vWA+wHTH+TPRs+wHTH+TPRs+APATPase+wHTH+TPRs	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+wHTH+TPRs+wHTH+TPRs+APATPase+wHTH+TPRs*→ ‖← AB_hydrolase	1767	Streptomyces sp. CB02923	GCA_001905005.1	actinobacteria
WP_073772252.1	vWA+STAND_NTPase+Trypsin+CASPASE+S1COLD	AB_hydrolase→ CASPASE+VMAP-M0+VMAP-C→ MoxR→ vWA+STAND_NTPase+Trypsin+CASPASE+S1COLD*→	1339	Streptomyces sp. CB02366	GCF_001905905.1	actinobacteria
WP_073777497.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ AB_hydrolase→ CASPASE+EAD2→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→	1463	Streptomyces sp. TSRI0445	GCF_001905405.1	actinobacteria
WP_073791958.1	vWA+cNMP_cyclase+TCAD13	AB_hydrolase→ CASPASE+VMAP-M2+VMAP-C→ MoxR→ vWA+cNMP_cyclase+TCAD13*→	1097	Streptomyces sp. CB01580	GCF_001905795.1	actinobacteria
WP_073793562.1	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+wHTH+TPRs+cNMP_cyclase*→	1289	Streptomyces uncialis	GCF_001905345.1	actinobacteria
WP_073801500.1	vWA+TPRs	AB_hydrolase→ CASPASE+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→	1170	Streptomyces sp. TSRI0261	GCF_001905485.1	actinobacteria
WP_073805364.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ AB_hydrolase→ CASPASE+EAD2→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→	1489	Streptomyces sp. TSRI0261	GCA_001905485.1	actinobacteria
WP_073848019.1	vWA+APATPase+wHTH+TPRs	cNMP_cyclase+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ‖← METALLOPROTEASE+TPRs← FXSXX-COOH-like← cNMP_binding+HTH_Crp_2	1197	Amycolatopsis sp. CB00013	GCA_001905755.1	actinobacteria
WP_073862966.1	vWA+TPRs	TCAD15‖Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→ Trypco1→	1139	Streptomyces sp. CB01249	GCA_001905735.1	actinobacteria
WP_073863467.1	vWA+TPRs	AB_hydrolase→ CASPASE+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→	1170	Streptomyces sp. CB01249	GCF_001905735.1	actinobacteria
WP_073866272.1	vWA+TPRs	TCAD15‖Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ Radical_SAM→ TIR+APATPase+TPRs→	936	Streptomyces sp. CB00072	GCF_001905575.1	actinobacteria
WP_073868984.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ AB_hydrolase→ CASPASE+EAD2→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→	1483	Streptomyces sp. CB00072	GCF_001905575.1	actinobacteria
WP_073881342.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→	1142	Streptomyces sp. CB00316	-	actinobacteria
WP_073892180.1	vWA+APATPase+wHTH+TPRs	-	1264	Saccharothrix sp. CB00851	-	actinobacteria
WP_073900317.1	vWA+APATPase+wHTH+TPRs	-	1427	Saccharothrix sp. CB00851	-	actinobacteria
WP_073912307.1	vWA+TPRs	TCAD15‖Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1083	Streptomyces sp. CB02009	GCF_001905825.1	actinobacteria
WP_073936870.1	vWA+APATPase+wHTH+TPRs	Trypsin+EAD2→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ‖← METALLOPROTEASE+TPRs← Radical_SAM← FXSXX-COOH‖Voltage_CLC→	1534	Streptomyces sp. CB02400	GCA_001905725.1	actinobacteria
WP_073938688.1	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD*→	1560	Streptomyces sp. TSRI0107	GCF_001905845.1	actinobacteria
WP_073939274.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ‖← Na_H_Exchanger‖CASPASE+EAD2→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→	1529	Streptomyces sp. TSRI0107	GCF_001905845.1	actinobacteria
WP_073958207.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→	1245	Streptomyces sp. TSRI0395	GCF_001905525.1	actinobacteria
WP_073958768.1	vWA+TPRs	AB_hydrolase→ CASPASE+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→	1170	Streptomyces sp. TSRI0395	GCF_001905525.1	actinobacteria
WP_073959593.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ AB_hydrolase→ CASPASE+EAD2→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→	1484	Streptomyces sp. TSRI0395	GCF_001905525.1	actinobacteria
WP_073963981.1	vWA+TPRs	TCAD15‖Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1135	Streptomyces sp. CB02460	GCA_001905705.1	actinobacteria
WP_074992219.1	vWA+Pkinase+cNMP_cyclase+Band7+HAD	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+cNMP_cyclase+Band7+HAD*→	1268	Streptomyces misionensis	GCA_900104815.1	actinobacteria
WP_075001997.1	vWA+TPRs	Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1069	Streptomyces qinglanensis	GCA_900111245.1	actinobacteria
WP_075020915.1	vWA+FtsK+FtsK+FtsK	Trypco1→ Trypsin+VMAP-M8+VMAP-C→ MoxR→ vWA+FtsK+FtsK+FtsK*→	1506	Actinomadura madurae	GCA_900115095.1	actinobacteria
WP_075029687.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	ADP_ribosyl_GH→ NUDIX→ Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→ SIR2→	1152	Streptomyces mirabilis	GCA_900112965.1	actinobacteria
WP_075128572.1	vWA+APATPase+wHTH+TPRs	cNMP_cyclase+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ‖← METALLOPROTEASE+TPRs← FXSXX-COOH-like← cNMP_binding+HTH_Crp_2	1204	Actinophytocola xanthii	GCA_001921205.1	actinobacteria
WP_075137510.1	vWA+APATPase+wHTH+TPRs	cNMP_cyclase+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ‖← METALLOPROTEASE+TPRs← FXSXX-COOH-like← cNMP_binding+HTH_Crp_2	1197	Actinophytocola xinjiangensis	GCA_001921215.1	actinobacteria
WP_075347515.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ AB_hydrolase→ CASPASE+EAD2→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→	1484	Streptomyces sp. MNU77	GCA_000935135.2	actinobacteria

acc	architecture	operon	len	species	gca	taxend
WP_075598587.1	vWA+FGS-fold_domain	-	862	Oscillatoriales cyanobacterium 'hensonii'	-	cyanobacteria
WP_075601459.1	vWA+FGS-fold_domain	EAD1+Trypsin→ ?→ EAD1+VMAP-M1+VMAP-C→ MoxR→ vWA+FGS-fold_domain*→ four_helix_bundle_protein→ RVT_1→ FGS-fold_domain→	860	Oscillatoriales cyanobacterium 'hensonii'	GCA_001939115.1	cyanobacteria
WP_075660888.1	vWA+TIR+FxsC_Cter(partial)	vWA+TIR+FxsC_Cter(partial)*→	730	Streptomyces acidiscabies	GCF_001941265.1	actinobacteria
WP_075661654.1	vWA+Pkinase+wHTH+cNMP_cyclase+Band7+HAD	vWA+Pkinase+wHTH+cNMP_cyclase+Band7+HAD*→	1037	Streptomyces acidiscabies	GCF_001941265.1	actinobacteria
WP_075692473.1	vWA+TIR+FxsC_Cter(partial)	vWA+TIR+FxsC_Cter(partial)*→	726	Streptomyces acidiscabies	GCF_001941285.1	actinobacteria
WP_075693252.1	vWA+Pkinase+wHTH+cNMP_cyclase+Band7+HAD	vWA+Pkinase+wHTH+cNMP_cyclase+Band7+HAD*→	1230	Streptomyces acidiscabies	GCF_001941285.1	actinobacteria
WP_075735350.1	vWA+Pkinase+wHTH+cNMP_cyclase+Band7+HAD	vWA+Pkinase+wHTH+cNMP_cyclase+Band7+HAD*→	1243	Streptomyces acidiscabies	GCF_001941275.1	actinobacteria
WP_075779362.1	vWA+TIR+FxsC_Cter(partial)	vWA+TIR+FxsC_Cter(partial)*→	726	Streptomyces acidiscabies	GCF_001941325.1	actinobacteria
WP_075779491.1	vWA+Pkinase+wHTH+cNMP_cyclase+Band7+HAD	vWA+Pkinase+wHTH+cNMP_cyclase+Band7+HAD*→	1227	Streptomyces acidiscabies	GCF_001941325.1	actinobacteria
WP_075779623.1	vWA+Pkinase+TPRs	Trypco2→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+TPRs*→	1028	Streptomyces acidiscabies	GCF_001941325.1	actinobacteria
WP_075779895.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→	1108	Streptomyces acidiscabies	GCF_001941325.1	actinobacteria
WP_075895039.1	vWA+APATPase+wHTH+TPRs	Radical_SAM→ PSE→ ‖← PSE‖FXSXX-COOH-like→ ?→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ‖← FXSXX-COOH-like‖cNMP_cyclase+EAD2→	1298	Actinomadura sp. CNU-125	GCA_001942465.1	actinobacteria
WP_075895313.1	vWA_protein	AB_hydrolase→ BTLCP+VMAP-M2+VMAP-C→ MoxR→ vWA_protein*→	821	Actinomadura sp. CNU-125	GCA_001942465.1	actinobacteria
WP_075896676.1	vWA+FGS-fold_domain	AB_hydrolase→ CASPASE+VMAP-M14+VMAP-C→ MoxR→ vWA+FGS-fold_domain*→ FGS-fold_domain→ four_helix_bundle_protein→	900	Moorea bouillonii	GCA_001942495.1	cyanobacteria
WP_075897253.1	vWA+FGS-fold_domain	EAD1+Trypsin→ EAD1+VMAP-M1+Calcineurin-like→ EAD1+VMAP-M1+VMAP-C→ MoxR→ vWA+FGS-fold_domain*→	862	Moorea bouillonii	GCA_001942495.1	cyanobacteria
WP_075925848.1	vWA_protein	Trypsin+EAD2→ VMAP-C→ MoxR→ ?→ vWA_protein*→ TIR+APATPase+TPRs→ ‖← DUF397‖Trypco1→ ‖← PSE← ?← PSE← PSE← DUF397	455	Nocardiopsis sp. CNR-923	GCA_001942255.1	actinobacteria
WP_075927196.1	vWA+APATPase+wHTH	Trypsin+VMAP-M8→ VMAP-C→ MoxR→ vWA+APATPase+wHTH*→	1058	Nocardiopsis sp. CNR-923	GCA_001942255.1	actinobacteria
WP_075971297.1	vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats	AB_hydrolase→ CASPASE+VMAP-M0+VMAP-C→ MoxR→ vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats*→	1195	Streptomyces sp. TN58	GCA_001941845.1	actinobacteria
WP_076044739.1	vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats	AB_hydrolase→ CASPASE+VMAP-M0+VMAP-C→ MoxR→ vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats*→	1193	Streptomyces amritsarensis	GCA_001953875.1	actinobacteria
WP_076096475.1	vWA+TPRs	TCAD15→ Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ Radical_SAM→ TIR+APATPase+TPRs→	1092	Streptomyces sp. IMTB 2501	GCA_001953885.1	actinobacteria
WP_076155767.1	vWA+TPRs	AB_hydrolase→ CASPASE+VMAP-M2+VMAP-C→ MoxR→ vWA+TPRs*→	805	Amycolatopsis coloradensis	GCA_001953865.1	actinobacteria
WP_076161090.1	vWA+APATPase+wHTH+TPRs	cNMP_cyclase+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ‖← METALLOPROTEASE+TPRs← FXSXX-COOH-like← cNMP_binding+HTH_Crp_2	1198	Amycolatopsis coloradensis	GCA_001953865.1	actinobacteria
WP_076819102.1	vWA+TPRs	Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ Voltage_CLC→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	929	Frankia sp. M16386	GCA_001983105.1	actinobacteria
WP_076821064.1	vWA+APATPase+wHTH+TPRs	EAD2+EAD1→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ‖← METALLOPROTEASE+TPRs	1517	Frankia sp. M16386	GCA_001983105.1	actinobacteria
WP_076831948.1	vWA+APATPase+wHTH+TPRs	EAD2+EAD1→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ‖← METALLOPROTEASE+TPRs	1598	Frankia sp. CcI49	GCA_001983215.1	actinobacteria
WP_076913890.1	vWA+REC	AB_hydrolase→ CASPASE+VMAP-M4+VMAP-C→ MoxR→ vWA+REC*→	1172	Burkholderia pseudomallei	GCA_001977425.1	betaproteobacteria
WP_076973926.1	vWA+APATPase+wHTH+TPRs	Trypsin+VMAP-M6+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ‖← METALLOPROTEASE+TPRs← Radical_SAM← Trypco1	1478	Streptomyces sp. M1013	GCA_001970135.1	actinobacteria
WP_076976234.1	vWA+TPRs	TCAD15→ Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1097	Streptomyces sp. M1013	GCA_001970135.1	actinobacteria
WP_076994244.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ‖← METALLOPROTEASE+TPRs← FXSXX-COOH-like‖EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs→ ‖← METALLOPROTEASE+TPRs← FXSXX-COOH-like	1432	Actinosynnema sp. ALI-1.44	GCA_001984155.1	actinobacteria
WP_076994249.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs→ ‖← METALLOPROTEASE+TPRs← FXSXX-COOH-like‖EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ‖← METALLOPROTEASE+TPRs← FXSXX-COOH-like	1394	Actinosynnema sp. ALI-1.44	GCA_001984155.1	actinobacteria
WP_077011609.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ‖← METALLOPROTEASE+TPRs← cNMP_cyclase+EAD2	1322	Saccharothrix sp. ALI-22-I	GCA_001984175.1	actinobacteria
WP_077058987.1	vWA+TPRs	TCAD15‖Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1097	Streptomyces sp. MP131-18	GCF_001984575.1	actinobacteria
WP_077060243.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→	1126	Streptomyces sp. MP131-18	GCA_001984575.1	actinobacteria
WP_077116335.1	vWA+TPRs	Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ Voltage_CLC→ METALLOPROTEASE→ TIR+APATPase+wHTH+TPRs→	801	Nocardia donostiensis	GCA_001989395.1	actinobacteria
WP_077193459.1	vWA+TPRs	TCAD15‖Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ TIR+APATPase+TPRs→	1136	Streptomyces lydicus	GCF_001984445.1	actinobacteria
WP_077692791.1	vWA+APATPase+wHTH+TPRs	Trypsin+VMAP-M0+VMAP-C→ vWA+APATPase+wHTH+TPRs*→ ‖← DUF397‖Trypco1→	1264	Nocardiopsis sinuspersici	GCA_001998325.1	actinobacteria
WP_077796725.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→	1114	Streptomyces sp. JHA26	GCF_002005565.1	actinobacteria
WP_078067203.1	vWA+TPRs	TCAD15‖PSE→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1145	Streptomyces jeddahensis	GCA_001642995.1	actinobacteria
WP_078075117.1	vWA+TPRs	TCAD15‖PSE→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1035	Streptomyces niveus	-	actinobacteria
WP_078095066.1	vWA+TPRs	TCAD15‖Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1099	Streptomyces sp. fd1-xmd	GCF_002007685.1	actinobacteria
WP_078095390.1	vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats	AB_hydrolase→ CASPASE+VMAP-M0+VMAP-C→ MoxR→ vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats*→	1192	Streptomyces sp. fd1-xmd	GCA_002007685.1	actinobacteria
WP_078490521.1	vWA+Pkinase+wHTH+TPRs	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ ‖← ?‖vWA+Pkinase+wHTH+TPRs*→	1072	Streptomyces scopuliridis	-	actinobacteria
WP_078496221.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ AB_hydrolase→ CASPASE+EAD2→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→	1479	Streptomyces sp. W007	GCF_000239075.1	actinobacteria
WP_078506948.1	vWA	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA*→ TIR+APATPase+TPRs→ PSE→ CASPASE+EAD2→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→	441	Streptomyces viridochromogenes	-	actinobacteria

acc	architecture	operon	len	species	gca	taxend
WP_078559684.1	vWA+wHTH+TPRs+wHTH+TPRs+BetaPropeller	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+wHTH+TPRs+wHTH+TPRs+BetaPropeller*→	1391	Streptomyces sp. PRh5	-	actinobacteria
WP_078610845.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ‖← METALLOPROTEASE+TPRs← FXSXX-COOH-like← ?← ?← Na_H_Exchanger	1444	Streptomyces	-	actinobacteria
WP_078621013.1	vWA+APATPase+wHTH+TPRs	vWA+APATPase+wHTH+TPRs*→ ‖← METALLOPROTEASE+TPRs← CASPASE+EAD2	1336	Streptomyces aurantiacus	-	actinobacteria
WP_078621095.1	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD*→	1658	Streptomyces sp. NRRL WC-3626	GCF_000718785.1	actinobacteria
WP_078621929.1	vWA+APATPase+wHTH+TPRs+NaeI	AB_hydrolase→ CASPASE+VMAP-M2+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs+NaeI*→	1286	Streptomyces sp. NRRL S-244	-	actinobacteria
WP_078625713.1	vWA+HTH+HTH+ParA-Soj-PloopNTPase(SIMIBI)	CASPASE+VMAP-M2+VMAP-C→ MoxR→ vWA+HTH+HTH+ParA-Soj-PloopNTPase(SIMIBI)*→ PSE→ PSE→ ‖← ?‖?→ ‖← ?‖?→ DUF397→	956	Streptomyces sp. CNB091	GCF_000377965.1	actinobacteria
WP_078630591.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ‖← METALLOPROTEASE+TPRs← FXSXX-COOH-like	1355	Streptomyces roseochromogenus	GCF_000497445.1	actinobacteria
WP_078633428.1	vWA+REase+cNMP_cyclase+CASPASE	AB_hydrolase→ CASPASE+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+REase+cNMP_cyclase+CASPASE*→	1160	Streptomyces antibioticus	GCF_002019855.1	actinobacteria
WP_078633957.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ vWA+APATPase+wHTH+TPRs*→ ‖← METALLOPROTEASE+TPRs← FXSXX-COOH-like← PSE‖METALLOPROTEASE+TPRs→	1358	Streptomyces antibioticus	GCF_002019855.1	actinobacteria
WP_078636541.1	vWA+APATPase+wHTH+TPRs	TCAD9+Pkinase+NACHT+HEAT_repeats→ EAD2+VMAP-M0+VMAP-C→ vWA→ MoxR→ vWA+APATPase+TPRs*→	991	Streptomyces antibioticus	GCF_002019855.1	actinobacteria
WP_078636543.1	vWA	TCAD9+Pkinase+NACHT+HEAT_repeats→ EAD2+VMAP-M0+VMAP-C→ vWA*→ MoxR→ vWA+APATPase+TPRs→	433	Streptomyces antibioticus	GCA_002019855.1	actinobacteria
WP_078639145.1	vWA+APATPase+wHTH+TPRs	PNP_UDP_1+EAD2→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ‖← METALLOPROTEASE+TPRs	1452	Streptomyces hygroscopicus	GCA_002021875.1	actinobacteria
WP_078640352.1	vWA+Pkinase+ZNR+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	SIR2→ ‖← ?‖Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ZNR+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→ Porphobil_deam+Porphobil_deamC→	1524	Streptomyces hygroscopicus	GCA_002021875.1	actinobacteria
WP_078641309.1	vWA+TPRs	AB_hydrolase→ CASPASE+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→	1171	Streptomyces hygroscopicus	GCA_002021875.1	actinobacteria
WP_078759921.1	vWA+APATPase+wHTH+TPRs	Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ‖← DUF397‖Trypco1→	1508	Marinactinospora thermotolerans	GCA_900167435.1	actinobacteria
WP_078841454.1	vWA+TPRs	TCAD15‖PSE→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1080	Streptomyces acidiscabies	GCF_001189015.1	actinobacteria
WP_078855504.1	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase*→	1130	Streptomyces sp. MBT28	-	actinobacteria
WP_078866458.1	vWA+TPRs	TCAD15‖PSE→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ TIR+APATPase+TPRs→	1198	Streptomyces sp. NRRL S-1448	-	actinobacteria
WP_078869289.1	vWA+APATPase+wHTH+TPRs	Trypsin+EAD2→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ‖← METALLOPROTEASE+TPRs← FXSXX-COOH-like	1320	Streptomyces sp. NRRL B-1347	-	actinobacteria
WP_078872795.1	vWA+TPRs	MoxR→ vWA+Trypsin+HDxxH+VMAP-M0+VMAP-C→ ‖← ?‖PSE→ MoxR→ ‖← ?‖vWA+TPRs*→ FXSXX-COOH→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1045	Streptomyces sp. NRRL S-1868	-	actinobacteria
WP_078872798.1	vWA+Trypsin+HDxxH+VMAP-M0+VMAP-C	TCAD15→ ?→ ?→ PSE→ ?→ MoxR→ vWA+Trypsin+HDxxH+VMAP-M0+VMAP-C*→ ‖← ?‖PSE→ MoxR→ ‖← ?‖vWA+TPRs→ FXSXX-COOH→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1090	Streptomyces sp. NRRL S-1868	-	actinobacteria
WP_078877222.1	vWA+TPRs	TCAD15‖Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1142	Streptomyces sp. 150FB	-	actinobacteria
WP_078884155.1	vWA+APATPase+wHTH+TPRs	Trypsin+EAD2→ EAD2+VMAP-M0+VMAP-C→ MoxR→ ?→ vWA+APATPase+wHTH+TPRs*→ ‖← METALLOPROTEASE+TPRs← Radical_SAM← FXSXX-COOH-like‖Voltage_CLC→	1363	Streptomyces sp. NRRL S-340	-	actinobacteria
WP_078885533.1	vWA+wHTH+TPRs+APATPase+wHTH+TPRs	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+wHTH+TPRs+APATPase+wHTH+TPRs*→ ‖← ?‖?→ ‖← AB_hydrolase	1438	Streptomyces sp. NBRC 110027	-	actinobacteria
WP_078889789.1	vWA+APATPase+wHTH+TPRs+SFI-helicase	AB_hydrolase→ CASPASE+VMAP-M2+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs+SFI-helicase*→	1581	Streptomyces sp. NRRL S-1813	GCF_000719605.1	actinobacteria
WP_078892246.1	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+HAD	Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+HAD*→	1619	Streptomyces olivaceus	-	actinobacteria
WP_078893851.1	vWA+PNP_UDP_1+APATPase+wHTH+TPRs	AB_hydrolase→ CASPASE+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+PNP_UDP_1+APATPase+wHTH+TPRs*→	1472	Streptomyces sp. NRRL S-1022	GCF_000720135.1	actinobacteria
WP_078906829.1	vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats	AB_hydrolase→ CASPASE+VMAP-M0+VMAP-C→ MoxR→ ‖← ?‖vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats*→	1158	Streptomyces sp. NRRL S-378	-	actinobacteria
WP_078914741.1	vWA+CASPASE+TCAD14+PIN+CCCH(ZNR)+FHA	Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ ‖← ?‖vWA+CASPASE+TCAD14+PIN+CCCH(ZNR)+FHA*→	1145	Streptomyces sp. NRRL S-384	-	actinobacteria
WP_078916501.1	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD*→	1579	Streptomyces viridochromogenes	-	actinobacteria
WP_078935568.1	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+wHTH+TPRs+cNMP_cyclase*→	1183	Streptomyces europaeiscabiei	-	actinobacteria
WP_078942262.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ AB_hydrolase→ CASPASE+EAD2→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→	1463	Streptomyces mediolani	GCF_000721685.1	actinobacteria
WP_078942771.1	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD*→	1583	Streptomyces viridochromogenes	-	actinobacteria
WP_078943028.1	vWA+APATPase+wHTH+TPRs	VMAP-M25+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ AB_hydrolase→ CASPASE+EAD2→ METALLOPROTEASE+TPRs→	1298	Streptomyces aureus	-	actinobacteria
WP_078946634.1	vWA+Pkinase+wHTH+TPRs	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+wHTH+TPRs*→	1081	Streptomyces sp. NRRL B-3648	GCF_001279545.1	actinobacteria
WP_078953405.1	vWA+APATPase+wHTH+TPRs+SFI-helicase	AB_hydrolase→ CASPASE+VMAP-M2+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs+SFI-helicase*→	1581	Streptomyces decoyicus	GCF_001270575.1	actinobacteria
WP_078957678.1	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD*→	1547	Streptomyces glaucescens	GCA_000761215.1	actinobacteria
WP_078961270.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ AB_hydrolase→ CASPASE+EAD2→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→	1484	Streptomyces	GCF_001189025.1	actinobacteria
WP_078968245.1	vWA+SFII-helicase+Trypsin+cNMP_cyclase+Coiled-coil+CASPASE	AB_hydrolase→ CASPASE+VMAP-M2+VMAP-C→ MoxR→ vWA+SFII-helicase+Trypsin+cNMP_cyclase+Coiled-coil+CASPASE*→	1796	Streptomyces	GCF_001280095.1	actinobacteria
WP_078969206.1	vWA+Pkinase+NUDIX	VMAP-M2+VMAP-C→ MoxR→ vWA+Pkinase+NUDIX*→	1259	Streptomyces cyaneogriseus	-	actinobacteria
WP_078969534.1	vWA+TPRs	TCAD15‖Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1095	Streptomyces cyaneogriseus	GCF_000931445.1	actinobacteria
WP_078970667.1	vWA+APATPase+wHTH+TPRs	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ‖← AB_hydrolase	1187	Streptomyces chattanoogensis	-	actinobacteria
WP_078978683.1	vWA+BetaPropeller	CASPASE+VMAP-M19+VMAP-C→ MoxR→ vWA+BetaPropeller*→	897	Streptomyces scabrisporus	GCA_002024165.1	actinobacteria
WP_079023028.1	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+wHTH+TPRs+cNMP_cyclase*→	1155	Streptomyces sp. NRRL B-24891	-	actinobacteria

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WP_079024941.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1095	Streptomyces leeuwenhoekii	GCF_001047315.1	actinobacteria
WP_079030148.1	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+HAD	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ ?→ MoxR→ vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+HAD*→	1542	Streptomyces ambofaciens	GCA_001267885.1	actinobacteria
WP_079041858.1	vWA+Pkinase+TPRs	vWA+Pkinase+TPRs*→	894	Streptomyces aureus	GCF_001418135.1	actinobacteria
WP_079044303.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ AB_hydrolase→ CASPASE+EAD2→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→	1484	Streptomyces amulatus	GCF_001434355.1	actinobacteria
WP_079051130.1	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD	Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD*→	1558	Streptomyces curacoi	-	actinobacteria
WP_079054844.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→	958	Streptomyces neyagawaensis	GCF_001418645.1	actinobacteria
WP_079059666.1	vWA+TIR+cNMP_cyclase+S1COLD+EAD2	AB_hydrolase→ CASPASE+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+TIR+cNMP_cyclase+S1COLD+EAD2*→	1102	Streptomyces violaceusniger	GCF_001509775.1	actinobacteria
WP_079065161.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like← Trypsin+EAD2← Trypco2||METALLOPROTEASE+TPRs→	1317	Streptomyces olivochromogenes	-	actinobacteria
WP_079065729.1	vWA+CASPASE+TIR+NUDIX	Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+CASPASE+TIR+NUDIX*→	1286	Streptomyces olivochromogenes	GCA_002335465.1	actinobacteria
WP_079078451.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1090	Streptomyces sp. CdTB01	-	actinobacteria
WP_079082984.1	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD*→	1536	Streptomyces antibioticus	GCF_001514065.1	actinobacteria
WP_079084658.1	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD*→	1646	Streptomyces sp. RV15	GCF_001514305.1	actinobacteria
WP_079104732.1	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+wHTH+TPRs+cNMP_cyclase*→	1153	Streptomyces europaeiscabiei	-	actinobacteria
WP_079123647.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ TIR+APATPase+TPRs→	1212	Streptomyces sp. NBRC 110611	GCF_001590865.1	actinobacteria
WP_079125114.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1105	Streptomyces lushanensis	GCF_001700515.1	actinobacteria
WP_079127044.1	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase	Trypco1→ PSE→ MoxR→ vWA+Pkinase+wHTH+TPRs+cNMP_cyclase*→	1217	Streptomyces sp. CC71	GCF_001595515.1	actinobacteria
WP_079127936.1	vWA+STAND_NTPase+BetaPropeller+REase(Mrr_cat-PDDEXK)	AB_hydrolase→ CASPASE+VMAP-M0+VMAP-C→ MoxR→ vWA+STAND_NTPase+BetaPropeller+REase(Mrr_cat-PDDEXK)*→	1081	Streptomyces niveus	GCF_001723055.1	actinobacteria
WP_079134774.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→	1479	Streptomyces sp. EN16	GCF_001746285.1	actinobacteria
WP_079138844.1	vWA+APATPase+wHTH+TPRs	vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← Trypsin+EAD2← Trypco2	1266	Streptomyces rubidus	GCF_001723065.1	actinobacteria
WP_079141625.1	vWA+cNMP_cyclase+Band7+HAD	vWA+cNMP_cyclase+Band7+HAD*→	949	Streptomyces sp. LUP30	-	actinobacteria
WP_079141871.1	vWA+TPRs	Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1109	Streptomyces sp. LUP30	-	actinobacteria
WP_079146592.1	vWA+APATPase+wHTH+TPRs	Trypco2→ EAD2+VMAP-M0+VMAP-C→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← Trypsin+EAD2||?→ Trypco2→	1259	Streptomyces griseochromogenes	-	actinobacteria
WP_079147211.1	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7*→	1401	Streptomyces griseochromogenes	GCF_001542625.1	actinobacteria
WP_079154905.1	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+HAD	Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+HAD*→	1616	Streptomyces pactum	-	actinobacteria
WP_079155447.1	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+HAD	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+HAD*→	1542	Streptomyces ambofaciens	GCA_001632865.1	actinobacteria
WP_079163728.1	vWA+APATPase+wHTH+TPRs	Trypco2→ EAD2+VMAP-M0+VMAP-C→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like← Trypsin+EAD2	1266	Streptomyces parvulus	GCF_001660045.1	actinobacteria
WP_079164118.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1095	Streptomyces leeuwenhoekii	GCF_001013905.1	actinobacteria
WP_079164533.1	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD*→ ?→ ?→ ?→ ||← ?||Radical_SAM→ Antibiotic_NAT→ TIR+FxsC_Cter→	1525	Streptomyces lincolnensis	GCA_001685355.1	actinobacteria
WP_079165222.1	vWA+SFII-helicase+Z1	AB_hydrolase→ CASPASE+VMAP-M2+VMAP-C→ MoxR→ vWA+SFII-helicase+Z1*→	1254	Streptomyces lincolnensis	-	actinobacteria
WP_079173956.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← Trypsin+EAD2← Trypco2||METALLOPROTEASE+TPRs→	1300	Streptomyces mirabilis	GCA_900112965.1	actinobacteria
WP_079176518.1	vWA+Pkinase+Pkinase+NaeI	Trypco2→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+Pkinase+NaeI*→	1494	Streptomyces sp. MUSC 14	GCF_001866675.1	actinobacteria
WP_079178870.1	vWA+TPRs	TCAD15||PSE→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ PSE→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1107	Streptomyces humi	-	actinobacteria
WP_079180720.1	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+wHTH+TPRs+cNMP_cyclase*→	1177	Streptomyces sp. CB02058	-	actinobacteria
WP_079182682.1	vWA+Pkinase+NaeI	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+NaeI*→	1103	Streptomyces sp. TSRI0281	GCF_001905125.1	actinobacteria
WP_079185913.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1243	Streptomyces sp. CB01580	-	actinobacteria
WP_079192457.1	vWA+wHTH+cNMP_cyclase+Band7+HAD	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+wHTH+cNMP_cyclase+Band7+HAD*→	1273	Streptomyces sp. CB01883	GCA_001905855.1	actinobacteria
WP_079192460.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← Na_H_Exchanger||AB_hydrolase→ CASPASE+EAD2→ FXSXX-COOH-like→ METALLOPROTEASE+TPRs→	1510	Streptomyces sp. CB01883	GCF_001905855.1	actinobacteria
WP_079193740.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ TIR+APATPase+TPRs→	1103	Streptomyces sp. CB02923	GCA_001905005.1	actinobacteria
WP_079195175.1	vWA+SWACOS+Trypsin+TIR+HTH	CASPASE+VMAP-M2+VMAP-C→ MoxR→ ||← ?||vWA+SWACOS+Trypsin+TIR+HTH*→	1121	Streptomyces sp. CB02400	GCF_001905725.1	actinobacteria
WP_079208172.1	vWA+FGS-fold_domain	AB_hydrolase→ PSE→ ||← PSE||EAD2+VMAP-M11+VMAP-C→ MoxR→ vWA+FGS-fold_domain*→	700	Microcystis aeruginosa	GCA_002025445.1	cyanobacteria
WP_079209937.1	vWA+FGS-fold_domain	Trypco1→ ||← ?||Trypsin+VMAP-M1+VMAP-C→ MoxR→ vWA+FGS-fold_domain*→	872	Microcystis aeruginosa	GCA_002025445.1	cyanobacteria
WP_079248443.1	vWA+TPRs	TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ ||← ?||vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	970	Streptomyces sp. MJM1172	-	actinobacteria
WP_079249393.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like	1355	Streptomyces sp. IMTB 2501	GCF_001953885.1	actinobacteria
WP_079250460.1	vWA+TPRs	TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1100	Streptomyces amritsarensis	GCF_001953875.1	actinobacteria
WP_079251228.1	vWA+TIR+FxsC_Cter(partial)	vWA+TIR+FxsC_Cter(partial)*→	631	Streptomyces acidiscabies	-	actinobacteria
WP_079259908.1	vWA+APATPase+wHTH+TPRs	PNP_UDP_1+EAD2→ ?→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like	1453	Streptomyces autolyticus	GCA_001983975.1	actinobacteria
WP_079273265.1	vWA+TPRs	TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1093	Streptomyces sp. TN58	GCF_001941845.1	actinobacteria
WP_079277810.1	vWA+APATPase+wHTH+TPRs	AB_hydrolase→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like← CASPASE+EAD2	1351	Streptomyces sp. CB03234	GCF_001905885.1	actinobacteria
WP_079309890.1	vWA_protein	MoxR→ vWA_protein*→	501	Streptomyces sp. GKU 895	GCA_002027195.1	actinobacteria
WP_079406085.1	vWA+TPRs	TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1103	Streptomyces sp. 3211	GCF_002028385.1	actinobacteria

acc	architecture	operon	len	species	gca	taxend
WP_079406523.1	vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats	AB_hydrolase→ CASPASE+VMAP-M0+VMAP-C→ MoxR→ vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats*→	1196	Streptomyces sp. 3211	GCF_002028385.1	actinobacteria
WP_079429737.1	vWA+TPRs	TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ ?→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1347	Streptomyces katrae	GCF_002028425.1	actinobacteria
WP_079430380.1	vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats	AB_hydrolase→ ||← ?||MoxR→ vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats*→	1369	Streptomyces katrae	GCA_003814735.1	actinobacteria
WP_079660314.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→	1108	Streptomyces sp. 3124.6	GCF_900129855.1	actinobacteria
WP_079662554.1	vWA+cNMP_cyclase+Band7+HAD	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+cNMP_cyclase+Band7+HAD*→	1118	Streptomyces sp. 3124.6	GCA_900129855.1	actinobacteria
WP_079663892.1	vWA+SFII-helicase+Z1	AB_hydrolase→ CASPASE+VMAP-M2+VMAP-C→ MoxR→ vWA+SFII-helicase+Z1*→	1363	Streptomyces sp. 3124.6	-	actinobacteria
WP_079664780.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1087	Streptomyces sp. 3124.6	GCF_900129855.1	actinobacteria
WP_081104772.1	vWA+HD+RelA+TGS	AB_hydrolase→ CASPASE+VMAP-M2+VMAP-C→ MoxR→ vWA+HD+RelA+TGS*→	1124	Mycobacterium fortuitum	GCF_001570465.1	actinobacteria
WP_081219385.1	vWA+TPRs	TCAD15||Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1101	Streptomyces sp. M41(2017)	GCA_002078175.1	actinobacteria
WP_081281385.1	vWA+HD+RelA+TGS	AB_hydrolase→ CASPASE+VMAP-M2+VMAP-C→ MoxR→ vWA+HD+RelA+TGS*→	973	Mycobacterium fortuitum	-	actinobacteria
WP_081438249.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ TIR+APATPase+TPRs→ ||← METALLOPROTEASE+TPRs	1496	Frankia sp. M16386	GCF_001983105.1	actinobacteria
WP_081511557.1	vWA+TPRs	Trypco1→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ Voltage_CLC→ METALLOPROTEASE→ TIR+APATPase+wHTH+TPRs→	824	Nocardia donostiensis	-	actinobacteria
WP_081522098.1	vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats	AB_hydrolase→ CASPASE+VMAP-M0+VMAP-C→ MoxR→ vWA+Trypsin+cNMP_cyclase+CCCH(TrebleClef)+Pentapeptide_repeats*→	1196	Streptomyces sp. Sge12	GCA_002080455.1	actinobacteria
WP_081522474.1	vWA+TPRs	TCAD15||Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1132	Streptomyces sp. Sge12	GCA_002080455.1	actinobacteria
WP_081551503.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	DUF397→ Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→	1116	Streptomyces sp. B9173	-	actinobacteria
WP_081552946.1	vWA+TPRs	TCAD15||PSE→ Trypsin+HDxxH+VMAP-M0+VMAP-C→ MoxR→ vWA+TPRs*→ FXSXX-COOH→ Radical_SAM→ METALLOPROTEASE+TPRs→ TIR+APATPase+TPRs→	1107	Streptomyces sp. B9173	-	actinobacteria
WP_081656248.1	vWA+FGS-fold_domain	Trypco1→ Trypsin+EAD9→ EAD9+EAD1+VMAP-C→ MoxR→ vWA+FGS-fold_domain*→ FGS-fold_domain→ four_helix_bundle_protein→ RVT_1→	972	Fischerella sp. PCC 9431	GCF_000447295.1	cyanobacteria
WP_081692359.1	vWA+MNS+MNS	CASPASE+VMAP-M1+VMAP-C→ MoxR→ vWA+MNS+MNS*→	1255	Planktothrix agardhii	GCF_000464825.1	cyanobacteria
WP_081736412.1	vWA+APATPase+wHTH+TPRs	cNMP_cyclase+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like← cNMP_binding+HTH_Crp_2	1473	Amycolatopsis orientalis	GCF_000478275.1	actinobacteria
WP_081748187.1	vWA+FGS-fold_domain	EAD1+Trypsin→ ?→ EAD1+VMAP-C→ MoxR→ vWA+FGS-fold_domain*→ four_helix_bundle_protein→ PSE→ ?→ RVT_1→ FGS-fold_domain→	694	Leptolyngbya sp. PCC 6406	GCF_000332095.2	cyanobacteria
WP_081974155.1	vWA+CASPASE+TCAD6+cNMP_cyclase+Antibiotic_NAT	AB_hydrolase→ CASPASE+VMAP-M2+VMAP-C→ MoxR→ vWA+CASPASE+TCAD6+cNMP_cyclase+Antibiotic_NAT*→	1198	Kitasatospora phosalacinea	GCF_000717185.1	actinobacteria
WP_081976007.1	vWA+APATPase+wHTH+TPRs	cNMP_cyclase+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like← cNMP_binding+HTH_Crp_2	1458	Amycolatopsis sp. MJM2582	GCA_000754115.1	actinobacteria
WP_082114514.1	vWA+APATPase+wHTH+TPRs	cNMP_binding+HTH_Crp_2||cNMP_cyclase+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like	1424	Lechevalieria aerocolonigenes	GCF_000955955.1	actinobacteria
WP_082122179.1	vWA+APATPase+wHTH+TPRs	EAD2+EAD1→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like	1380	Frankia sp. CpI1-S	GCA_000948395.1	actinobacteria
WP_082172447.1	vWA+FGS-fold_domain	FGS-fold_domain→ ||← ?← ?||EAD4+VMAP-M3+VMAP-C→ MoxR→ vWA+FGS-fold_domain*→ ?→ FGS-fold_domain→	600	Limnoraphis robusta	GCF_000972705.2	cyanobacteria
WP_082824563.1	vWA+TPRs	VMAP-C_protein→ MoxR→ vWA+TPRs*→	696	Arthrospira platensis	-	cyanobacteria
WP_082857577.1	vWA+APATPase+wHTH+TPRs	cNMP_cyclase+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like← cNMP_binding+HTH_Crp_2	1457	Amycolatopsis regifaucium	GCA_900113515.1	actinobacteria
WP_083103842.1	vWA	EAD2+VMAP-M0+VMAP-C→ vWA*→	490	Streptomyces gilvosporeus	GCA_002082195.1	actinobacteria
WP_083255164.1	vWA+APATPase+wHTH+TPRs	cNMP_cyclase+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like← cNMP_binding+HTH_Crp_2	1470	Amycolatopsis orientalis	GCF_000943515.2	actinobacteria
WP_083401471.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs→ ||← METALLOPROTEASE+TPRs||EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs	1518	Frankia sp. EUN1h	GCF_001854645.1	actinobacteria
WP_083466592.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like← ?||EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs→ ||← METALLOPROTEASE+TPRs	1425	Kibdelosporangium sp. MJ126-NF4	GCF_000826545.1	actinobacteria
WP_083507376.1	vWA+APATPase+wHTH+TPRs	EAD2+EAD1→ EAD2+VMAP-M0+VMAP-C→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like	1390	Frankia sp. ACN1ag	GCF_001414035.1	actinobacteria
WP_083619629.1	vWA+MACRODOMAIN+GUN4+DO-GTPase2	vWA+MACRODOMAIN+GUN4+DO-GTPase2*→	1224	Planktothrix serta	GCA_900010725.1	cyanobacteria
WP_083650068.1	vWA+APATPase+wHTH+TPRs	cNMP_cyclase+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like← cNMP_binding+HTH_Crp_2	1458	Amycolatopsis sp. CB00013	GCF_001905755.1	actinobacteria
WP_084210794.1	vWA+APATPase+wHTH+TPRs	cNMP_binding+HTH_Crp_2→ ?→ cNMP_cyclase+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs	1487	Pseudonocardia acaciae	GCF_000620785.1	actinobacteria
WP_084265700.1	vWA+Pkinase+DO-GTPase2	Trypsin+VMAP-M8+VMAP-C→ MoxR→ vWA+Pkinase+DO-GTPase2*→	1099	Actinomadura macra	GCF_001552215.1	actinobacteria
WP_084555188.1	vWA+FGS-fold_domain	cNMP_cyclase+VMAP-M1+VMAP-C→ MoxR→ vWA+FGS-fold_domain*→ FGS-fold_domain→	826	Phormidium ambiguum	GCF_001904725.1	cyanobacteria
WP_084641579.1	vWA+APATPase+wHTH+TPRs	cNMP_cyclase+EAD2→ EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs||cNMP_cyclase+EAD2→ EAD2+VMAP-M0+VMAP-C→ MoxR→ TIR+APATPase+TPRs→ ||← METALLOPROTEASE+TPRs	1486	Amycolatopsis balhimycina	GCA_003947255.1	actinobacteria
WP_084749695.1	vWA+APATPase+wHTH+TPRs	cNMP_cyclase+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← FXSXX-COOH-like← cNMP_binding+HTH_Crp_2	1462	Amycolatopsis coloradensis	GCF_001953865.1	actinobacteria
WP_084763081.1	vWA+MNS+GUN4+EAD10+BetaPropeller	EAD10+VMAP-M1+VMAP-C→ MoxR→ vWA+MNS+GUN4+EAD10+BetaPropeller*→	1529	[Scytonema hofmanni] UTEX B 1581	GCF_000582685.1	cyanobacteria
WP_084896381.1	vWA+wHTH+TPRs+wHTH+TPRs+APATPase+wHTH+TPRs	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+wHTH+TPRs+wHTH+TPRs+APATPase+wHTH+TPRs*→	1788	Streptomyces sp. CB03238	GCA_002099185.1	actinobacteria
WP_084989906.1	vWA+FGS-fold_domain	HTH+VMAP-M9+VMAP-C→ MoxR→ vWA+FGS-fold_domain*→ ||← ?← ?← ?← PSE||?→ FGS-fold_domain→	964	Microcystis aeruginosa	GCA_002095975.1	cyanobacteria
WP_085207283.1	vWA+REase+cNMP_cyclase+CASPASE	AB_hydrolase→ CASPASE+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+REase+cNMP_cyclase+CASPASE*→	1172	Streptomyces sp. Amel2xC10	GCA_900177255.1	actinobacteria
WP_085214149.1	vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+wHTH+TPRs+cNMP_cyclase+Band7+HAD*→	1501	Streptomyces sp. Amel2xC10	GCA_900177255.1	actinobacteria
WP_085564588.1	vWA+Pkinase+cNMP_cyclase+Band7+HAD	Trypco1→ Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+cNMP_cyclase+Band7+HAD*→	1308	Streptomyces griseofuscus	GCA_002114065.1	actinobacteria

acc	architecture	operon	len	species	gca	taxend
WP_085923529.1	vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)	Trypco1→ Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+ParA-Soj-PloopNTPase(SIMIBI)*→	1127	Streptomyces platensis	-	actinobacteria
WP_085983492.1	vWA+APATPase+wHTH+TPRs	EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+wHTH+TPRs*→ ||← METALLOPROTEASE+TPRs← cNMP_cyclase+EAD2	1336	Saccharothrix espanaensis	GCF_000328705.1	actinobacteria
WP_086560182.1	vWA+APATPase+GGDEF+EAD2+VMAP-M0+VMAP-C	Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+APATPase+GGDEF+EAD2+VMAP-M0+VMAP-C*→	1327	Streptomyces africanus	GCF_002150735.1	actinobacteria
WP_086706666.1	vWA+TIR+cNMP_cyclase+S1COLD+EAD2	AB_hydrolase→ CASPASE+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+TIR+cNMP_cyclase+S1COLD+EAD2*→	1102	Streptomyces castelarensis	GCF_002154275.1	actinobacteria
WP_089154134.1	vWA+Trypsin+Coiled-coil	Trypco1+Trypsin+VMAP-M0+VMAP-C→ MoxR→ vWA+Trypsin+Coiled-coil*→ Glyco_hydro_16+Ricin_B_lectin→ ||← ?||?→ DUF397→	1004	Micromonospora sp. NBS 11-29	GCF_002140155.1	actinobacteria
WP_096617002.1	vWA+REC+CASPASE+FGS-fold_domain	EAD1+Trypsin→ ?→ EAD1+VMAP-M1+VMAP-C→ ||← ?||VMAP-C(partial)→ MoxR→ vWA+REC+CASPASE+FGS-fold_domain*→	1263	Calothrix sp. NIES-4101	GCA_004296455.1	cyanobacteria
WP_097965258.1	vWA+Pkinase+APATPase+TPRs	Trypsin+EAD2+VMAP-M0+VMAP-C→ MoxR→ vWA+Pkinase+APATPase+TPRs*→	1310	Streptomyces sp. or20	GCF_002551305.1	actinobacteria
WP_098754349.1	vWA+Pkinase+Pkinase+TPRs	vWA+Pkinase+Pkinase+TPRs*→	1734	Streptomyces sp. Ru87	GCA_002573955.1	actinobacteria
WP_100179620.1	vWA+REC+REC+GAF+GAF+GAF+Acylphosphatase+CASPASE	AB_hydrolase→ CASPASE+VMAP-M4+VMAP-C→ MoxR→ vWA+REC+REC+GAF+GAF+GAF+Acylphosphatase+CASPASE*→	1802	Bradyrhizobium sp. TSA1	GCA_002776695.1	alphaproteobacteria

iSTAND ternary systems

acc	architecture	operon	len	species	gca	taxend
ABG51300.1	iSTAND	iSTAND*→ MoxR→ TM+TM+vWA+TM+TM+TM+TM+TM+TM→	378	Trichodesmium erythraeum IMS101	GCA_000014265.1	cyanobacteria
ACC83829.1	EAD9+iSTAND	CASPASE+EAD9→ EAD9+iSTAND*→ STAND_NTPase→ MoxR(fragment)→ helical_region(leucine-richLWxKmotif)+vWA→??+REC→ GUN4→	326	Nostoc punctiforme PCC 73102	GCA_000020025.1	cyanobacteria
ACK70921.1	HTH+iSTAND	TM||HTH+iSTAND*→ MoxR→ helical_region(leucine-richLWxKmotif)+vWA→	416	Gloeothece citriformis PCC 7424	GCA_000021825.1	cyanobacteria
AEE50346.1	EAD11+iSTAND	TM+TM+TM+TM+STAND_NTPase+TM+TM+TM+TM→||←STAND_NTPase+REase←TM||HTH→ PIN+DUF3368→ EAD11+iSTAND*→ MoxR→||←vWA←??+beta-sandwich(Ig-like?)	356	Haliscomenobacter hydrossis DSM 1100	GCA_000212735.1	bacteroidetes
AEE54384.1	CASPASE+iSTAND	CASPASE+iSTAND*→ MoxR→ vWA+??+FGS-fold_domain+FGS-fold_domain+FGS-fold_domain+FGS-fold_domain→	548	Haliscomenobacter hydrossis DSM 1100	GCA_000212735.1	bacteroidetes
AEJ01436.1	TIR+iSTAND	TIR+iSTAND*→ MoxR→ TM+TM+vWA+TM+FGS-fold_domain→	436	Nitrosomonas sp. Is79A3	GCA_000219585.1	betaproteobacteria
AFY52644.1	Trypsin+iSTAND	Trypco1→ Trypsin+iSTAND*→ MoxR→ helical_region(leucine-richLWxKmotif)+vWA→ vWA+FGS-fold_domain→	504	Rivularia sp. PCC 7116	GCA_000316665.1	cyanobacteria
AFZ01471.1	CASPASE+iSTAND	CASPASE+iSTAND*→ STAND_NTPase(fragment)→	527	Calothrix sp. PCC 6303	GCA_000317435.1	cyanobacteria
AFZ27597.1	Coiled-coil+iSTAND	CASPASE+EAD9→ Coiled-coil+iSTAND*→	335	Cylindrospermum stagnale PCC 7417	GCA_000317535.1	cyanobacteria
AOY79837.1	Coiled-coil+iSTAND	Coiled-coil+iSTAND*→ MoxR→ helical_region(leucine-richLWxKmotif)+TM+Calx-beta?+TM+vWA→	342	Moorea producens JHB	GCA_001854205.1	cyanobacteria
ATY32529.1	Trypsin+iSTAND	rve_3→ Trypsin+iSTAND*→ MoxR→	494	Sphingomonas sp. Cra20	GCA_002796605.1	alphaproteobacteria
AUB37286.1	EAD9+iSTAND	EAD9+iSTAND*→ MoxR→ helical_region(leucine-richLWxKmotif)+vWA→??+TM→ CASPASE(fragment)→	328	Nostoc flagelliforme CCNUN1	GCA_002813575.1	cyanobacteria
BAI89278.1	Coiled-coil+iSTAND	SLH+OprB→||←TM||RadC-like_JAB+sGTPase→ Coiled-coil+iSTAND*→ MoxR→ helical_region(leucine-richLWxKmotif)+vWA→ TA_antitoxin(DUF1902)→ Ntox45→ HEPN→	630	Arthrospira platensis NIES-39	GCA_000210375.1	cyanobacteria
BAY12344.1	EAD9+iSTAND	EAD9+iSTAND*→ MoxR→ helical_region(leucine-richLWxKmotif)+vWA→ Cation_ATPase→ Calcineurin→	322	Calothrix sp. NIES-2098	GCA_002368175.1	cyanobacteria
BAY13982.1	Coiled-coil+iSTAND	Coiled-coil+iSTAND*→ MoxR→ helical_region(leucine-richLWxKmotif)+TM+Calx-beta?+TM+vWA→ vWA+FGS-fold_domain→	341	Calothrix sp. NIES-2098	GCA_002368175.1	cyanobacteria
BAY41492.1	iSTAND	Pentapeptide_repeats+TM+TM+TM+TM+TM+TM+TM+Pentapeptide_repeats→ Pentapeptide_repeats→ STNAD_NTPase+TM+TM+TM+TM+TM+TM+TM→ iSTAND*→ MoxR→ TM+TM+vWA→||←DDE_endonuclease←PAIREDC-HTH||beta-rich_jelly-roll?→	359	Nostoc sp. NIES-2111	GCA_002368215.1	cyanobacteria
BAY43400.1	iSTAND	iSTAND*→ MoxR→ helical_region(leucine-richLWxKmotif)+vWA→ TM+Pentapeptide_repeats+TM+TM+TM+TM+TM+TM+TM+Pentapeptide_repeats→||←TM+TM+TM+TM+TM	312	Scytonema sp. HK-05	GCA_002368235.1	cyanobacteria
BAZ19856.1	EAD8+iSTAND	EAD8+Trypsin→ EAD8+iSTAND*→ MoxR→ helical_region(leucine-richLWxKmotif)+vWA→ REase→ vWA+GTPase-AIG→	361	Scytonema sp. NIES-4073	GCA_002368435.1	cyanobacteria
BAZ48964.1	HTH+iSTAND	HTH+iSTAND*→ MoxR→ helical_region(leucine-richLWxKmotif)+vWA→	383	Nostoc sp. NIES-4103	GCA_002368335.1	cyanobacteria
BBD55736.1	??+HTH+iSTAND	??+HTH+iSTAND*→ MoxR→ helical_region(leucine-richLWxKmotif)+vWA→	431	Planktothrix agardhii NIES-204	GCA_003609755.1	cyanobacteria
CAL77009.1	Trypsin+iSTAND	Trypco2→ Trypsin+iSTAND*→ MoxR→2TM+vWA+22TM→??+TM→??→	499	Bradyrhizobium sp. ORS 278	GCA_000026145.1	alphaproteobacteria
CBS89362.1	Trypsin+iSTAND	Trypco2→ Trypsin+iSTAND*→ MoxR→2TM+vWA+22TM→	501	Azospirillum lipoferum 4B	GCA_000283655.1	alphaproteobacteria
CUR12819.1	Death-like.bact-prob+iSTAND	Death-like.bact-prob+iSTAND*→ MoxR→ helical_region(leucine-richLWxKmotif)+vWA→ vWA+TPRs+CASPASE→??→	368	Planktothrix paucivesiculata PCC 9631	GCA_900009265.1	cyanobacteria
CUR34706.1	HTH+iSTAND	HTH+iSTAND*→ MoxR→ helical_region(leucine-richLWxKmotif)+vWA→	342	Planktothrix tepida PCC 9214	GCA_900009145.1	cyanobacteria
CUS33832.1	TIR+iSTAND	DUF805(3TM_protein)→??→ DUF805(3TM_protein)→ TM+TM+TM→ TIR+iSTAND*→ MoxR→ TM+TM+vWA+TM+TM→	463	Candidatus Nitrospira nitrosa	GCA_001458735.1	nitrospirae
EAZ90085.1	CASPASE+VMAP-M11	AB_hydrolase→ CASPASE+VMAP-M11*→ MoxR→ helical_region(leucine-richLWxKmotif)+vWA→ vWA+FGS-fold_domain→	553	Crocosphaera chwakensis CCY0110	GCA_000169335.1	cyanobacteria
EDN69714.1	iSTAND	PNP_UDP_1→ PNP_UDP_1(fragment)→ iSTAND*→ HTH→ MoxR→	199	Beggiatoa sp. PS	GCA_000170715.1	gammaproteobacteria
EDX78652.1	HTH+iSTAND	TM||HTH+iSTAND*→ MoxR→	363	Coleofasciculus chthonoplastes PCC 7420	GCA_000155555.1	cyanobacteria
EKD10616.1	Coiled-coil+iSTAND	SLH+OprB→ RadC-like_JAB+sGTPase→ Coiled-coil+iSTAND*→ MoxR→ helical_region(leucine-richLWxKmotif)+vWA→ TA_antitoxin(DUF1902)→ HicA_toxin→ Ntox45→	622	Arthrospira platensis C1	GCA_000307915.1	cyanobacteria
EKE99441.1	Coiled-coil+iSTAND	TM+DUF218→||←??←??||Coiled-coil+iSTAND*→ MoxR→	327	Tolypothrix sp. PCC 7601	GCA_000300115.1	cyanobacteria
EKF00758.1	HTH+STAND_NTPase+macroglobulin-like+CASPASE+??	HTH+STAND_NTPase+macroglobulin-like+CASPASE+??*→ CASPASE→ Pkinase+STAND_NTPase+macroglobulin-like+CASPASE→ CASPASE→ Coiled-coil→	1058	Tolypothrix sp. PCC 7601	GCA_000300115.1	cyanobacteria
ERN41330.1	iSTAND	??→ iSTAND*→ MoxR→ TM+TM+vWA+TM→	371	Rubidibacter lacunae KORDI 51-2	GCA_000473895.1	cyanobacteria

acc	architecture	operon	len	species	gca	taxend
ERN41366.1	CASPASE+iSTAND	←Trypco1||CASPASE+iSTAND*→ MoxR→ helical_region(leucine-richLWxKmotif)+vWA→ BetaPropeller+TPRs+FGE-sulfatase→ FGS-fold_domain→	516	Rubidibacter lacunae KORDI 51-2	GCA_000473895.1	cyanobacteria
ETR67316.1	DRHyd+iSTAND	DRHyd+iSTAND*→??→ GspA-ATPase(fragment)→	370	Candidatus Magnetoglobus multicellularis str. Araruama	GCA_000516475.1	deltaproteobacteria
ETR67363.1	DRHyd+iSTAND	DRHyd+iSTAND*→ MoxR→	409	Candidatus Magnetoglobus multicellularis str. Araruama	GCA_000516475.1	deltaproteobacteria
ETR68943.1	iSTAND(fragment)	iSTAND(fragment)*→??→??→	131	Candidatus Magnetoglobus multicellularis str. Araruama	GCA_000516475.1	deltaproteobacteria
ETR70369.1	TIR+iSTAND	TIR+iSTAND*→	434	Candidatus Magnetoglobus multicellularis str. Araruama	GCA_000516475.1	deltaproteobacteria
ETR71372.1	ZnR+ZnR+TIR+iSTAND	STNAD_NTPase+REase7→ ZnR+ZnR+TIR+iSTAND*→ MoxR→	493	Candidatus Magnetoglobus multicellularis str. Araruama	GCA_000516475.1	deltaproteobacteria
EXI79137.1	TIR+iSTAND	TIR+iSTAND*→ MoxR→ TM+TM→ vWA+TIR→ TM+FGS-fold_domain→	471	Candidatus Accumulibacter sp. BA-92	GCA_000585055.1	betaproteobacteria
GAK59821.1	TIR+iSTAND	TIR+iSTAND*→ GspA-ATPase(fragment)→ Ploop_inactive→	455	Candidatus Vecturithrix granuli	GCA_000739535.1	bacteria
GBF81152.1	HTH+iSTAND	HTH+iSTAND*→ MoxR→	411	Aphanothece sacrum FPU1	GCA_003864295.1	cyanobacteria
GCE31429.1	wHTH+TPRs+STAND_NTPase+wHTH+TPRs	wHTH+TPRs+STAND_NTPase+wHTH+TPRs*→	1250	Dictyobacter alpinus	GCA_003967575.1	chloroflexi
KEI68398.1	??+HTH+iSTAND	??+HTH+iSTAND*→ MoxR→ vWA+FGE-sulfatase→	429	Planktothrix agardhii NIVA-CYA 126/8	GCA_000710505.1	cyanobacteria
KFB67381.1	iSTAND	iSTAND*→ MoxR→	283	Candidatus Accumulibacter sp. SK-01	GCA_000584955.2	betaproteobacteria
KHD04797.1	Coiled-coil+iSTAND	Coiled-coil+iSTAND*→	252	Candidatus Thiomargarita nelsonii	-	gammaproteobacteria
KIF23001.1	iSTAND	iSTAND*→ MoxR→??→	255	Aphanocapsa montana BDHKU210001	GCA_000817745.1	cyanobacteria
KIF28928.1	EAD9+iSTAND	EAD9+iSTAND*→ MoxR→??→	330	Hassallia byssoidea VB512170	GCA_000817785.1	cyanobacteria
KIF42870.1	EAD9+iSTAND	TM+TM+TM+TM+TM→ EAD9+iSTAND*→	261	Lyngbya confervoides BDU141951	GCA_000817775.1	cyanobacteria
KIJ79200.1	DRHyd+iSTAND	cyclic_phosphodiesterase→ OppC_N+TM+BPD_transp_1→ DRHyd+iSTAND*→	401	Tolypothrix campylonemoides VB511288	GCA_000828075.2	cyanobacteria
KPA09311.1	TM+TM+iSTAND	TM+TM+iSTAND*→	338	Candidatus Magnetomorum sp. HK-1	GCA_001292585.1	deltaproteobacteria
KPA11637.1	DRHyd+iSTAND	DRHyd+iSTAND*→	345	Candidatus Magnetomorum sp. HK-1	GCA_001292585.1	deltaproteobacteria
KPA12577.1	iSTAND	iSTAND*→ MoxR→??+FGE-sulfatase→	212	Candidatus Magnetomorum sp. HK-1	GCA_001292585.1	deltaproteobacteria
KPA12842.1	TIR+iSTAND	TIR+iSTAND*→ STAND_NTPase→	447	Candidatus Magnetomorum sp. HK-1	GCA_001292585.1	deltaproteobacteria
KPA13794.1	TM+TM+iSTAND	TM+TM+iSTAND*→ MoxR→	338	Candidatus Magnetomorum sp. HK-1	GCA_001292585.1	deltaproteobacteria
KPA15048.1	iSTAND	iSTAND*→ MoxR→||←tRNA_anti-codon+tRNA-synt_2||REC+PAS+NtrC-AAA+FIS-HTH→ REC+cNMP_cyclase→ HAM→	264	Candidatus Magnetomorum sp. HK-1	GCA_001292585.1	deltaproteobacteria
KPA15524.1	iSTAND(fragment)	Nucleoside_deoxyribosyltransferas?→ iSTAND(fragment)*→	160	Candidatus Magnetomorum sp. HK-1	GCA_001292585.1	deltaproteobacteria
KPA17452.1	ZnR+ZnR+TIR+iSTAND	ZnR+ZnR+TIR+iSTAND*→ MoxR→ TM+TM+vWA+TM+FGS-fold_domain→	522	Candidatus Magnetomorum sp. HK-1	GCA_001292585.1	deltaproteobacteria
KPA18269.1	TIR+iSTAND	TIR+iSTAND*→ MoxR→ TM+TM+vWA+TM+PEGA+PEGA+FGS-fold_domain→	466	Candidatus Magnetomorum sp. HK-1	GCA_001292585.1	deltaproteobacteria
KPQ40050.1	Coiled-coil+iSTAND	Coiled-coil+iSTAND*→ MoxR→ helical_region(leucine-richLWxKmotif)+vWA→	570	Phormidium sp. OSCR	GCA_001314905.1	cyanobacteria
KPQ40445.1	CASPASE+iSTAND	←Trypco1||CASPASE+iSTAND*→ MoxR→ helical_region(leucine-richLWxKmotif)+vWA→ vWA+FGS-fold_domain→	524	Phormidium sp. OSCR	GCA_001314905.1	cyanobacteria
KPV52199.1	Coiled-coil+iSTAND	STAND_NTPase→ Coiled-coil+iSTAND*→ STAND_NTPase→	358	Kouleothrix aurantiaca	GCA_001399705.1	chloroflexi
KRB42991.1	Coiled-coil+iSTAND	CASPASE→ Coiled-coil+iSTAND*→ MoxR→ helical_region(leucine-richLWxKmotif)+vWA→ CASPASE+Pkinase→	309	Terrabacter sp. Root181	GCA_001428505.1	actinobacteria

acc	architecture	operon	len	species	gca	taxend
KST64486.1	CASPASE+iSTAND	??+Coiled-coil+TM+TM←??||CASPASE+APATPase+wTHT+TPR→ CASPASE+iSTAND*→ MoxR→ helical_region(leucine-richLWxKmotif)+vWA→	525	Mastigocoleus testarum BC008	GCA_001456025.1	cyanobacteria
KXU90039.1	TIR+iSTAND	DUF805(3TM_protein)→ TM+TM+TM→ TIR+iSTAND*→ MoxR→ TM+TM+vWA+TM+TM→??→??→||←??	457	Paraburkholderia monticola	GCA_001580545.1	betaproteobacteria
KYC36464.1	Coiled-coil+iSTAND	Coiled-coil+iSTAND*→	290	Scytonema hofmannii PCC 7110	GCA_000346485.2	cyanobacteria
KYC38261.1	iSTAND	PNP_UDP_1+EAD9→ iSTAND*→ MoxR→ helical_region(leucine-richLWxKmotif)+vWA+FGS-fold_domain→	304	Scytonema hofmannii PCC 7110	GCA_000346485.2	cyanobacteria
KYC41250.1	EAD9+iSTAND	EAD9+iSTAND*→ MoxR→ helical_region(leucine-richLWxKmotif)+vWA→??+CHASE+TM+TM→	326	Scytonema hofmannii PCC 7110	GCA_000346485.2	cyanobacteria
KYC44054.1	BetaPropeller+iSTAND	BetaPropeller+iSTAND*→	317	Scytonema hofmannii PCC 7110	GCA_000346485.2	cyanobacteria
OCQ92168.1	??+HTH+iSTAND	??→??+HTH+iSTAND*→ MoxR→	433	Oscillatoriales cyanobacterium USR001	GCA_001698425.1	cyanobacteria
OCQ93508.1	Death-like.bact-prob+iSTAND	??+Death-like-bact-prob+Trypsin→??→ Death-like.bact-prob+iSTAND*→ MoxR→ helical_region(leucine-richLWxKmotif)+vWA→	442	Nostoc sp. MBR 210	GCA_001698435.1	cyanobacteria
OCQ97673.1	HTH+iSTAND	HTH+iSTAND*→ MoxR→ helical_region(leucine-richLWxKmotif)+vWA→??+CASPASE→	355	Nostoc sp. MBR 210	GCA_001698435.1	cyanobacteria
OCR02031.1	EAD1+CASPASE+iSTAND	EAD1+CASPASE+iSTAND*→ MoxR→ helical_region(leucine-richLWxKmotif)+vWA→ vWA+EAD1-unk5+CASPASE→	616	Oscillatoriales cyanobacterium USR001	GCA_001698425.1	cyanobacteria
OCR02802.1	HTH+iSTAND	HTH+iSTAND*→ MoxR→	429	Oscillatoriales cyanobacterium USR001	GCA_001698425.1	cyanobacteria
OCR02924.1	CASPASE+iSTAND	CASPASE+iSTAND*→ MoxR→ helical_region(leucine-richLWxKmotif)+vWA→ Ntox45→ HEPN→??→	546	Oscillatoriales cyanobacterium USR001	GCA_001698425.1	cyanobacteria
ODH02967.1	EAD1+VMAP-M1+iSTAND	EAD1+VMAP-M1+iSTAND*→ MoxR→ helical_region(leucine-richLWxKmotif)+vWA→ TM+sGTPase→	471	Nostoc sp. KVJ20	GCA_001712795.1	cyanobacteria
ODN56964.1	HTH+iSTAND	HTH+iSTAND*→ MoxR→ helical_region(leucine-richLWxKmotif)+vWA→ vWA+FGS-fold_domain→	377	Scytonema millei VB511283	GCA_000817735.2	cyanobacteria
OEJ75068.1	iSTAND	iSTAND*→ MoxR→ helical_region(leucine-richLWxKmotif)+vWA+FGS-fold_domain→ Four-helical-protein→ RVT→	333	Desertifilum sp. IPPAS B-1220	GCA_001746915.1	cyanobacteria
OJY86315.1	DRHyd+iSTAND	??||DRHyd+iSTAND*→ MoxR→ TM+TM+beta-sandwich(Ig-like?)+vWA+TM+??+LRRs?→ TM+ATP-synt_A→ TM+TM→ ATP-synt_B→	388	Sphingobacteriales bacterium 40-81	GCA_001899605.1	bacteroidetes
OKH60575.1	??+iSTAND	pJV1-spdB3?→ cNMP_cyclase→??+iSTAND*→ MoxR→ helical_region(leucine-richLWxKmotif)+vWA→ vWA+FGS-fold_domain→	347	Scytonema sp. HK-05	GCA_001904675.1	cyanobacteria
OLT60416.1	Trypsin+iSTAND	Trypsin+iSTAND*→ MoxR→ helical_region(leucine-richLWxKmotif)+vWA→	454	Moorea bouillonii PNG	GCA_001942495.1	cyanobacteria
ONN59423.1	Death-like.bact-prob+iSTAND	Death-like-bact-prob+Trypsin→??→ Death-like.bact-prob+iSTAND*→ MoxR→	369	Mastigocladus laminosus UU774	-	cyanobacteria
OQP57790.1	TIR+HATPase?	TIR+HATPase?*→ MoxR→ TM+beta-sandwich(Ig-like?)+TM+vWA+TM+??→	419	Niastella vici	GCA_002077945.1	bacteroidetes
OQW38836.1	TIR+iSTAND	TIR+iSTAND*→ MoxR→ TM→ TM+vWA+TM+FGS-fold_domain→	421	Proteobacteria bacterium SG_bin4	GCA_002083395.1	proteobacteria
OQX97257.1	iSTAND	TIR→ iSTAND*→ MoxR→ Coiled-coil+??→??+DrHyd+APATPase+wHTH+TPR→ TPRs→	298	Bacteroidetes bacterium 4572_128	GCA_002084355.1	bacteroidetes
OWY22263.1	TIR+iSTAND	TIR+iSTAND*→ MoxR→ TM+beta-sandwich(Ig-like?)+TM+vWA+TM+TM+TPRs+BetaPropeller→ ZnR→||←TM||MazG+MazG→	431	Sphingobacteriales bacterium TSM_CSS	GCA_002212985.1	bacteroidetes
PAX57114.1	EAD9+iSTAND	CASPASE+EAD9→ EAD9+iSTAND*→ MoxR(fragment)→	334	Calothrix elsteri CCALA 953	GCA_002289455.1	cyanobacteria
PHI20256.1	EAD11+iSTAND	EAD11+iSTAND*→ MoxR→ beta-sandwich(Ig-like?)+TM+vWA+TM+OmpA→	394	Lewinellaceae bacterium SD302	GCA_002591745.1	bacteroidetes
PKO80078.1	DRHyd+iSTAND	DRHyd+iSTAND*→ MoxR→ vWA→??+TIR+CASPASE→	450	Betaproteobacteria bacterium HGW-Betaproteobacteria-13	GCA_002842325.1	betaproteobacteria
PNK01636.1	Trypsin+iSTAND	Trypco1→ Trypsin+iSTAND*→ MoxR→	503	Cylindrospermopsis raciborskii S07	GCA_002893205.1	cyanobacteria
PSB54106.1	EAD1+CASPASE+iSTAND	EAD1+CASPASE+iSTAND*→ MoxR→	621	filamentous cyanobacterium Phorm 6	GCA_003003725.1	cyanobacteria
PSM31871.1	Coiled-coil??+iSTAND	Coiled-coil??+iSTAND*→ MoxR→ helical_region(leucine-richLWxKmotif)+vWA→??→ EAD7+EAD7+EAD7+EAD7+VWA→||←??	340	Haliangium sp. UPWRP_2	GCA_002212765.2	deltaproteobacteria
PSN17482.1	iSTAND	iSTAND*→ MoxR→ helical_region(leucine-richLWxKmotif)+vWA→ Coiled-coil→	237	filamentous cyanobacterium CCP5	GCA_003017785.1	cyanobacteria
PSR11591.1	EAD11+iSTAND	EAD11+iSTAND*→ MoxR→ TM+beta-rich_region+TM+vWA→	374	Bacteroidetes bacterium	GCA_003023605.1	bacteroidetes
PZN72517.1	TIR+iSTAND	TIR+iSTAND*→ MoxR→	467	Candidatus Methyloumidiphilus alinensis	GCA_003242955.1	gammaproteobacteria
PZN77012.1	iSTAND	??→ iSTAND*→ MoxR→ TM+TM+vWA+TM+FGE-sulfatase→	325	Candidatus Methyloumidiphilus alinensis	GCA_003242955.1	gammaproteobacteria
PZN82957.1	EAD9+iSTAND	DrHyd+EAD9→ EAD9+iSTAND*→ MoxR→ helical_region(leucine-richLWxKmotif)+vWA→	344	Candidatus Methyloumidiphilus alinensis	GCA_003242955.1	gammaproteobacteria
RAM51670.1	HTH+iSTAND	HTH+iSTAND*→ MoxR→	354	Hapalosiphonaceae cyanobacterium JJU2	GCA_003261315.1	cyanobacteria
RIJ88564.1	Trypsin+iSTAND	Trypco1→ Trypsin+iSTAND*→	335	Candidatus Brocadia sp.	GCA_003577195.1	planctomycetes

acc	architecture	operon	len	species	gca	taxend
RKW05163.1	Ploop_NTPase(RecA-like?)	HTH+DDE_transposase→ STAND_NTPase→ Ploop_NTPase(RecA-like?)*→	191	Capnocytophaga sp.	GCA_003638885.1	bacteroidetes
RKZ39497.1	iSTAND	iSTAND*→	257	Gammaproteobacteria bacterium	GCA_003645185.1	gammaproteobacteria
RKZ83713.1	Trypsin+iSTAND	??→ Trypco1→||←??||Trypsin+iSTAND*→ MoxR→ HTH→	512	Gammaproteobacteria bacterium	GCA_003646175.1	gammaproteobacteria
RKZ89871.1	iSTAND	HTH→||←??||iSTAND*→ DUF4065→??→ MoxR→	358	Gammaproteobacteria bacterium	GCA_003645315.1	gammaproteobacteria
RKZ91146.1	TM+TM+iSTAND	TM+TM+iSTAND*→	318	Gammaproteobacteria bacterium	GCA_003646175.1	gammaproteobacteria
RKZ93584.1	CASPASE+iSTAND	EAD-unk2→ CASPASE+iSTAND*→ HTH→ MoxR→??→??+DUF4351→	447	Gammaproteobacteria bacterium	GCA_003646175.1	gammaproteobacteria
RMF22456.1	Coiled-coil+iSTAND(fragment)	Coiled-coil+iSTAND(fragment)*→	158	Bacteroidetes bacterium	GCA_003695465.1	bacteroidetes
RMF26839.1	iSTAND(fragment)	iSTAND(fragment)*→ MoxR→ TM+beta-sandwich(Ig-like?)→	239	Bacteroidetes bacterium	GCA_003695465.1	bacteroidetes
RMG26468.1	CASPASE+iSTAND	??||CASPASE+iSTAND*→ TM+TM+vWA+??+BetaPropeller→	491	Bacteroidetes bacterium	GCA_003696835.1	bacteroidetes
RMG30280.1	CASPASE+iSTAND	REC+Alkaline_phosphatase-like→ CASPASE+iSTAND*→??→ Radical_SAM→	495	Bacteroidetes bacterium	GCA_003696835.1	bacteroidetes
RMG84230.1	EAD11+iSTAND	EAD11+iSTAND*→ STAND(fragment)→	354	Bacteroidetes bacterium	GCA_003696485.1	bacteroidetes
SAL85251.1	Trypsin+iSTAND	Trypco2→ Trypsin+iSTAND*→ MoxR→ TM+LRRs→	535	Caballeronia choica	GCA_001544535.2	betaproteobacteria
SEB22698.1	TIR+iSTAND	TIR+iSTAND*→ MoxR→ TM+TM+vWA+BetaPropeller+PASTA→	439	Variovorax sp. YR216	GCA_900107745.1	betaproteobacteria
SEH05005.1	??+CASPASE+iSTAND	PseudoU_synth||??→??+CASPASE+iSTAND*→	718	Thiotrichales bacterium HS_08	GCA_900099115.2	gammaproteobacteria
SEH05860.1	Trypsin+iSTAND	Trypsin+iSTAND*→	341	Thiotrichales bacterium HS_08	GCA_900099115.2	gammaproteobacteria
WP_017306429.1	??+iSTAND	??+iSTAND*→ MoxR→ helical_region(leucine-richLWxKmotif)+vWA→ TM→||←Y1_Tnp	401	Spirulina subsalsa	GCF_000314005.1	cyanobacteria
WP_017318743.1	EAD9+iSTAND	EAD9+iSTAND*→ MoxR→ helical_region(leucine-richLWxKmotif)+vWA→	324	Mastigocladopsis repens	GCF_000315565.1	cyanobacteria
WP_017660035.1	CASPASE+iSTAND	NTP_transferase→ BetaPropeller+AB_hydrolase→||←Trypco1||CASPASE+iSTAND*→ MoxR→ helical_region(leucine-richLWxKmotif)+vWA→||←HicB_lk_antitox||vWA+FGS-fold_domain→ FGS-fold_domain→	520	Geitlerinema sp. PCC 7105	GCF_000332355.1	cyanobacteria
WP_018400346.1	HTH+iSTAND	HTH+iSTAND*→ MoxR→ helical_region(leucine-richLWxKmotif)+vWA→	377	filamentous cyanobacterium ESFC-1	GCF_000380225.1	cyanobacteria
WP_018401004.1	??+iSTAND	NfeD||??→??+iSTAND*→ MoxR→	399	filamentous cyanobacterium ESFC-1	GCF_000380225.1	cyanobacteria
WP_019493547.1	Coiled-coil+iSTAND	Coiled-coil+iSTAND*→ MoxR→ helical_region(leucine-richLWxKmotif)+vWA+FGS-fold_domain→	304	Calothrix sp. PCC 7103	GCF_000331305.1	cyanobacteria
WP_020531248.1	TIR+iSTAND	TIR+iSTAND*→ MoxR→	437	Flexithrix dorotheae	GCF_000379765.1	bacteroidetes
WP_020536784.1	EAD11+iSTAND	EAD11+iSTAND*→ MoxR→??+beta-sandwich(Ig-like?)+TM+vWA+TM+FGE-sulfatase→||←TPRs	363	Lewinella cohaerens	GCF_000379805.1	bacteroidetes
WP_020569053.1	EAD11+iSTAND	EAD11+iSTAND*→ MoxR→	379	Lewinella persica	GCF_000373105.1	bacteroidetes
WP_020569756.1	Coiled-coil+iSTAND	Coiled-coil+iSTAND*→ MoxR→ TM+TM+??TM+??+CASPASE→	361	Lewinella persica	GCF_000373105.1	bacteroidetes
WP_026722524.1	iSTAND	TIR→ iSTAND*→ MoxR→ helical_region(leucine-richLWxKmotif)+vWA→	276	Fischerella sp. PCC 9431	GCF_000447295.1	cyanobacteria
WP_028091549.1	EAD9+iSTAND	EAD9+iSTAND*→ MoxR→ TM+TM+??+Amidase→ RVT→	356	Dolichospermum circinale	GCF_000426905.1	cyanobacteria
WP_028158837.1	TIR+iSTAND	TIR+iSTAND*→ MoxR→ TM+TM+vWA+TM+Sel1→??→	453	Bradyrhizobium japonicum	GCF_000472745.1	alphaproteobacteria
WP_028668053.1	CASPASE+iSTAND	CASPASE+iSTAND*→ MoxR→ vWA→ CASPASE+LRRs→ SUI→??→	647	Runella zeae	GCF_000423565.1	bacteroidetes
WP_038297199.1	EAD9+iSTAND	EAD9+iSTAND*→ MoxR→ helical_region(leucine-richLWxKmotif)+vWA→	327	[Scytonema hofmanni] UTEX B 1581	GCF_000582685.1	cyanobacteria
WP_047155941.1	Death-like.bact-prob+iSTAND	-	369	Trichodesmium erythraeum	-	cyanobacteria
WP_052486108.1	TIR+iSTAND	TIR+iSTAND*→ MoxR→	427	Scytonema tolypothrichoides	GCF_000828085.2	cyanobacteria
WP_061996503.1	Pkinase+STAND_NTPase+wHTH+TPRs+GGDEF	Pkinase+STAND_NTPase+wHTH+TPRs+GGDEF*→	1806	Clostridium sp. ATCC 25772	GCF_001573875.1	firmicutes
WP_066426097.1	??+iSTAND	??+iSTAND*→ MoxR→ helical_region(leucine-richLWxKmotif)+vWA→	386	Anabaena sp. 4-3	GCF_001597745.1	cyanobacteria
WP_071187406.1	EAD9+iSTAND	Trypco1→ Trypsin+EAD9→ EAD9+iSTAND*→ MoxR→ helical_region(leucine-richLWxKmotif)+vWA→7TMR-HDED+Beta-rich+HTH+FGS-fold_domain→	339	Trichormus sp. NMC-1	GCF_001858025.1	cyanobacteria
WP_072720293.1	??+iSTAND	??+iSTAND*→ MoxR→ vWA→||←Y1_Tnp||HTH+RNase_H+ZnR→ FGS-fold_domain→	403	Planktothrix tepida	-	cyanobacteria
WP_081755753.1	DRHyd+iSTAND	DRHyd+iSTAND*→ MoxR→ vWA→??+TIR+APATPase+TPRs+Pentapeptide_repeats→	428	Desulfovibrio magneticus	GCF_000526455.1	deltaproteobacteria
WP_081881197.1	Coiled-coil+Ploop_NTPase	Coiled-coil+Ploop_NTPase*→ REase→||←SLOG||??→ TM→ DUF262+??+DUF1524(HNH?)→	644	Ghiorsea bivora	GCF_000744415.1	zetaproteobacteria
WP_081968917.1	CASPASE+iSTAND	CASPASE+iSTAND*→ MoxR→ vWA→??+SGNH_hydrolase+CASPASE→	698	Phaeodactylibacter xiamenensis	GCF_000759025.1	bacteroidetes
WP_084170174.1	wHTH+STAND_NTPase	METHYLASE→||←TM+Cupin+AraC-HTH+AraC-HTH||AB_hydrolase→ wHTH+STAND_NTPase*→	664	Paraburkholderia ferrariae	GCF_000685035.1	betaproteobacteria
WP_088242757.1	EAD9+iSTAND	EAD9+iSTAND*→ MoxR→ helical_region(leucine-richLWxKmotif)+vWA→ vWA+FGS-fold_domain→	327	Calothrix rhizosoleniae	GCF_900185595.1	cyanobacteria
WP_088242861.1	EAD4+iSTAND	EAD4+iSTAND*→ MoxR→	426	Calothrix rhizosoleniae	GCF_900185595.1	cyanobacteria

acc	architecture	operon	len	species	gca	taxend
WP_088278871.1	TIR+iSTAND	TIR+iSTAND*→ MoxR→ BetaPropeller+FGS-fold_domain→	495	Ideonella sp. A 288	GCF_002198735.1	betaproteobacteria
WP_113510333.1	iSTAND	iSTAND*→ MoxR→ TM+TM+vWA+TM+Sel1→	277	Rhizobiales bacterium	GCF_900469875.1	alphaproteobacteria
WP_124143316.1	??+iSTAND	??+iSTAND*→ MoxR→	395	Okeania hirsuta	GCF_003838225.1	cyanobacteria

FtsH ternary systems

acc	architecture	operon	len	species	gca	taxend
WP_015348943.1	inactive_FtsH+FtsH	Radical_SAM→ X6→ X5→ inactive_FtsH+FtsH*→ X3_analog→ a/b_unk+NEFF1+TPR_region→ MoxR→?→ helical_unk+ivWA→	705	Myxococcus stipitatus	GCF_000331735.1	deltaproteobacteria
PCJ17226.1	inactive_FtsH+FtsH	Radical_SAM→?→ X5→ inactive_FtsH+FtsH*→ X3_analog→??+NEFF1→ PSE→ PSE→ helical_unk+ivWA→	691	Candidatus Cloacimonetes bacterium	GCA_002402105.1	bacteria
WP_013563425.1	inactive_FtsH+FtsH	inactive_FtsH+FtsH*→ X3_analog→??+TPRs+NEFF1→ MoxR→ helical_unk+ivWA→	750	Isosphaera pallida	GCF_000186345.1	planctomycetes
PID39910.1	inactive_FtsH+FtsH	Radical_SAM→ X6→ X5→ inactive_FtsH+FtsH*→ X3_analog→ a/b_unk+NEFF1+TPR_region→ MoxR→ helical_unk+ivWA→	738	Proteobacteria bacterium	GCA_002747355.1	proteobacteria
WP_090492713.1	inactive_FtsH+FtsH	Radical_SAM→ X6→ X5→ inactive_FtsH+FtsH*→ X3_analog→ a/b_unk+NEFF1+TPR_region→ MoxR→ helical_unk+ivWA→	706	Myxococcus virescens	GCF_900101905.1	deltaproteobacteria
WP_095958505.1	inactive_FtsH+FtsH	Radical_SAM→ X6→ X5→ inactive_FtsH+FtsH*→ X3_analog→ a/b_unk+NEFF1+TPR_region→ MoxR→ helical_unk+ivWA→	706	Myxococcus macrosporus	GCF_002305895.1	deltaproteobacteria
WP_140790498.1	inactive_FtsH+FtsH	Radical_SAM→ X6→ X5→ inactive_FtsH+FtsH*→ X3_analog→ a/b_unk+NEFF1+TPR_region→ MoxR→ helical_unk+ivWA→	708	Myxococcus xanthus	GCF_006401215.1	deltaproteobacteria
WP_140798142.1	inactive_FtsH+FtsH	Radical_SAM→ X6→ X5→ inactive_FtsH+FtsH*→ X3_analog→ a/b_unk+NEFF1+TPR_region→ MoxR→ helical_unk+ivWA→	706	Myxococcus xanthus	GCF_006400955.1	deltaproteobacteria
WP_140862181.1	inactive_FtsH+FtsH	Radical_SAM→ X6→ X5→ inactive_FtsH+FtsH*→ X3_analog→ a/b_unk+NEFF1+TPR_region→ MoxR→ helical_unk+ivWA→	706	Myxococcus xanthus	GCF_006401635.1	deltaproteobacteria
WP_141255298.1	inactive_FtsH+FtsH	Radical_SAM→ X6→ X5→ inactive_FtsH+FtsH*→ X3_analog→ a/b_unk+NEFF1+TPR_region→ MoxR→ helical_unk+ivWA→	706	Myxococcus	GCF_006518195.1	deltaproteobacteria
WP_141592591.1	inactive_FtsH+FtsH	Radical_SAM→ X6→ X5→ inactive_FtsH+FtsH*→ X3_analog→ a/b_unk+NEFF1+TPR_region→ MoxR→ helical_unk+ivWA→	706	Myxococcus sp. AB025A	GCF_006547365.1	deltaproteobacteria
WP_141619821.1	inactive_FtsH+FtsH	Radical_SAM→ X6→ X5→ inactive_FtsH+FtsH*→ X3_analog→ a/b_unk+NEFF1+TPR_region→ MoxR→ helical_unk+ivWA→	706	Myxococcus sp. AB024B	GCF_006547355.1	deltaproteobacteria
WP_046713160.1	inactive_FtsH+FtsH	Radical_SAM→ X6→ X5→ inactive_FtsH+FtsH*→ X3_analog→ a/b_unk+NEFF1+TPR_region→ MoxR→||←?||helical_unk+ivWA→	705	Myxococcus fulvus	GCF_000988565.1	deltaproteobacteria
RCK81659.1	inactive_FtsH+FtsH	inactive_FtsH+FtsH*→?→?→ MoxR→ helical_unk+ivWA→ Radical_SAM→ RadSAM_pep→	695	Candidatus Ozemobacter sibiricus	GCA_003327425.1	bacteria
PKL48731.1	inactive_FtsH+FtsH	inactive_FtsH+FtsH*→?→ MoxR→ helical_unk+ivWA→ Radical_SAM→ RadSAM_pep→?→ X5→	698	Candidatus Riflebacteria bacterium HGW-Riflebacteria-2	GCA_002839435.1	bacteria
PCC71843.1	inactive_FtsH+FtsH	Radical_SAM→?→ X5→ inactive_FtsH+FtsH*→ X3_analog→?→ MoxR→ helical_unk+ivWA→	700	Nannocystis exedens	GCA_002343915.1	deltaproteobacteria
WP_096329841.1	inactive_FtsH+FtsH	Radical_SAM→?→ X5→ inactive_FtsH+FtsH*→ X3_analog→?→ MoxR→ helical_unk+ivWA→	704	Nannocystis exedens	GCF_900112715.1	deltaproteobacteria
WP_011552959.1	inactive_FtsH+FtsH	Radical_SAM→ X6→ X5→ inactive_FtsH+FtsH*→ X3_analog→ a/b_unk+NEFF1+TPR_region→ MoxR→?→ helical_unk+ivWA→	706	Myxococcus	GCF_000012685.1	deltaproteobacteria
WP_002635065.1	inactive_FtsH+FtsH	Radical_SAM→ X6→ X5→ inactive_FtsH+FtsH*→ X3_analog→ a/b_unk+NEFF1+TPR_region→ MoxR→ helical_unk+ivWA→	706	Myxococcus hansupus	GCF_000280925.3	deltaproteobacteria
WP_095985475.1	inactive_FtsH+FtsH	Radical_SAM→ X6→ X5→ inactive_FtsH+FtsH*→ X3_analog→ a/b_unk+NEFF1+TPR_region→ MoxR→ helical_unk+ivWA→?→?→||←Radical_SAM	705	Cystobacter fuscus	GCF_002305875.1	deltaproteobacteria
WP_002627974.1	inactive_FtsH+FtsH	Radical_SAM→ X6→?→ X5→ inactive_FtsH+FtsH*→ X3_analog→ a/b_unk+NEFF1+TPR_region→ MoxR→ helical_unk+ivWA→?→?→||←Radical_SAM	705	Cystobacter fuscus	GCF_000335475.2	deltaproteobacteria
WP_013939476.1	inactive_FtsH+FtsH	X6→ X5→ inactive_FtsH+FtsH*→ X3_analog→ a/b_unk+NEFF1+TPR_region→ MoxR→ helical_unk+ivWA→?→?→||←Radical_SAM	706	Myxococcus macrosporus	GCF_000219105.1	deltaproteobacteria
WP_071896885.1	inactive_FtsH+FtsH	Radical_SAM→ X6→ X5→ inactive_FtsH+FtsH*→ X3_analog→ a/b_unk+NEFF1+TPR_region→ MoxR→ helical_unk+ivWA→?→?→||←Radical_SAM	705	Cystobacter ferrugineus	GCF_001887355.1	deltaproteobacteria
PKL44251.1	inactive_FtsH+FtsH	inactive_FtsH+FtsH*→?→ MoxR→ helical_unk+ivWA→ Radical_SAM→ RadSAM_pep→?→ X5→	699	Candidatus Riflebacteria bacterium HGW-Riflebacteria-1	GCA_002839445.1	bacteria
WP_074957489.1	inactive_FtsH+FtsH	Radical_SAM→ X6→ X5→ inactive_FtsH+FtsH*→ X3_analog→ a/b_unk+NEFF1+TPR_region→ MoxR→||←?||helical_unk+vWA→	705	Myxococcus fulvus	GCF_900111765.1	deltaproteobacteria
MBM74108.1	inactive_FtsH+FtsH	Radical_SAM→?→ X5→ inactive_FtsH+FtsH*→ X3_analog→?→ MoxR→??+ivWA→||←?||STAND_NTPase→	715	Proteobacteria bacterium	GCA_002722755.1	proteobacteria
MBK05551.1	inactive_FtsH+FtsH	Radical_SAM→?→ X5→ inactive_FtsH+FtsH*→ X3_analog→?→ MoxR←?||helical_unk+vWA→	737	Deltaproteobacteria bacterium	GCA_002720785.1	deltaproteobacteria
WP_129628747.1	inactive_FtsH+FtsH	TPRs→?→?→??+vWA+FGS-fold_domain→ inactive_FtsH+FtsH*→ REase→→ MoxR	600	Oscillochloris sp. Chuk17	GCF_004138135.1	chloroflexi
WP_006562442.1	inactive_FtsH+FtsH	TPRs→?→?→??+vWA+FGS-fold_domain→ inactive_FtsH+FtsH*→ MoxR→?→?→ STAND_NTPase→	598	Oscillochloris trichoides	GCF_000152145.1	chloroflexi
WP_141322754.1	inactive_FtsH+FtsH	Radical_SAM→ X6→ X5→ inactive_FtsH+FtsH*→ X3_analog→ a/b_unk+NEFF1+TPR_region→ MoxR→||←?||helical_unk+ivWA→	705	Myxococcus sp. AB022	GCF_006518215.1	deltaproteobacteria
WP_020473751.1	inactive_FtsH+FtsH	Radical_SAM→?→ Radical_SAM→ X6→ X5→ inactive_FtsH+FtsH*→ X3_analog→?→ a/b_unk+NEFF+TPR_region→	714	Zavarzinella formosa	GCF_000255705.1	planctomycetes
WP_082839483.1	inactive_FtsH+FtsH	Radical_SAM→ X6→ X5→ inactive_FtsH+FtsH*→ X3_analog→ a/b_unk+NEFF1+TPR_region→ a/b_unk+NEFF1+TPR_region→	740	Gemmata sp. SH-PL17	GCF_001610855.1	planctomycetes
VFJ42630.1	inactive_FtsH+FtsH	Radical_SAM.Ammememo→ TIR→ TIR+Pkinase+inactive_Ploop_NTPase+Ploop_NTPase→ Ploop_NTPase→ small_peptide→??→ inactive_FtsH+FtsH*→??→ MoxR→??+ivWA	582	Candidatus Kentron sp. FM	-	gammaproteobacteria
WP_051865898.1	inactive_FtsH+FtsH	EAD1+CASPASE→ RING(inactive)+RING→ E1+UFD→ EAD1+Ubl-Nterm+Ubl+E2→ JAB-N+JAB→ X1→ inactive_FtsH+FtsH*→ MoxR→ X2→ X3→ TPRs→ low_complexity+a/b_unk+TPR_repeat←BetaPropeller+vWA←RadSAM_pep←RADICAL_SAM.Ammemo	615	Streptomyces griseus	GCF_000720255.1	actinobacteria
WP_015197961.1	inactive_FtsH+FtsH	E1+UFD→ EAD8+Trypsin→ TPRs+FGS-fold_domain→ EAD8+EAD1→ EAD1+Ubl-Nterm+Ubl+E2→ JAB-N+JAB→ X1→ inactive_FtsH+FtsH*→ TPRs+C-type_lectin→ MoxR→?→ X3→ TPRs+C-type_lectin→ TPRs+C-type_lectin→?→ Clp_N_repeats+vWA←RADICAL_SAM.Ammemo	663	Calothrix parietina	GCF_000317435.1	cyanobacteria
WP_079310654.1	inactive_FtsH+FtsH	E1+UFD→ E1+UFD→ EAD1+Ubl-Nterm+Ubl+E2→ JAB_N+JAB→ X1→ inactive_FtsH+FtsH*→ MoxR→ X2→ X3→ PSE→?→ beta_propeller(frag?)	624	Streptomyces sp. GKU 895	GCF_002027195.1	actinobacteria
WP_081970790.1	inactive_FtsH+FtsH	E1+UFD→ EAD1+Ubl-Nterm+Ubl+E2→ JAB_N+JAB→ X1→ inactive_FtsH+FtsH*→ MoxR→ X2→ X3→ TPRs→ low_complexity+a/b_unk+TPR_repeat→ BetaPropeller+vWA→||←RadSAM_pep←RADICAL_SAM.Ammemo	561	Dactylosporangium aurantiacum	GCF_000716715.1	actinobacteria
WP_093170141.1	inactive_FtsH+FtsH	E1+UFD→ EAD1+Ubl-Nterm+Ubl+E2→ JAB_N+JAB→ X1→ inactive_FtsH+FtsH*→ MoxR→ X2→ X3→ TPRs→ low_complexity+a/b_unk+TPR_repeat→ BetaPropeller+vWA→||←RadSAM_pep	616	Sinosporangium album	GCF_900100605.1	actinobacteria

acc	architecture	operon	len	species	gca	taxend
WP_052745217.1	inactive_FtsH+FtsH	←DO-GTPase2←Pkinase+TM||EAD1+CASPASE→ RING(inactive)+RING→ E1+UFD→ EAD1+Ubl-Nterm+Ubl+E2→ JAB_N+JAB*→ X1→ inactive_FtsH+FtsH→ MoxR→??→ X2→ X3→ TPRs→ low_complexity+a/b_unk+TPR_repeat→ BetaPropeller+vWA→||←RadSAM_pep←RADICAL_SAM.Ammemo←MPTase←RadSAM.X1	639	Streptomyces sp. WM6386	GCF_000972385.1	actinobacteria
WP_052067792.1	inactive_FtsH+FtsH	←TM+??←TM+coiled-coil←GAP1-N2+GAP1-M+??←DO-GTPase2←Pkinase+TM||EAD1+CASPASE→ RING(inactive)+RING→ E1+UFD→ EAD1+Ubl-Nterm+Ubl+E2→ JAB_N+JAB→ X1→ inactive_FtsH+FtsH*→ MoxR→ X2→ X3→ TPRs→ low_complexity+a/b_unk+TPR_repeat→ BetaPropeller+vWA→||←RadSAM_pep←RADICAL_SAM.Ammemo←MPTase	628	Streptomyces mirabilis	GCF_000746395.1	actinobacteria
WP_067128135.1	inactive_FtsH+FtsH	EAD1+CASPASE→ RING(inactive)+RING→ E1+UFD→ EAD1+Ubl-Nterm+Ubl+E2→ JAB_N+JAB→ X1→ inactive_FtsH+FtsH*→ MoxR→ X2→ X3→ TPRs→?→ BetaPropeller+vWA←RadSAM_pep←RADICAL_SAM.Ammemo←MPTase	637	Streptomyces yokosukanensis	GCF_001514035.1	actinobacteria
TCO52884.1	inactive_FtsH+FtsH	←TM+??←TM+coiled-coil←GAP1-N2+GAP1-M+??←DO-GTPase2←Pkinase+TM||EAD1+CASPASE→ RING(inactive)+RING→ E1+UFD→ EAD1+Ubl-Nterm+Ubl+E2→ JAB_N+JAB→ X1→ inactive_FtsH+FtsH*→ MoxR→ X2→ X3→ TPRs→ low_complexity+a/b_unk+TPR_repeat→ BetaPropeller+vWA→||←RadSAM_pep←RADICAL_SAM.Ammemo	611	Actinocrispum wychmicini	GCA_004345645.1	actinobacteria
WP_020645963.1	inactive_FtsH+FtsH	EAD1+CASPASE→ RING(inactive)+RING→ E1+UFD→ EAD1+Ubl-Nterm+Ubl+E2→ JAB_N+JAB→ X1→ inactive_FtsH+FtsH*→ MoxR→ X2→ X3→ TPRs→ low_complexity+a/b_unk+TPR_repeat→ BetaPropeller+vWA→||←RadSAM_pep←RADICAL_SAM.Ammemo←TM+TM	599	Amycolatopsis balhimycina	GCF_000384295.1	actinobacteria
WP_093947432.1	inactive_FtsH+FtsH	EAD1+CASPASE→ RING(inactive)+RING→ E1+UFD→ EAD1+Ubl-Nterm+Ubl+E2→ JAB_N+JAB→ X1→ inactive_FtsH+FtsH*→ MoxR→ X2→ X3→ TPRs→ low_complexity+a/b_unk+TPR_repeat→ BetaPropeller+vWA→||←RadSAM_pep←RADICAL_SAM.Ammemo←TM+TM	599	Amycolatopsis sp. H5	GCF_002234595.1	actinobacteria
WP_126270580.1	inactive_FtsH+FtsH	EAD1+CASPASE→ RING(inactive)+RING→ E1+UFD→ EAD1+Ubl-Nterm+Ubl+E2→ JAB_N+JAB→ X1→ inactive_FtsH+FtsH*→ MoxR→ X2→ X3→ TPRs→ low_complexity+a/b_unk+TPR_repeat→ BetaPropeller+vWA→||←RadSAM_pep←RADICAL_SAM.Ammemo	624	Streptomyces sp. GGCR-6	GCF_003955715.1	actinobacteria
WP_132124194.1	inactive_FtsH+FtsH	←TM+??←TM+coiled-coil←GAP1-N2+GAP1-M+??←DO-GTPase2←Pkinase+TM||EAD1+CASPASE→ RING(inactive)+RING→ E1+UFD→ EAD1+Ubl-Nterm+Ubl+E2→ JAB_N+JAB→ X1→ inactive_FtsH+FtsH*→ MoxR→ X2→ X3→ TPRs→ low_complexity+a/b_unk+TPR_repeat→ BetaPropeller+vWA→||←RadSAM_pep←RADICAL_SAM.Ammemo	587	Actinocrispum wychmicini	GCF_004345645.1	actinobacteria
WP_132804228.1	inactive_FtsH+FtsH	EAD1+CASPASE→ RING(inactive)+RING→ E1+UFD→ EAD1+Ubl-Nterm+Ubl+E2→ JAB_N+JAB→ X1→ inactive_FtsH+FtsH*→ MoxR→ X2→ X3→ TPRs→ low_complexity+a/b_unk+TPR_repeat→ BetaPropeller+vWA→||←RadSAM_pep←RADICAL_SAM.Ammemo	624	Streptomyces sp. BK042	GCF_004343295.1	actinobacteria
WP_136970956.1	inactive_FtsH+FtsH	←RadSAM_pep←RADICAL_SAM.Ammemo←BetaPropeller+vWA||Prok_Ring(degenerate)+Prok_Ring→ E1+UFD→ EAD1+Ubl-Nterm+Ubl+E2→ JAB-N+JAB→ X1→ inactive_FtsH+FtsH*→ MoxR→	662	Polyangium sorediatum	-	deltaproteobacteria
WP_092557310.1	inactive_FtsH+FtsH	Trypsin+EAD1→ BetaPropeller+vWA→ RADICAL_SAM.Ammemo→ RadSAM_pep→ RING(inactive)+RING→ E1+UFD→ EAD1+Ubl-Nterm+Ubl+E2→ JAB_N+JAB→ X1→ inactive_FtsH+FtsH*→ MoxR→ X2→ X3→ TPRs→ low_complexity+a/b_unk+TPR_repeat→ CASPASE+Ploop_NTPase→ BetaPropeller→ ABhydrolase+TIR→ EAD1+TIR→ BetaPropeller+vWA→	660	Actinoplanes derwentensis	GCF_900104725.1	actinobacteria
WP_051927025.1	inactive_FtsH+FtsH	EAD1+CASPASE→ RING(inactive)+RING→ E1+UFD→ EAD1+Ubl-Nterm+Ubl+E2→ JAB_N+JAB→ X1→ inactive_FtsH+FtsH*→ MoxR→ X2→ X3→ TPRs→ low_complexity+a/b_unk+TPR_repeat→ BetaPropeller+vWA→||←RadSAM_pep←RADICAL_SAM.Ammemo←MPTase←RadSAM.X1	636	Streptomyces durhamensis	GCF_000725475.1	actinobacteria
WP_053662245.1	inactive_FtsH+FtsH	EAD1+CASPASE→ RING(inactive)+RING→ E1+UFD→ EAD1+Ubl-Nterm+Ubl+E2→ JAB_N+JAB→ X1→ inactive_FtsH+FtsH*→ MoxR→ X2→ X3→ TPRs→ low_complexity+a/b_unk+TPR_repeat→ BetaPropeller+vWA→||←RadSAM_pep←RADICAL_SAM.Ammemo←MPTase←RadSAM.X1	639	Streptomyces sp. MMG1121	GCF_001280015.1	actinobacteria
WP_071384075.1	inactive_FtsH+FtsH	EAD1+CASPASE→ RING(inactive)+RING→ E1+UFD→ EAD1+Ubl-Nterm+Ubl+E2→ JAB_N+JAB→ X1→ inactive_FtsH+FtsH*→ MoxR→ X2→ X3→ TPRs→ low_complexity+a/b_unk+TPR_repeat→ BetaPropeller+vWA→||←RadSAM_pep←RADICAL_SAM.Ammemo←MPTase←RadSAM.X1	634	Streptomyces sp. MUSC 1	GCF_001866665.1	actinobacteria
WP_069777255.1	inactive_FtsH+FtsH	←TM+??←TM+coiled-coil←GAP1-N2+GAP1-M+??←DO-GTPase2←Pkinase+TM||EAD1+CASPASE→ RING(inactive)+RING→ E1+UFD→ EAD1+Ubl-Nterm+Ubl+E2→ JAB_N+JAB→ X1→ inactive_FtsH+FtsH*→ MoxR→ X2→ X3→ TPRs→ low_complexity+a/b_unk+TPR_repeat→||←BetaPropeller+vWA←RadSAM_pep←RADICAL_SAM.Ammemo←MPTase	638	Streptomyces punicescabiei	GCF_001735805.1	actinobacteria
WP_051115179.1	inactive_FtsH+FtsH	Clp_N_repeats+vWA→ Clp_N_repeats+vWA→ Clp_N_repeats+vWA→ Clp_N_repeats+vWA→ Clp_N_repeats+vWA→ Clp_N_repeats+vWA→??→??+4TM→ EAD1+CASPASE→ RADICAL_SAM.Ammemo→ RadSAM_pep→ RING(inactive)+RING→ E1+UFD→ EAD1+Ubl-Nterm+Ubl+E2→ JAB_N+JAB→ X1→ inactive_FtsH+FtsH*→ MoxR→ X2→?→ TPRs→ low_complexity+a/b_unk+TPRs→	689	Actinoplanes globisporus	GCF_000379645.1	actinobacteria
WP_133930094.1	inactive_FtsH+FtsH	EAD1+CASPASE→ RING(inactive)+RING→ E1+UFD→ EAD1+Ubl-Nterm+Ubl+E2→ JAB_N+JAB→ X1→ inactive_FtsH+FtsH*→ MoxR→ X2→ X3→ TPRs→ low_complexity+a/b_unk+TPRs→||←BetaPropeller+vWA←RadSAM_pep←RADICAL_SAM.Ammemo	615	Streptomyces sp. BK161	GCF_004364215.1	actinobacteria
TQS46759.1	inactive_FtsH+FtsH	BetaPropeller+vWA→ BetaPropeller+vWA→ BetaPropeller+vWA→||←TIR+EAD1||BetaPropeller+vWA→ RADICAL_SAM.Ammemo→ RadSAM_pep→ RING(inactive)+RING→ E1+UFD→ EAD1+Ubl-Nterm+Ubl+E2→ JAB_N+JAB→ X1→ inactive_FtsH+FtsH*→ MoxR→ X2→ X3→ TPRs→ low_complexity+a/b_unk+TPRs→	716	Cryptosporangium sp. A-T 5661	GCA_006912135.1	actinobacteria
WP_071371602.1	inactive_FtsH+FtsH	←TM+??←TM+coiled-coil←GAP1-N2+GAP1-M+??←DO-GTPase2←Pkinase+TM||EAD1+CASPASE→ CASPASE(frag)→ CASPASE(frag)→ CASPASE(frag)→ RING(inactive)+RING→ E1+UFD→ EAD1+Ubl-Nterm+Ubl+E2→ JAB_N+JAB→ X1→ inactive_FtsH+FtsH*→ MoxR→ X2→ X3→ TPRs→ low_complexity+a/b_unk+TPR_repeat→||←BetaPropeller+vWA←RadSAM_pep←RADICAL_SAM.Ammemo←MPTase	634	Streptomyces sp. MUSC 14	-	actinobacteria
QBG49801.1	inactive_FtsH+FtsH	E1+UFD→ EAD1+Ubl-Nterm+Ubl+E2→ JAB_N+JAB→ X1→ inactive_FtsH+FtsH*→ MoxR→ TPRs→?→ EAD1+CASPASE→	758	Streptomyces spiramyceticus	-	actinobacteria
WP_136931981.1	inactive_FtsH+FtsH	←RadSAM_pep←Radical_SAM←BetaPropeller+vWA||Prok_Ring→ E1+UFD→ EAD1+Ubl-Nterm+Ubl+E2→ JAB-N+JAB→ X1→ inactive_FtsH+FtsH*→ MoxR→?→ TPRs→ low_complexity+a/b_unk+TPRs→	662	Polyangium fumosum	GCF_005144585.1	deltaproteobacteria
WP_130402109.1	inactive_FtsH+FtsH	Clp_N_repeats+vWA→??→??+4TM→ EAD1+CASPASE→ RING(inactive)+RING→ E1+UFD→ EAD1+Ubl-Nterm+Ubl+E2→ JAB_N+JAB→ X1→ inactive_FtsH+FtsH*→ MoxR→ TPRs→ low_complexity+a/b_unk+TPR_repeat→	681	Micromonospora violae	GCF_004217135.1	actinobacteria
KPA11743.1	inactive_FtsH+FtsH	TIR+??→||←?||Ubl+E2→ JAB-N+JAB→ inactive_FtsH+FtsH*→ E1+UFD→ TPRs+FGS-fold_domain→	743	Candidatus Magnetomorum sp. HK-1	GCA_001292585.1	deltaproteobacteria
WP_086686847.1	inactive_FtsH+FtsH	RadSAM_pep→ RING(inactive)+RING→ E1+UFD→ Trypsc2→ TCAD4+CASPASE+EAD1→ EAD1+Ubl-Nterm+Ubl+E2→ JAB_N+JAB→ X1→ inactive_FtsH+FtsH*→ TPRs+FGS-fold_domain→ MoxR→?→?→ FGS-fold_domain→||←?||?→||←BetaPropeller+vWA||RADICAL_SAM.Ammemo→	660	Nostoc sp. T09	GCF_002154695.1	cyanobacteria
WP_109500344.1	inactive_FtsH+FtsH	EAD1+CASPASE→ RING(inactive)+RING→ E1+UFD→ EAD1+Ubl-Nterm+Ubl+E2→ JAB_N+JAB→ X1→ inactive_FtsH+FtsH*→ MoxR→ X2→ X3→ TPRs→ low_complexity+a/b_unk+TPR_repeat→||←BetaPropeller+vWA←RadSAM_pep←RADICAL_SAM.Ammemo	626	Streptomyces sp. Act143	GCF_003143935.1	actinobacteria
ETR70572.1	inactive_FtsH+FtsH	inactive_FtsH+FtsH*→ inactive_FtsH+FtsH→ Prok_Ring+Prok_Ring→ E1+UFD→ TIR+??→ Ubl+E2→ JAB_N2→ JAB→	235	Candidatus Magnetoglobus multicellularis str. Araruama	GCA_000516475.1	deltaproteobacteria
SDT45767.1	inactive_FtsH+FtsH	Trypsin+EAD1→ BetaPropeller+vWA→ RADICAL_SAM.Ammemo→ RadSAM_pep→ RING(inactive)+RING→ E1+UFD→ EAD1+Ubl-Nterm+Ubl+E2→ JAB_N+JAB→ X1→ inactive_FtsH+FtsH*→ MoxR→ X2→ X3→ TPRs→ low_complexity+a/b_unk+TPR_repeat→ CASPASE+Ploop_NTPase→ beta_propeller→ ABhydrolase+TIR→ EAD1+TIR→ BetaPropeller+vWA→	668	Actinoplanes derwentensis	GCA_900104725.1	actinobacteria
RMG09056.1	inactive_FtsH+FtsH	MPTase→||←Prok-RING+TM←?←Prok-RING+TM+TM←Band7←Band7||inactive_FtsH+FtsH*→ X3_analog→	793	Planctomycetes bacterium	GCA_003695705.1	planctomycetes
WP_083304944.1	inactive_FtsH+FtsH	RadSAM_pep→ Prok_Ring(degenerate)+Prok_Ring→ X1→ TPRs→ inactive_FtsH+FtsH*→ MoxR→?→?→ TPRs+FGS-fold_domain→→||←?||?→?→||←RADICAL_SAM.Ammemo	622	Moorea producens	GCF_001767235.1	cyanobacteria
WP_009740764.1	inactive_FtsH+FtsH	E1+UFD→ EAD1+Ubl-Nterm+Ubl+E2→ JAB_N+JAB→ X1→ X1→ inactive_FtsH+FtsH*→ MoxR→ Clathrin+DnaJ_CXXCXGXG+DnaJ_C→ low_complexity+a/b_unk+TPR_repeat→||←?←TIR	712	Frankia sp. QA3	GCF_000262465.1	actinobacteria
WP_097261157.1	inactive_FtsH+FtsH	RING(inactive)+RING→ E1+UFD→ EAD1+Ubl-Nterm+Ubl+E2→||←PSE→ X1→ inactive_FtsH+FtsH*→ MoxR→?→?→ TPRs→ low_complexity+a/b_unk+TPR_repeat→ BetaPropeller+vWA→||←RadSAM_pep←RADICAL_SAM.Ammemo	622	Streptomyces sp. TLI_55	GCF_900206255.1	actinobacteria
WP_058554410.1	inactive_FtsH+FtsH	RING(inactive)+RING→ E1+UFD→ helical_X+TIR→ EAD1+Ubl-Nterm+Ubl+E2→||←PSE||?→ inactive_FtsH+FtsH*→ MoxR→ BetaPropeller+vWA→ X2→ X3?→ TPRs→ low_complexity+a/b_unk+TPR_repeat→||←?||BetaPropeller+vWA→ HTH→ RADICAL_SAM.Ammemo→ RadSAM_pep→	677	Thiohalocapsa sp. ML1	GCF_001469165.1	gammaproteobacteria
WP_131767338.1	inactive_FtsH+FtsH	RadSAM_pep→ RING(inactive)+RING→ E1+?→ TIR→||←?←?←?||X1→ inactive_FtsH+FtsH*→ MoxR→	461	Frankia symbiont of Datisca glomerata	GCF_900634715.1	actinobacteria
WP_012825462.1	inactive_FtsH+FtsH	beta_propeller+vWA→ X1→ inactive_FtsH+FtsH*→ MoxR→ X2→ X3→?→ Radical_SAM→ RadSAM_pep→	691	Haliangium ochraceum	GCF_000024805.1	deltaproteobacteria
WP_047223339.1	inactive_FtsH+FtsH	X1→ inactive_FtsH+FtsH*→ MoxR→ X2→	749	Frankia coriariae	GCF_001017755.1	actinobacteria
OGK06825.1	inactive_FtsH+FtsH	inactive_FtsH+FtsH*→?→ MoxR→	699	Candidatus Riflebacteria bacterium GWC2_50_8	GCA_001787855.1	bacteria
WP_131796573.1	inactive_FtsH+FtsH	inactive_FtsH+FtsH*→ MoxR→	452	Frankia symbiont of Datisca glomerata	GCF_900635405.1	actinobacteria

acc	architecture	operon	len	species	gca	taxend
RKZ47050.1	inactive_FtsH+FtsH	inactive_FtsH+FtsH*→?→	662	Gammaproteobacteria bacterium	GCA_003645185.1	gammaproteobacteria
OIP44723.1	inactive_FtsH+FtsH	X5→ inactive_FtsH+FtsH*→	723	Deltaproteobacteria bacterium CG2_30_63_29	GCA_001873925.1	deltaproteobacteria
PJB47822.1	inactive_FtsH+FtsH	X5→ inactive_FtsH+FtsH*→	723	Deltaproteobacteria bacterium CG_4_9_14_3_um_filter_63_12	GCA_002789955.1	deltaproteobacteria
CEF49305.1	inactive_FtsH+FtsH	X6→ X5→ inactive_FtsH+FtsH*→	700	uncultured bacterium	GCA_000821145.1	bacteria
WP_141643777.1	inactive_FtsH+FtsH	Radical_SAM→ X6→ X5→ inactive_FtsH+FtsH*→ X3_analog→ a/b_unk+NEFF1+TPR_region→ MoxR→	705	Myxococcus sp. AM401	GCF_006636215.1	deltaproteobacteria
WP_071102283.1	inactive_FtsH+FtsH	inactive_FtsH+FtsH*→ MoxR→?→||←?←?||X2→	660	Moorea producens	GCF_001854205.1	cyanobacteria
WP_010040329.1	inactive_FtsH+FtsH	Radical_SAM→ X6→ X5→ inactive_FtsH+FtsH*→ X3_analog→ a/b_unk+NEFF1+TPR_region→ a/b_unk+NEFF1+TPR_region→	748	Gemmata obscuriglobus	GCF_000171775.1	planctomycetes
RLS40983.1	inactive_FtsH+FtsH	X5→ inactive_FtsH+FtsH*→ X3_analog→?+NEFF+?→ MoxR→	720	Planctomycetes bacterium	GCA_003669555.1	planctomycetes
MBH25655.1	inactive_FtsH+FtsH	inactive_FtsH+FtsH*→ X3_analog→	730	Myxococcales bacterium	GCA_002716585.1	deltaproteobacteria
MBK06498.1	inactive_FtsH+FtsH	inactive_FtsH+FtsH*→ X3_analog→	723	Deltaproteobacteria bacterium	GCA_002720785.1	deltaproteobacteria
TNE49083.1	inactive_FtsH+FtsH	inactive_FtsH+FtsH*→ X3_analog→	725	Deltaproteobacteria bacterium	GCA_006226375.1	deltaproteobacteria
WP_088257901.1	inactive_FtsH+FtsH	inactive_FtsH+FtsH*→ X3_analog→	722	Fimbriiglobus ruber	GCF_002197845.1	planctomycetes
TET34120.1	inactive_FtsH+FtsH	X5→ inactive_FtsH+FtsH*→?→?→ X3_analog→	729	Planctomycetes bacterium	GCA_004376375.1	planctomycetes
PZR18634.1	inactive_FtsH+FtsH	X5→ inactive_FtsH+FtsH*→ X3_analog→	704	Archangium gephyra	GCA_003243425.1	deltaproteobacteria
WP_006976996.1	inactive_FtsH+FtsH	X5→ inactive_FtsH+FtsH*→ X3_analog→?→ a/b_unk+NEFF+TPRs	707	Plesiocystis pacifica	GCF_001170895.1	deltaproteobacteria
HBI41239.1	inactive_FtsH+FtsH	X6→ X5→ inactive_FtsH+FtsH*→	716	Planctomycetales bacterium	GCA_003508275.1	planctomycetes
WP_106395424.1	inactive_FtsH+FtsH	Radical_SAM→ X6→ X5→ inactive_FtsH+FtsH*→	706	Enhygromyxa salina	GCF_002994615.1	deltaproteobacteria
WP_131772555.1	inactive_FtsH+FtsH	inactive_FtsH+FtsH*→ MoxR→ X2→||←?||TPRs→	511	Frankia symbiont of Coriaria nepalensis	GCF_900635385.1	actinobacteria
WP_013873919.1	inactive_FtsH+FtsH	X1→ inactive_FtsH+FtsH*→ MoxR→ X2→||←?||TPRs→	735	Frankia	GCF_000177615.2	actinobacteria
WP_076843094.1	inactive_FtsH+FtsH	X1→ inactive_FtsH+FtsH*→ MoxR→ X2→?→ TPRs→	744	Frankia sp. BMG5.30	GCF_001983005.1	actinobacteria

β-propeller containing ternary systems

acc	architecture	operon	len	species	gca	taxend
OFY83689.1	extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1+Ribosomal_L12_insert	bpX4→ MoxR→ bpX2→ extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1+Ribosomal_L12_insert*→ bpX3→	846	Bacteroidetes bacterium RIFCSPLOWO2_12_FULL_35_15	GCA_001769385.1	bacteroidetes
AFM05601.1	extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1+Ribosomal_L12_insert	bpX4→?→ MoxR→?→ bpX2→ extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1+Ribosomal_L12_insert*→	873	Bernardetia litoralis DSM 6794	GCA_000265505.1	bacteroidetes
POR24865.1	extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1+Ribosomal_L12_insert	bpX4→ MoxR→ bpX2→ extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1+Ribosomal_L12_insert*→ abpX3+2TM+TPR_region→	803	Flavobacterium columnare	GCA_002916795.1	bacteroidetes
OXA84853.1	extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1+Ribosomal_L12_insert	bpX4→ MoxR→ bpX2→ extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1+Ribosomal_L12_insert*→	851	Flavobacterium hydatis	GCA_002217335.1	bacteroidetes
SEN93879.1	extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1+Ribosomal_L12_insert	bpX4→ MoxR→ bpX2→ extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1+Ribosomal_L12_insert*→ abpX3+2TM+TPR_region→	845	Flavobacterium sp. fv08	GCA_900110335.1	bacteroidetes
KOY86779.1	extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1	bpX4→ MoxR→ bpX2→ extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*→	767	bacterium 336/3	GCA_001281695.1	bacteria
WP_128150033.1	extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1	bpX4→ MoxR→ bpX2→ extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*→ bpX3+4TM→2TM+TPR_region→	779	Apibacter sp. HY041	GCF_004014855.1	bacteroidetes
PWK28201.1	extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1	bpX4→ MoxR→ bpX2→ extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*→ bpX3+TPR_region→	808	Arcicella aurantiaca	GCA_003148625.1	bacteroidetes
WP_052599568.1	extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1	bpX4→ MoxR→ bpX2→ extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*→ bpX3+TPR_region→	776	Aureispira sp. CCB-QB1	GCF_000724545.1	bacteroidetes
PSL46654.1	extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1	MoxR→ bpX2→ extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*→ bpX3+TPR_region+beta_propeller→	789	Chitinophaga niastensis	GCA_003014755.1	bacteroidetes
RBL92136.1	extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1	bpX4→ MoxR→ bpX2→ extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*→ bpX3+TPR_region+beta_propeller→	787	Chitinophaga sp. GDMCC 1.1325	GCA_003308995.1	bacteroidetes
RFM30704.1	extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1	bpX4→ MoxR→ bpX2→ extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*→ bpX3+TPR_region+beta_propeller→ HTH+TetR_C→	775	Chitinophaga sp. K20C18050901	GCA_003412465.1	bacteroidetes
PWV51444.1	extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1	bpX4→ MoxR→ bpX2→ extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*→ bpX3+TPR_region+beta_propeller→ HTH+TetR_C→	817	Chitinophaga sp. S165	GCA_003182155.1	bacteroidetes
SEW36401.1	extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1	bpX4→ MoxR→ bpX2→ extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*→ bpX3+TPR_region+beta_propeller→ HTH+TetR_C→	597	Chitinophaga sp. YR573	GCA_900110995.1	bacteroidetes
SFO49267.1	extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1	bpX4→ MoxR→ bpX2→ extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*→ bpX3+TPR_region+beta_propeller→	829	Chitinophaga sp. YR627	GCA_900114995.1	bacteroidetes
SDQ16602.1	extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1	MoxR→ bpX2→ extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*→ bpX3+4TM→2TM+TPR_region→	802	Chryseobacterium soldanellicola	GCA_900100115.1	bacteroidetes
ABG58961.1	extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1	bpX4→ MoxR→ bpX2→ extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*→ bpX3+TPR_region→	843	Cytophaga hutchinsonii ATCC 33406	GCA_000014145.1	bacteroidetes
WP_108823377.1	extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1	bpX4→ MoxR→ bpX2→ extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*→ bpX3+TPR_region→	770	Dysgonomonas sp. Marseille-P4361	GCF_900343125.1	bacteroidetes
BAV07989.1	extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1	bpX4→ MoxR→ bpX2→ extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1→ *extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*→* bpX3+TPR_region→	883	Filimonas lacunae	GCA_002355595.1	bacteroidetes
PVY14782.1	extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1	bpX4→ MoxR→ bpX2→ extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*→ bpX3+TPR_region→	874	Filimonas sp. YR581	GCA_003097095.1	bacteroidetes
KIC92612.1	extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1	bpX4→ MoxR→ bpX2→ extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*→ bpX3+TPR_region→	783	Flavihumibacter solisilvae	GCA_000814475.1	bacteroidetes
KYP15344.1	extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1	bpX4→ MoxR→ bpX2→ extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*→ bpX3+TPR_region→	772	Flavihumibacter sp. CACIAM 22H1	GCA_001601815.1	bacteroidetes
ANE49440.1	extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1	bpX4→ MoxR→ bpX2→ extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*→ bpX3→	781	Flavisolibacter tropicus	GCA_001644645.1	bacteroidetes
AWH86615.1	extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1	bpX4→ MoxR→ bpX2→ extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*→ abpX3+2TM+TPR_region→	801	Flavobacterium album	GCA_003096035.1	bacteroidetes
WP_052705351.1	extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1	bpX4→ MoxR→ bpX2→ extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*→ bpX3+4TM→2TM+TPR_region→	845	Flavobacterium sp. 316	GCF_000967805.1	bacteroidetes
AEE53802.1	extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1	bpX4→ MoxR→ bpX2→ extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*→ bpX3+TPR_region+beta_propeller→	819	Haliscomenobacter hydrossis DSM 1100	GCA_000212735.1	bacteroidetes
PJJ59945.1	extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1	bpX4→ MoxR→ bpX2→ extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*→ bpX3+2TM+TPR_region+beta_propeller→	828	Hymenobacter chitinivorans DSM 11115	GCA_002797555.1	bacteroidetes
RTQ48805.1	extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1	MoxR→ bpX2→ extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*→	836	Hymenobacter gummosus	GCA_003970915.1	bacteroidetes
SNR82429.1	extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1	bpX4→ MoxR→ bpX2→ extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*→ bpX3+TPR_region+beta_propeller→	813	Hymenobacter mucosus	GCA_900188255.1	bacteroidetes
WP_022821708.1	extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1	bpX4→ MoxR→ bpX2→ extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*→	823	Hymenobacter norwichensis	GCF_000420705.1	bacteroidetes

acc	architecture	operon	len	species	gca	taxend
RSK36273.1	extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1	MoxR→ bpX2→ extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*→	830	Hymenobacter sp. 9PBR-2	GCA_003944705.1	bacteroidetes
EDP94883.1	extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1	bpX4→ MoxR→ bpX2→ extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*→ bpX3+4TM→2TM+TPR_region→	799	Kordia algicida OT-1	GCA_000154725.1	bacteroidetes
RKR84050.1	extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1	bpX4→ MoxR→ bpX2→ extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*→	788	Mucilaginibacter gracilis	GCA_003633615.1	bacteroidetes
EHQ24573.1	extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1	extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*→ bpX3+TPR_region+beta_propeller→	784	Mucilaginibacter paludis DSM 18603	GCA_000166195.3	bacteroidetes
RVU02898.1	extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1	bpX4→ MoxR→ bpX2→ extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*→ bpX3+2TM+TPR_region+beta_propeller→	791	Mucilaginibacter sp. YBJ-36	GCA_004005815.1	bacteroidetes
AEW02126.1	extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1	bpX4→ MoxR→ bpX2→ extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*→ bpX3+TPR_region+beta_propeller→	836	Niastella koreensis GR20-10	GCA_000246855.1	bacteroidetes
KRT17467.1	extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1	bpX4→ MoxR→ bpX2→ extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*→ bpX3+2TM+TPR_region+beta_propeller→	791	Pedobacter ginsenosidimutans	GCA_001442625.1	bacteroidetes
RQO30278.1	extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1	bpX4→ MoxR→ bpX2→ extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*→ bpX3+4TM→2TM+TPR_region→	787	Taibaiella sp. KBW10	GCA_003852495.1	bacteroidetes
PQO39541.1	extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1	bpX4→ MoxR→ bpX2→ extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*→ bpX3+TPR_region+beta_propeller→	917	Blastopirellula marina	GCA_002967765.1	planctomycetes
OWK46343.1	extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1	bpX2→ extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*→ bpX3+TPR_region+beta_propeller→	969	Fimbriiglobus ruber	GCA_002197845.1	planctomycetes
AMV26576.1	extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1	bpX4→ MoxR→ bpX2→ extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*→ bpX3+TPR_region+beta_propeller→	960	Gemmata sp. SH-PL17	GCA_001610855.1	planctomycetes
RUL85748.1	extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1	bpX4→ MoxR→ bpX2→ extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*→	960	Isosphaeraceae bacterium GM2012	GCA_003977685.1	planctomycetes
SFH92940.1	extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1	bpX4→ MoxR→ bpX2→ extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*→ bpX3+TPR_region+beta_propeller→	904	Planctomicrobium piriforme	GCA_900113665.1	planctomycetes
AMV18939.1	extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1	bpX4→ MoxR→ bpX2→ extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*→ bpX3+TPR_region+beta_propeller→	939	Planctomyces sp. SH-PL14	GCA_001610835.1	planctomycetes
RIK61979.1	extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1	MoxR→ bpX2→ extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*→	969	Planctomycetes bacterium	GCA_003576915.1	planctomycetes
RLS72559.1	extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1	bpX4→ MoxR→ bpX2→ extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*→ bpX3+2TM+TPR_region+??→	920	Planctomycetes bacterium	GCA_003669275.1	planctomycetes
OYP36357.1	extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1	bpX4→ MoxR→ bpX2→ extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*→ bpX3+TPR_region+beta_propeller→	923	Rhodopirellula sp. MGV	GCA_002251265.1	planctomycetes
WP_044252884.1	extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1	MoxR→ bpX2→ extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*→ bpX3+TPR_region+beta_propeller→	934	Rhodopirellula sp. SWK7	-	planctomycetes
WP_068134229.1	extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1	bpX4→ MoxR→ bpX2→ extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*→ bpX3+TPR_region+beta_propeller→	926	Roseimaritima ulvae	GCF_001642915.1	planctomycetes
WP_010582785.1	extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1	extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*→ bpX3+TPR_region+beta_propeller→	912	Schlesneria paludicola	GCF_000255655.1	planctomycetes
SIO62481.1	extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1	bpX4→ MoxR→ bpX2→ extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*→ bpX3+TPR_region+beta_propeller→	930	Singulisphaera sp. GP187	GCA_900129635.1	planctomycetes
WP_020472485.1	extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1	extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*→	910	Zavarzinella formosa	GCF_000255705.1	planctomycetes
WP_124744879.1	extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1	bpX4→ MoxR→ bpX2→ extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*→ bpX3+TPR_region→	770	Glaciecola sp. THG-3.7	GCF_003856375.1	gammaproteobacteria
EDY17134.1	extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1	bpX4→ MoxR→ bpX2→ extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*→ bpX3+TPR_region+beta_propeller→	928	Chthoniobacter flavus Ellin428	GCA_000173075.1	verrucomicrobia
EEF58752.1	extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1	bpX4→ MoxR→ bpX2→ extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*→?→ bpX3+TPR_region+beta_propeller→	799	Pedosphaera parvula Ellin514	GCA_000172555.1	verrucomicrobia
RBP36328.1	extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1	bpX4→ MoxR→ bpX2→ extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*→ bpX3+TPR_region+beta_propeller→	841	Roseimicrobium gellanilyticum	GCA_003315205.1	verrucomicrobia
PTY04067.1	extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1	extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*→	1028	Verrucomicrobia bacterium LW23	GCA_003054695.1	verrucomicrobia
WP_009959261.1	extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1	bpX4→ MoxR→ bpX2→ extended_strand+helical_region+vWA+beta_propeller+beta_rich_region+bpX1*→ bpX3+TPR_region+beta_propeller→	896	Verrucomicrobium spinosum	GCF_000172155.1	verrucomicrobia
WP_030304647.1	vWA+beta_propeller	MoxR→ bpX5→ vWA+beta_propeller*→ bpX6+TMs+TPRs+Betapropeller→	599	Streptomyces sp. NRRL F-6131	GCF_000719695.1	actinobacteria
PJI85297.1	vWA+beta_propeller	MoxR→?→ vWA+beta_propeller*→	626	Yoonia maricola	GCA_002797915.1	alphaproteobacteria
ODA19159.1	vWA+beta_propeller	MoxR→ bpX5→ vWA+beta_propeller*→ bpX6+TPRs+Betapropeller→	586	Achromobacter xylosoxidans	GCA_001707535.1	betaproteobacteria
KPC53758.1	vWA+beta_propeller	MoxR→ bpX5→ vWA+beta_propeller*→ bpX6+TPRs+Betapropeller→	605	Amantichitinum ursilacus	GCA_001294205.1	betaproteobacteria
SMC19581.1	vWA+beta_propeller	MoxR→ bpX5→ vWA+beta_propeller*→ bpX6+TMs+TPRs+Betapropeller→	597	Andreprevotia lacus DSM 23236	GCA_900176275.1	betaproteobacteria
AAQ60410.1	vWA+beta_propeller	MoxR→ bpX5→ vWA+beta_propeller*→	597	Chromobacterium violaceum ATCC 12472	GCA_000007705.1	betaproteobacteria
RFP17714.1	vWA+beta_propeller	MoxR→ bpX5→ vWA+beta_propeller*→ bpX6+TMs+TPRs+Betapropeller→	583	Duganella sp. BJB489	GCA_003416915.1	betaproteobacteria
KQZ25959.1	vWA+beta_propeller	MoxR→ bpX5→ vWA+beta_propeller*→ bpX6+TMs+TPRs+Betapropeller→	589	Duganella sp. Root1480D1	GCA_001427305.1	betaproteobacteria
WP_051057605.1	vWA+beta_propeller	MoxR→ bpX5→ vWA+beta_propeller*→?→ bpX6+TPRs+Betapropeller→	602	Herbaspirillum sp. B39	GCF_000333495.1	betaproteobacteria
SHH13774.1	vWA+beta_propeller	MoxR→ bpX5→ vWA+beta_propeller*→ bpX6+TMs+TPRs+Betapropeller→	611	Massilia sp. CF038	GCA_900129765.1	betaproteobacteria
ATQ78387.1	vWA+beta_propeller	MoxR→ bpX5→ vWA+beta_propeller→ *vWA+beta_propeller*→ bpX6+TPRs+Betapropeller→	594	Massilia violaceinigra	GCA_002752675.1	betaproteobacteria
RAS17227.1	bpX6+TPRs+Betapropeller←vWA+beta_propeller	MoxR→ bpX5→ vWA+beta_propeller*→ bpX6+TPRs+Betapropeller→||←?←BetaPropeller←BetaPropeller	601	Microvirgula sp. AG722	GCA_003269145.1	betaproteobacteria
ANH68664.1	vWA+beta_propeller	MoxR→ bpX5→ vWA+beta_propeller*→ bpX6+TMs+TPRs+Betapropeller→	652	Mitsuaria sp. 7	GCA_001653795.1	betaproteobacteria
CBJ39465.1	vWA+beta_propeller	MoxR→ bpX5→ vWA+beta_propeller*→ bpX6+TMs+TPRs+Betapropeller→	614	Ralstonia solanacearum CMR15	GCA_000427195.1	betaproteobacteria
ARN22671.1	vWA+beta_propeller	MoxR→ bpX5→ vWA+beta_propeller*→ bpX6+TMs+TPRs+Betapropeller→	599	Rhizobacter gummiphilus	GCA_002116905.1	betaproteobacteria
KQW02656.1	vWA+beta_propeller	MoxR→ bpX5→ vWA+beta_propeller*→ bpX6+TPRs+Betapropeller→	607	Rhizobacter sp. Root1221	GCA_001425785.1	betaproteobacteria
RQP22489.1	vWA+beta_propeller	MoxR→ bpX5→ vWA+beta_propeller*→ bpX6+TMs+TPRs+Betapropeller→	616	Rhizobacter sp. S-16	GCA_003852895.1	betaproteobacteria
SDW66728.1	vWA+beta_propeller	MoxR→ bpX5→ vWA+beta_propeller*→ bpX6+TMs+TPRs+Betapropeller→	619	Variovorax sp. YR634	GCA_900106655.1	betaproteobacteria
KFA87837.1	vWA+beta_propeller	bpX5→ vWA+beta_propeller*→ bpX6+TPRs+Betapropeller→	609	Archangium violaceum Cb vi76	GCA_000733295.1	deltaproteobacteria

acc	architecture	operon	len	species	gca	taxend
RJS21768.1	vWA+beta_propeller	MoxR→ bpX5→ vWA+beta_propeller*→ bpX6+TPRs+Betapropeller→	606	Corallococcus sp. H22C18031201	GCA_003600865.1	deltaproteobacteria
AKF84122.1	vWA+beta_propeller	bpX5→ vWA+beta_propeller*→	640	Myxococcus fulvus 124B02	GCA_000988565.1	deltaproteobacteria
ATB51059.1	vWA+beta_propeller	MoxR→ bpX5→ vWA+beta_propeller*→ bpX6+TPRs+Betapropeller→	606	Myxococcus macrosporus DSM 14697	GCA_002305895.1	deltaproteobacteria
ABF92814.1	vWA+beta_propeller	MoxR→ bpX5→ vWA+beta_propeller*→ bpX6+TPRs+Betapropeller→	608	Myxococcus xanthus DK 1622	GCA_000012685.1	deltaproteobacteria
OTQ06733.1	vWA+beta_propeller	MoxR→ bpX5→ vWA+beta_propeller*→ bpX6+TMs+TPRs+Betapropeller→	588	Gilliamella apicola	GCA_002141575.1	gammaproteobacteria
ABC29563.1	vWA+beta_propeller	MoxR→ bpX5→ vWA+beta_propeller*→ bpX6+TPRs+Betapropeller→	623	Hahella chejuensis KCTC 2396	GCA_000012985.1	gammaproteobacteria
WP_022951101.1	vWA+beta_propeller	MoxR→ bpX5→ vWA+beta_propeller*→ bpX6+TPRs+Betapropeller→	608	Leucothrix mucor	GCF_000419525.1	gammaproteobacteria
WP_064748987.1	vWA+beta_propeller	MoxR→ bpX5→ vWA+beta_propeller*→	616	Lysobacter antibioticus	GCF_000336385.2	gammaproteobacteria
BAV97131.1	vWA+beta_propeller	MoxR→ bpX5→ vWA+beta_propeller*→ bpX6+TPRs+Betapropeller→	605	Lysobacter enzymogenes	GCA_002355975.1	gammaproteobacteria
KRA21135.1	vWA+beta_propeller	MoxR→ bpX5→ vWA+beta_propeller*→ bpX6+TPRs+Betapropeller→	608	Lysobacter sp. Root604	GCA_001427505.1	gammaproteobacteria
KRB02264.1	vWA+beta_propeller	MoxR→ bpX5→ vWA+beta_propeller*→ bpX6+TPRs+Betapropeller→	620	Lysobacter sp. Root690	GCA_001427785.1	gammaproteobacteria
PNL50802.1	vWA+beta_propeller	RADICAL_SAM.Ammemo→?→ MoxR→ bpX5→ vWA+beta_propeller*→ bpX6+TPRs+Betapropeller→	637	Proteus mirabilis	GCA_002206145.2	gammaproteobacteria
EKT57597.1	vWA+beta_propeller	bpX5→ vWA+beta_propeller*→	628	Providencia sneebia DSM 19967	GCA_000314895.2	gammaproteobacteria
KIH83594.1	vWA+beta_propeller	MoxR→ bpX5→ vWA+beta_propeller*→ bpX6+TMs+TPRs+Betapropeller→	606	Pseudomonas batumici	GCA_000820515.1	gammaproteobacteria
WP_117164965.1	vWA+beta_propeller	MoxR→ bpX5→ vWA+beta_propeller*→ bpX6+TMs+TPRs+Betapropeller→	598	Pseudomonas cichorii	GCF_003415775.1	gammaproteobacteria
WP_029532585.1	vWA+beta_propeller	MoxR→ PSE→ vWA+beta_propeller*→?→ TPRs+Betapropeller→	573	Pseudomonas fuscovaginae	GCF_000467005.1	gammaproteobacteria
RMP14790.1	vWA+beta_propeller	MoxR→ bpX5→ vWA+beta_propeller*→ bpX6+TMs+TPRs+Betapropeller→	610	Pseudomonas marginalis pv. marginalis	GCA_003700875.1	gammaproteobacteria
RMR06475.1	vWA+beta_propeller	vWA+beta_propeller*→	617	Pseudomonas savastanoi pv. glycinea	GCA_003701285.1	gammaproteobacteria
WP_122602356.1	vWA+beta_propeller	MoxR→ bpX5→ vWA+beta_propeller*→ bpX6+TMs+TPRs+Betapropeller→	608	Pseudomonas sp. 286	GCF_900582885.1	gammaproteobacteria
KIV62454.1	vWA+beta_propeller	MoxR→ bpX5→ vWA+beta_propeller*→ bpX6+TMs+TPRs+Betapropeller→	610	Pseudomonas sp. FeS53a	GCA_000931385.1	gammaproteobacteria
WP_082033854.1	vWA+beta_propeller	MoxR→ bpX5→ vWA+beta_propeller*→	614	Pseudomonas sp. PI1	GCF_000812405.1	gammaproteobacteria
BAQ80643.1	vWA+beta_propeller	MoxR→ bpX5→ vWA+beta_propeller*→ bpX6+TMs+TPRs+Betapropeller→	605	Pseudomonas sp. St29	GCA_001547915.1	gammaproteobacteria
SNZ04485.1	vWA+beta_propeller	MoxR→ bpX5→ vWA+beta_propeller*→ bpX6+TPRs+Betapropeller→	614	Pseudomonas sp. URIL14HWK12:I9	GCA_900215525.1	gammaproteobacteria
ODU30905.1	vWA+beta_propeller	MoxR→ bpX5→ vWA+beta_propeller*→ bpX6+TPRs+Betapropeller→	598	Xanthomonadaceae bacterium SCN 69-320	GCA_001725155.1	gammaproteobacteria
PPT63983.1	vWA+beta_propeller	MoxR→ bpX5→ vWA+beta_propeller*→ bpX6+TPRs+Betapropeller→	616	Xanthomonas arboricola	GCA_002940525.1	gammaproteobacteria
KMM74478.1	vWA+beta_propeller	MoxR→ bpX5→ vWA+beta_propeller*→ bpX6+TPRs+Betapropeller→	616	Xanthomonas sp. NCPPB 1128	GCA_001043115.1	gammaproteobacteria
WP_020510239.1	ClpN_repeats+vWA	ClpN_repeats+vWA→ ClpN_repeats+vWA→ ClpN_repeats+vWA→ *ClpN_repeats+vWA*→ ClpN_repeats+vWA→ ClpN_repeats+vWA→?→?→ EAD1+CASPASE→	1040	Actinoplanes globisporus	GCF_000379645.1	actinobacteria
SDT45587.1	beta_propeller+helical_linker+vWA	??→ Trypsin+EAD1→ beta_propeller+helical_linker+vWA*→ RADICAL_SAM.Ammemo→ RadSAM_pep→?→ E1+UFD→ EAD1+Ubl-Nterm+Ubl+E2→	1145	Actinoplanes derwentensis	GCA_900104725.1	actinobacteria
SDT45954.1	beta_propeller+helical_linker+vWA	low_complexity+a/b_unk+TPR_repeat→ CASPASE+Ploop_NTPase→ BetaPropeller→ a/b_hydrolase→ EAD1+TIR→ beta_propeller+helical_linker+vWA*→	1137	Actinoplanes derwentensis	GCA_900104725.1	actinobacteria
OXM68678.1	beta_propeller+helical_linker+vWA	MoxR→?→ X3→ TPRs→ low_complexity+TPRs→ beta_propeller+helical_linker+vWA*→||←RadSAM_pep←RADICAL_SAM.Ammemo	1038	Amycolatopsis sp. H5	GCA_002234595.1	actinobacteria
WP_033359495.1	beta_propeller+helical_linker+vWA	MoxR→?→ X3→ TPRs→ low_complexity+TPRs→ beta_propeller+helical_linker+vWA*→||←RadSAM_pep←RADICAL_SAM.Ammemo	1005	Dactylosporangium aurantiacum	GCF_000716715.1	actinobacteria
KLL11673.1	beta_propeller+helical_linker+vWA	beta_propeller+helical_linker+vWA*→	858	Frankia coriariae	GCA_001017755.1	actinobacteria
SDG79101.1	beta_propeller+helical_linker+vWA	TPRs→ low_complexity+TPRs→ beta_propeller+helical_linker+vWA*→||←RadSAM_pep	1050	Sinosporangium album	GCA_900100605.1	actinobacteria
AZP16236.1	beta_propeller+helical_linker+vWA	beta_propeller+helical_linker+vWA*→||←RadSAM_pep←RADICAL_SAM.Ammemo	1043	Streptomyces sp. GGCR-6	GCA_003955715.1	actinobacteria
KOV61826.1	←beta_propeller+helical_linker+vWA	X3→ TPRs→ low_complexity+TPRs→ beta_propeller+helical_linker+vWA*→||←RadSAM_pep←RADICAL_SAM.Ammemo	1055	Streptomyces sp. MMG1121	GCA_001280015.1	actinobacteria
OUL34959.1	←beta_propeller+helical_linker+vWA	X3→ TPRs+C-type_lectin→||←?||low_complexity+TPRs→ beta_propeller+helical_linker+vWA*→||←RADICAL_SAM.Ammemo	771	Nostoc sp. T09	GCA_002154695.1	cyanobacteria
WP_053332818.1	beta_propeller+helical_linker+vWA	beta_propeller+helical_linker+vWA*→ TPRs→	870	Haliangium ochraceum	GCF_000024805.1	deltaproteobacteria
WP_082673981.1	beta_propeller+helical_linker+vWA	X3→ TPRs→ low_complexity+TPRs→||←?||beta_propeller+helical_linker+vWA*→	1188	Thiohalocapsa sp. ML1	GCF_001469165.1	gammaproteobacteria
KHD04278.1	helical_linker+vWA	helical_linker+vWA*→	424	Candidatus Thiomargarita nelsonii	-	gammaproteobacteria
RKZ47048.1	helical_linker+vWA	helical_linker+vWA*→	424	Gammaproteobacteria bacterium	GCA_003645185.1	gammaproteobacteria
WP_035921195.1	vWA	vWA*→	273	Frankia sp. QA3	GCF_000262465.1	actinobacteria
ETR67287.1	vWA	vWA*→	221	Candidatus Magnetoglobus multicellularis str. Araruama	GCA_000516475.1	deltaproteobacteria

acc	architecture	operon	len	species	gca	taxend
ETR65220.1	vWA	vWA*→	229	Candidatus Magnetoglobus multicellularis str. Araruama	GCA_000516475.1	deltaproteobacteria
WP_086758355.1	vWA	vWA*→	152	Streptomyces scabiei	GCF_002156075.1	actinobacteria

GAP1-N1-type GTPase centric systems

acc	architecture	operon	len	species	gca	taxend
ADY35731.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→?→ DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	662	Bacteroides salanitronis DSM 18170	GCA_000190575.1	bacteroidetes
AEL07773.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→	822	Xanthomonas campestris pv. raphani 756C	GCA_000221965.1	gammaproteobacteria
AGS80673.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ PNP_UDP_1+EAD1→	845	Leptospira phage vb_LkmZ_Bejolso9-LE1	GCA_002603685.1	dsdna viruses, no rna stage
AIJ49675.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ CASPASE+EAD1→	830	Comamonas testosteroni TK102	GCA_000739375.1	betaproteobacteria
AJX95795.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	704	Burkholderia pseudomallei PB08298010	GCA_000959345.1	betaproteobacteria
AMV35122.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→||←EAD1+Trypsin	844	Pirellula sp. SH-Sr6A	GCA_001610875.1	planctomycetes
ASL44118.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	688	Burkholderia sp. AD24	GCA_002220305.1	betaproteobacteria
ASR53154.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	871	Blastomonas fulva	GCA_003431825.1	alphaproteobacteria
AUC22653.1	GAP1-N1+GAP1-M+GAP1-C+PNP_UDP_1	GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+PNP_UDP_1*→	1031	Polaribacter sejongensis	GCA_002814075.1	bacteroidetes
BBC81760.1	GAP1-N1+GAP1-M+GAP1-C	AB_hydrolase+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	677	Acetobacter orientalis	GCA_003966365.1	alphaproteobacteria
BBD02433.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	881	Sphingobium sp. YG1	GCA_003609795.1	alphaproteobacteria
CDG51235.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ CASPASE+EAD1→	820	Halomonas sp. A3H3	GCA_000982975.1	gammaproteobacteria
CNI41896.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	651	Yersinia pekkanenii	GCA_001152565.1	gammaproteobacteria
CRE86890.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	838	Yersinia intermedia	GCA_001319925.1	gammaproteobacteria
CUQ34010.1	GAP1-N1	DO-GTPase1→ GAP1-N1*→	43	Prevotella copri	GCA_001405915.1	bacteroidetes
EEQ09204.1	GAP1-N1+GAP1-M+GAP1-C	DO-GTPase2.1(fragment)→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	589	Yersinia mollaretii ATCC 43969	GCA_000167995.1	gammaproteobacteria
EGG75068.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	884	Gluconacetobacter sp. SXCC-1	GCA_000208635.2	alphaproteobacteria
EIT67703.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	904	Hydrocarboniphaga effusa AP103	GCA_000271305.1	gammaproteobacteria
EJF69446.1	GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ DO-GTPase1→ GAP1-M+GAP1-C*→	793	Pseudomonas sp. Ag1	GCA_000278565.1	gammaproteobacteria
EJP17918.1	GAP1-N1	GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1*→	61	Leptospira interrogans str. FPW2026	GCA_000243895.3	spirochaetes
EKO23840.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	668	Leptospira interrogans str. UI 12621	GCA_000244275.3	spirochaetes
EKR43466.1	GAP1-N1+GAP1-M+GAP1-C	GAP1-N1+GAP1-M+GAP1-C*→	350	Leptospira interrogans serovar Grippotyphosa str. UI 08368	GCA_000244135.3	spirochaetes
EMG74074.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	679	Salmonella enterica subsp. enterica serovar Newport str. SH111077	GCA_000344825.1	gammaproteobacteria
EMS40767.1	GAP1-N1+GAP1-M+GAP1-C	CASPASE+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	650	Methylobacterium mesophilicum SR1.6/6	GCA_000364445.1	alphaproteobacteria
ENV08026.1	GAP1-N1+GAP1-M+GAP1-C	GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→ EAD1→ CASPASE+EAD1→	395	Acinetobacter sp. CIP 56.2	GCA_000368445.1	gammaproteobacteria
ERV84201.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	840	Pseudomonas aeruginosa BWHPSA028	GCA_000481145.1	gammaproteobacteria
ESZ35911.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	876	Mesorhizobium sp. L2C067A000	GCA_000502855.1	alphaproteobacteria
ETR71189.1	GAP1-N1+GAP1-M+GAP1-C	GrpE→?→?→ GrpE→ DO-GTPase2.1→ GAP1-N1+GAP1-M+GAP1-C*→	276	Candidatus Magnetoglobus multicellularis str. Araruama	GCA_000516475.1	deltaproteobacteria
EWG65005.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	651	Enterobacter sp. DC3	GCA_000568155.1	gammaproteobacteria
GAN50643.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	858	Methylobacterium sp. ME121	GCA_000974725.1	alphaproteobacteria
KDD14872.1	GAP1-N1+GAP1-M+GAP1-C	DO-GTPase2.1(fragment)→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	855	Bordetella bronchiseptica MBORD731	GCA_000698985.1	betaproteobacteria
KDL57610.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	651	Klebsiella variicola	GCA_000694595.1	gammaproteobacteria
KEC69694.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ DO-GTPase2.1→ GAP1-N1+GAP1-M+GAP1-C*→	907	Rhizobium leguminosarum bv. phaseoli CCGM1	GCA_000705615.1	alphaproteobacteria
KFB70201.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ CASPASE+EAD1→	829	Candidatus Accumulibacter sp. SK-01	GCA_000584955.2	betaproteobacteria
KIA82238.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ GAP1-N1+GAP1-M+GAP1-C*→	873	Chromobacterium piscinae	GCA_000812585.1	betaproteobacteria
KIP94692.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ CASPASE+EAD1→	829	Pseudomonas fluorescens	GCA_000834545.1	gammaproteobacteria
KIU30546.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	879	Methylobacterium radiotolerans	GCA_000878385.1	alphaproteobacteria
KJS35250.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→	749	Rhodospirillaceae bacterium BRH_c57	GCA_000961745.1	alphaproteobacteria
KJS38336.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	694	Hyphomonas sp. BRH_c22	GCA_000961795.1	alphaproteobacteria

acc	architecture	operon	len	species	gca	taxend
KMS75234.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ CASPASE+EAD1→	824	Streptomyces viridochromogenes	GCA_001047325.1	actinobacteria
KOR33477.1	GAP1-N1+GAP1-M+GAP1-C	GAP1-N1+GAP1-M+GAP1-C*→	1014	Achromatium sp. WMS3	GCA_001276615.1	gammaproteobacteria
KPW87077.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ GAP1-N1+GAP1-M+GAP1-C*→	880	Pseudomonas congelans	GCA_001400775.1	gammaproteobacteria
KQU31117.1	GAP1-N1+GAP1-M+GAP1-C	GAP1-N1+GAP1-M+GAP1-C*→	494	Methylobacterium sp. Leaf94	GCA_001426045.1	alphaproteobacteria
KQV53300.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	820	Pelomonas sp. Root1217	GCA_001425705.1	betaproteobacteria
KVK81003.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→||←?||DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	676	Burkholderia ubonensis	GCA_001526225.1	betaproteobacteria
KVM36471.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→||←?||DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	704	Burkholderia ubonensis	GCA_001527385.1	betaproteobacteria
KVT48317.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	871	Burkholderia ubonensis	GCA_001528875.1	betaproteobacteria
KXG12688.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ CASPASE+EAD1→	827	Pseudomonas aeruginosa	GCA_001560865.1	gammaproteobacteria
KYF95748.1	GAP1-N1+GAP1-M+GAP1-C	GAP1-N1+GAP1-M+GAP1-C*→||←DO-GTPase1←ZnR+DO-GTPase2.1←GAP2	868	Sorangium cellulosum	GCA_001589295.1	deltaproteobacteria
KZB53811.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR(fragment)+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	674	Thalassospira xiamenensis	GCA_001613855.1	alphaproteobacteria
OCX33136.1	GAP1-N1+GAP1-M+GAP1-C	DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	872	Bradyrhizobium sp. UASWS1016	GCA_001705105.1	alphaproteobacteria
OFW09671.1	GAP1-N1+GAP1-M+GAP1-C	DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	905	Acidobacteria bacterium RIFCSPLOWO2_12_FULL_59_11	GCA_001767115.1	acidobacteria
OGB06618.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	687	Burkholderiales bacterium RIFCSPHIGHO2_02_FULL_64_19	GCA_001772075.1	betaproteobacteria
OHC26956.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	581	Pseudomonadales bacterium RIFCSPLOWO2_12_59_9	GCA_001830395.1	gammaproteobacteria
OJW12786.1	GAP1-N1+GAP1-M+GAP1-C	TIR+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	712	Mucilaginibacter sp. 44-25	GCA_001898335.1	bacteroidetes
OJW81738.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ PNP_UDP_1+EAD1→	792	Bacteroidetes bacterium 46-16	GCA_001897835.1	bacteroidetes
OJX35082.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ CASPASE+EAD1→	822	Burkholderiales bacterium 68-20	GCA_001898665.1	betaproteobacteria
OKO35123.1	GAP1-N1+GAP1-M+GAP1-C	GAP2→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→ EAD1→	381	Acinetobacter baumannii	GCA_001874765.1	gammaproteobacteria
OKO42867.1	GAP1-N1+GAP1-M+GAP1-C	PNP_UDP_1+EAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→ EAD1→	582	Acinetobacter baumannii	GCA_001874765.1	gammaproteobacteria
OLF53922.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ CASPASE+EAD1→	819	Pseudomonas chlororaphis	GCA_001921865.1	gammaproteobacteria
OQW76544.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	880	Proteobacteria bacterium ST_bin14	GCA_002083655.1	proteobacteria
OUM77232.1	GAP1-N1+GAP1-M+GAP1-C	GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	304	Acinetobacter baumannii	GCA_001432265.1	gammaproteobacteria
OUN76202.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→?→ DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	657	Alistipes sp. An54	GCA_002159375.1	bacteroidetes
OWK25036.1	GAP1-N1+GAP1-M+GAP1-C	GAPEAD1→ GAP2→ GAP1-N1+GAP1-M+GAP1-C*→?→ Calcineurin→	336	Rhizobium yanglingense	GCA_002200935.1	alphaproteobacteria
OYX25764.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→??+EAD1→ EAD1+Trypsin→	834	Flavobacteriales bacterium 32-35-8	GCA_002280395.1	bacteroidetes
OYY94018.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	Calcineurin+EAD1→||←?||GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→	730	Hydrogenophilales bacterium 28-61-23	GCA_002281555.1	proteobacteria
PCI26491.1	GAP1-N1+GAP1-M+GAP1-C+PNP_UDP_1	GAP2→ DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+PNP_UDP_1*→	1045	SAR324 cluster bacterium	GCA_002401295.1	deltaproteobacteria
PCI68527.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→	829	Gammaproteobacteria bacterium	GCA_002401655.1	gammaproteobacteria
PCI83911.1	GAP1-N1+GAP1-M+GAP1-C+CASPASE	GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+CASPASE*→	930	Ectothiorhodospiraceae bacterium	GCA_002401775.1	gammaproteobacteria
PCI90653.1	GAP1-N1+GAP1-M+GAP1-C+CASPASE	GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+CASPASE*→	930	Ectothiorhodospiraceae bacterium	GCA_002401775.1	gammaproteobacteria
PHV10311.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	689	Chitinimonas sp. BJB300	GCA_002735695.1	betaproteobacteria
PHV25597.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ CASPASE+EAD1→	779	Janthinobacterium sp. BJB426	GCA_002735705.1	betaproteobacteria
PIL47826.1	GAP1-N1+GAP1-M+GAP1-C	PNP_UDP_1+EAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	489	Acinetobacter baumannii	GCA_002760695.1	gammaproteobacteria
PIL52425.1	GAP1-N1+GAP1-M+GAP1-C	PNP_UDP_1+EAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	469	Acinetobacter baumannii	GCA_002760725.1	gammaproteobacteria
PIL53638.1	GAP1-N1+GAP1-M+GAP1-C	PNP_UDP_1+EAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	383	Acinetobacter baumannii	GCA_002760715.1	gammaproteobacteria
PIL63415.1	GAP1-N1+GAP1-M+GAP1-C	PNP_UDP_1+EAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	161	Acinetobacter baumannii	GCA_002760785.1	gammaproteobacteria
PIL66775.1	GAP1-N1+GAP1-M+GAP1-C	GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	228	Acinetobacter baumannii	GCA_002760765.1	gammaproteobacteria
PIL69197.1	GAP1-N1+GAP1-M+GAP1-C	ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	212	Acinetobacter baumannii	GCA_002760825.1	gammaproteobacteria
PIL82486.1	GAP1-N1+GAP1-M+GAP1-C	GAP1-N1+GAP1-M+GAP1-C*→	426	Acinetobacter baumannii	GCA_002760895.1	gammaproteobacteria
PKG61900.1	GAP1-N1+GAP1-M+GAP1-C	DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	645	Psychrobacter sp. Choline-02u-13	GCA_002836235.1	gammaproteobacteria
PKM46863.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	683	Gammaproteobacteria bacterium HGW-Gammaproteobacteria-1	GCA_002840095.1	gammaproteobacteria
PKM75314.1	GAP1-N1+GAP1-M+GAP1-C	DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	639	Firmicutes bacterium HGW-Firmicutes-17	GCA_002841525.1	firmicutes
PKO39589.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ PSE→ GAP1-N1+GAP1-M+GAP1-C*→	689	Betaproteobacteria bacterium HGW-Betaproteobacteria-6	GCA_002842145.1	betaproteobacteria
PKP48546.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ PNP_UDP_1+EAD1→	829	Bacteroidetes bacterium HGW-Bacteroidetes-11	GCA_002842665.1	bacteroidetes
PLT23558.1	GAP1-N1+GAP1-M+GAP1-C	GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	378	Psychrobacter sp. MES7-P7E	GCA_002863645.1	gammaproteobacteria

acc	architecture	operon	len	species	gca	taxend
PMH59968.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	611	Vibrio lentus	GCA_002873265.1	gammaproteobacteria
PMH70067.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	PNP_UDP_1+EAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ SLATT→	805	Vibrio splendidus	GCA_002878555.1	gammaproteobacteria
PRY19984.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ PNP_UDP_1+EAD1→	815	Pseudosporangium ferrugineum	GCA_003002065.1	actinobacteria
PRY35997.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ PNP_UDP_1+EAD1→	813	Spirosoma oryzae	GCA_003002825.1	bacteroidetes
PSH02583.1	GAP1-N1+GAP1-M+GAP1-C	DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	418	Acidobacteria bacterium	GCA_003010405.1	acidobacteria
SAQ17800.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	651	Klebsiella oxytoca	GCA_900084005.1	gammaproteobacteria
SAY47011.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	855	Komagataeibacter rhaeticus	GCA_900086575.1	alphaproteobacteria
SDC45789.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	872	Variovorax sp. CF079	GCA_900101545.1	betaproteobacteria
SDF29865.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	643	Bradyrhizobium sp. R5	GCA_900101405.1	alphaproteobacteria
SDP87527.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	873	Pseudomonas congelans	GCA_900103225.1	gammaproteobacteria
SDQ38520.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	888	Pseudomonas sp. UC 17F4	GCA_900101695.1	gammaproteobacteria
SDX24507.1	GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-M+GAP1-C*→	728	Lysobacter enzymogenes	GCA_900106525.1	gammaproteobacteria
SDY57230.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	873	Pseudomonas syringae	GCA_900107345.1	gammaproteobacteria
SEA61952.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	653	Acidovorax soli	GCA_900107605.1	betaproteobacteria
SED79523.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	874	Paraburkholderia caballeronis	GCA_900104845.1	betaproteobacteria
SEQ94678.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	653	Litorimicrobium taeanense	GCA_900110775.1	alphaproteobacteria
SER37675.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ CASPASE+EAD1→	828	Giesbergeria anulus	GCA_900111115.1	betaproteobacteria
SFB61072.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→ SLATT→	689	Azotobacter beijerinckii	GCA_900112015.1	gammaproteobacteria
SFD88056.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	690	Blastococcus sp. DSM 46838	GCA_900112815.1	actinobacteria
SFU95039.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	880	Pseudomonas sp. OV546	GCA_900116845.1	gammaproteobacteria
SHI10396.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	653	Sporobacter termitidis DSM 10068	GCA_900130065.1	firmicutes
SIR73769.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	888	Pseudomonas putida	GCA_900156185.1	gammaproteobacteria
SLY49252.1	GAP1-N1+GAP1-M+GAP1-C	GAPEAD1→ GAP2→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	651	Klebsiella pneumoniae	GCA_900174015.1	gammaproteobacteria
SOD32715.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ CASPASE+EAD1→	825	Serratia sp. JKS296	GCA_900215445.1	gammaproteobacteria
WP_000583717.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ PNP_UDP_1+EAD1→	842	Leptospira interrogans	GCA_000216135.3	spirochaetes
WP_002184169.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ PNP_UDP_1+EAD1→	842	Leptospira interrogans	GCA_000306495.2	spirochaetes
WP_002551483.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ CASPASE(frag)→ PSE→ CASPASE+EAD1→	834	Pseudomonas savastanoi	GCA_000164015.3	gammaproteobacteria
WP_003585899.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	644	Rhizobium leguminosarum	GCA_000271785.1	alphaproteobacteria
WP_004293833.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→?→ DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	663	Bacteroides	GCA_000738065.1	bacteroidetes
WP_004624951.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	655	[Clostridium] termitidis	GCA_000350485.1	firmicutes
WP_004911050.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ CASPASE+EAD1→	826	Acinetobacter junii	GCA_000368665.1	gammaproteobacteria
WP_005142132.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	PNP_UDP_1+EAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→	798	Acinetobacter	GCA_001896005.1	gammaproteobacteria
WP_005265695.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	PNP_UDP_1+EAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→	798	Acinetobacter	GCA_000369745.1	gammaproteobacteria
WP_005682844.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→?→ DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	663	Bacteroides	GCA_001404375.1	bacteroidetes
WP_005792628.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	681	Acidovorax delafieldii	GCA_000175235.1	betaproteobacteria
WP_006889296.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	PNP_UDP_1+EAD1→ GAP2→||←?||GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→	814	Methylobacter tundripaludum	GCA_000190755.3	gammaproteobacteria
WP_006964510.1	GAP1-N1+GAP1-M+GAP1-C	??+PNP_UDP_1+EAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→?→ EAD1→	621	Desulfotignum phosphitoxidans	GCA_000350545.1	deltaproteobacteria
WP_007244465.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ GAP1-N1+GAP1-M+GAP1-C*→	870	Pseudomonas syringae group genomosp. 3	GCA_002966555.1	gammaproteobacteria
WP_007766092.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ PSE→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ CASPASE+EAD1→	813	Rhizobium sp. CF080	GCA_000282095.2	alphaproteobacteria
WP_007888757.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	609	Roseburia inulinivorans	GCA_000174195.1	firmicutes
WP_009169750.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	634	Clostridium sp. DL-VIII	GCA_000230835.1	firmicutes
WP_009284468.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ PNP_UDP_1+EAD1→	828	Fibrisoma limi	GCA_000296815.2	bacteroidetes
WP_009518308.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ CASPASE+EAD1→	826	Acinetobacter baumannii	GCA_000314635.1	gammaproteobacteria
WP_010208169.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ GAP1-N1+GAP1-M+GAP1-C*→	866	Pseudomonas syringae group genomosp. 3	GCF_000177455.1	gammaproteobacteria
WP_010335847.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	896	Sphingobium yanoikuyae	-	alphaproteobacteria
WP_010801596.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→?→ DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	664	Parabacteroides	GCA_000364265.1	bacteroidetes
WP_011103173.1	GAP1-N1+GAP1-M+GAP1-C	DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	650	Pseudomonas syringae group genomosp. 3	GCF_000007805.1	gammaproteobacteria
WP_011965441.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→?→ DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	659	Bacteroides vulgatus	GCA_000012825.1	bacteroidetes
WP_011995908.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ CASPASE+EAD1→	824	Xanthobacter autotrophicus	GCA_000017645.1	alphaproteobacteria
WP_012406443.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	666	Paraburkholderia phymatum	GCA_000020045.1	betaproteobacteria
WP_012548896.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→?→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	603	Aliivibrio salmonicida	GCA_000196495.1	gammaproteobacteria
WP_012723147.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	871	Pseudomonas fluorescens	GCA_000009225.1	gammaproteobacteria

acc	architecture	operon	len	species	gca	taxend
WP_012806743.1	GAP1-N1+GAP1-M+GAP1-C	GAP1-N1+GAP1-M+GAP1-C*→	696	Candidatus Accumulibacter phosphatis	GCA_000024165.1	betaproteobacteria
WP_013593491.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ CASPASE+EAD1→	822	Acidovorax avenae	GCA_000176855.2	betaproteobacteria
WP_014682791.1	GAP1-N1+GAP1-M+GAP1-C	GAP2→ DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	789	Deinococcus gobiensis	GCA_000252445.1	deinococci
WP_015073721.1	GAP1-N1+GAP1-M+GAP1-C	CASPASE+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	664	Gluconobacter oxydans	GCA_000311765.1	alphaproteobacteria
WP_015241824.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ CASPASE+EAD1→	825	Sinorhizobium meliloti	GCA_000320385.2	alphaproteobacteria
WP_017050961.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	PNP_UDP_1+EAD1→ GAP2→ ZnR(fragment)+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ SLATT→	809	Vibrio ordalii	GCA_000287135.2	gammaproteobacteria
WP_017258880.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	882	Pedobacter arcticus	GCF_000302595.1	bacteroidetes
WP_018632651.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	649	Neomegalonema perideroedes	GCF_000374145.1	alphaproteobacteria
WP_019600192.1	GAP1-N1+GAP1-M+GAP1-C+PNP_UDP_1	GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+PNP_UDP_1*→	1034	Rhodonellum	GCA_000473765.1	bacteroidetes
WP_020123514.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ CASPASE+EAD1→	765	Streptomyces canus	GCF_000383615.1	actinobacteria
WP_021205085.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	871	Pseudomonas aeruginosa	GCA_000455705.1	gammaproteobacteria
WP_021446629.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ CASPASE+EAD1→	828	Alcaligenes sp. EGD-AK7	GCA_000465875.3	betaproteobacteria
WP_022696794.1	GAP1-N1+GAP1-M+GAP1-C+DNA-glycosylase+EAD1	GAP2→ DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+DNA-glycosylase+EAD1*→ CASPASE+EAD1→	810	Euryhalocaulis caribicus	GCF_000412185.1	alphaproteobacteria
WP_023775588.1	GAP1-N1+GAP1-M+GAP1-C	GAP1-N1+GAP1-M+GAP1-C*→	511	Mesorhizobium sp. LNHC229A00	GCA_000502415.1	alphaproteobacteria
WP_023783068.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	643	Mesorhizobium sp. LNHC220B00	GCA_000502395.1	alphaproteobacteria
WP_023802006.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR(fragment)+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	677	Mesorhizobium sp. L48C026A00	GCA_000502375.1	alphaproteobacteria
WP_023808270.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	880	Mesorhizobium sp. L2C085B000	GCA_000502895.1	alphaproteobacteria
WP_024138975.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ DO-GTPase2.1(fragment)→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	629	Salmonella enterica	GCF_000344825.1	gammaproteobacteria
WP_024658860.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	876	Pseudomonas syringae	GCF_000452545.1	gammaproteobacteria
WP_025177520.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	671	Leptospira interrogans	GCA_002074835.1	spirochaetes
WP_025381480.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ CASPASE+EAD1→	820	Yersinia similis	GCA_000582515.1	gammaproteobacteria
WP_025626868.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→	662	Vibrio parahaemolyticus	GCF_000490295.1	gammaproteobacteria
WP_025726211.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→?→ DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	664	Bacteroides sp. 14(A)	GCF_000526555.1	bacteroidetes
WP_026768844.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ PNP_UDP_1+EAD1→	846	Asinibacterium sp. OR53	GCF_000515315.1	bacteroidetes
WP_027604116.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	879	Pseudomonas	GCA_900177315.1	gammaproteobacteria
WP_027988968.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ CASPASE+EAD1→	825	Sinorhizobium meliloti	GCA_004001485.1	alphaproteobacteria
WP_028170393.1	GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-M+GAP1-C*→	783	Bradyrhizobium japonicum	GCA_000807315.1	alphaproteobacteria
WP_028672472.1	GAP1-N1+GAP1-M+GAP1-C	DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	867	Saccharospirillum impatiens	GCF_000423605.1	gammaproteobacteria
WP_029095773.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	611	Budvicia aquatica	GCA_002591785.1	gammaproteobacteria
WP_032370172.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→?→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ PNP_UDP_1+EAD1→ PNP_UDP_1→	818	Rhodococcus fascians	GCF_000760995.1	actinobacteria
WP_032389288.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→?→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ PNP_UDP_1+EAD1→ PNP_UDP_1→	818	Rhodococcus fascians	GCF_000761035.1	actinobacteria
WP_032815283.1	GAP1-N1+GAP1-M+GAP1-C	DO-GTPase2.1(fragment)→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	564	Yersinia mollaretii	GCF_000167995.1	gammaproteobacteria
WP_032899633.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	872	Pseudomonas sp. Agl	GCF_000278565.1	gammaproteobacteria
WP_033159517.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	PNP_UDP_1+EAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→	811	Methylomonas sp. LW13	GCA_000702925.2	gammaproteobacteria
WP_033840772.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	877	Bordetella bronchiseptica	GCF_000698985.1	betaproteobacteria
WP_035621591.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→??+EAD1→ EAD1+Trypsin→	845	Flavobacterium hydatis	GCA_000737695.1	bacteroidetes
WP_036748648.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	PNP_UDP_1+EAD1→ GAP2→ ZnR(fragment)+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ SLATT→	810	Photobacterium galatheae	GCA_000695255.1	gammaproteobacteria
WP_037146786.1	GAP1-M+GAP1-C+??	Calcineurin+GAPEAD1→ GAP2→ DO-GTPase2.1→ DO-GTPase1→ GAP1-M+GAP1-C+??*→	784	Rhizobium	GCA_003150695.1	alphaproteobacteria
WP_038637402.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	PNP_UDP_1+EAD1→ GAP2→ ZnR(fragment)+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ SLATT→	809	Pseudoalteromonas piratica	GCA_000788395.1	gammaproteobacteria
WP_038698912.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→?→??+EAD1→ EAD1+Trypsin→	850	Sphingobacterium sp. ML3W	GCA_000747525.1	bacteroidetes
WP_038799205.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ CASPASE+EAD1→	829	Burkholderia pseudomallei	GCA_000773415.1	betaproteobacteria
WP_039013431.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→	828	Cupriavidus sp. IDO	GCA_000812465.1	betaproteobacteria
WP_039045051.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	PNP_UDP_1+EAD1→ GAP2→ ZnR(fragment)+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ SLATT→	807	Plesiomonas shigelloides	GCF_000813415.1	gammaproteobacteria
WP_039487494.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	869	Pectobacterium polaris	GCA_000749915.1	gammaproteobacteria
WP_039554384.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	PNP_UDP_1+EAD1→ GAP2→ ZnR(fragment)+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ SLATT→	809	Vibrio vulnificus	GCA_000746665.1	gammaproteobacteria
WP_039766187.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	870	Pseudomonas fluorescens	GCA_000817905.1	gammaproteobacteria
WP_039894283.1	GAP1-N1+GAP1-M+GAP1-C	CASPASE+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	657	Methylobacterium mesophilicum	GCF_000364445.1	alphaproteobacteria
WP_039999911.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	880	Acetobacteraceae	GCA_002762195.1	alphaproteobacteria
WP_040455186.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	887	Hydrocarboniphaga effusa	GCF_000271305.1	gammaproteobacteria
WP_041583905.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→?→ DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	663	Bacteroides salanitronis	GCF_000190575.1	bacteroidetes
WP_041766525.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	701	Paraburkholderia caribensis	GCA_003028645.1	betaproteobacteria
WP_042387557.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	871	Pseudescherichia vulneris	GCA_000759795.1	gammaproteobacteria

acc	architecture	operon	len	species	gca	taxend
WP_043393687.1	GAP1-N1+GAP1-M+GAP1-C	GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	905	Archangium violaceum	GCA_000733295.1	deltaproteobacteria
WP_043607170.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	673	Novosphingobium sp. B-7	GCF_000410015.1	alphaproteobacteria
WP_043816345.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	656	Aeromonas salmonicida	GCA_001643285.1	gammaproteobacteria
WP_044342662.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ CASPASE+EAD1→	828	Pseudomonas oryzihabitans	GCA_000935305.1	gammaproteobacteria
WP_045379206.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	430	Vibrio campbellii	GCF_000818335.1	gammaproteobacteria
WP_045419498.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	ZnR(fragment)+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ SLATT→	809	Vibrio jasicida	GCF_000818715.1	gammaproteobacteria
WP_045492829.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	PNP_UDP_1+EAD1→ GAP2→ ZnR(fragment)+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ SLATT→	809	Vibrio hyugaensis	GCF_000818475.1	gammaproteobacteria
WP_045576370.1	GAP1-N1+GAP1-M+GAP1-C	GAP1-N1+GAP1-M+GAP1-C*→	668	Desulfosporosimus sp. I2	GCA_000960765.1	firmicutes
WP_045628704.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	608	Vibrio vulnificus	GCF_000959835.1	gammaproteobacteria
WP_045752253.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→??+EAD1→ EAD1+Trypsin→	847	Sphingobacterium sp. PM2-P1-29	GCA_000938735.2	bacteroidetes
WP_046017835.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	656	Marinomonas sp. S3726	GCA_000967665.1	gammaproteobacteria
WP_046064071.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ CASPASE+EAD1→	826	Pseudomonas kilonensis	GCA_000968575.1	gammaproteobacteria
WP_046067188.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR(fragment)+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	676	Sinorhizobium meliloti	GCA_000968555.1	alphaproteobacteria
WP_046463994.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	872	Pseudomonas syringae group genomosp. 3	GCA_000980905.1	gammaproteobacteria
WP_046689645.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	671	Leptospira santarosai	GCA_000988105.2	spirochaetes
WP_046951455.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	671	Leptospira santarosai	GCA_001981455.1	spirochaetes
WP_047110447.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	PNP_UDP_1+EAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ SLATT→	807	Vibrio vulnificus	GCA_001013325.1	gammaproteobacteria
WP_047535633.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ CASPASE+EAD1→	823	Shewanella sp. ZOR0012	GCF_000798835.1	gammaproteobacteria
WP_048399784.1	GAP1-N1+GAP1-M	-	1007	Candidatus Achromatium palustre	-	gammaproteobacteria
WP_048503675.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→??+EAD1→ EAD1+Trypsin→	843	Chryseobacterium sp. BLS98	GCA_001045445.1	bacteroidetes
WP_048580951.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ CASPASE+EAD1→	765	Streptomyces viridochromogenes	GCF_001047325.1	actinobacteria
WP_049614825.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	658	Yersinia pekkanenii	GCF_001152565.1	gammaproteobacteria
WP_050085962.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	869	Yersinia	GCF_001140765.1	gammaproteobacteria
WP_050103946.1	GAP1-N1+GAP1-M+GAP1-C	GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	869	Yersinia pseudotuberculosis	GCA_001136465.1	gammaproteobacteria
WP_050537229.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	669	Yersinia mollaretii	GCA_001319605.1	gammaproteobacteria
WP_050586283.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ CASPASE+EAD1→	745	Pseudomonas syringae	GCF_000452605.1	gammaproteobacteria
WP_050594058.1	GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-M+GAP1-C*→	739	Mesorhizobium sp. L2C067A000	GCF_000502855.1	alphaproteobacteria
WP_050642156.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	644	Eubacterium sp. SB2	GCF_001244405.1	firmicutes
WP_052246573.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	785	Chromobacterium piscinae	GCF_000812585.1	betaproteobacteria
WP_052516912.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	890	Methylobacterium radiotolerans	GCA_002221455.1	alphaproteobacteria
WP_052820524.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	878	Agrobacterium sp. SUL3	GCA_001263295.1	alphaproteobacteria
WP_053349796.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	PNP_UDP_1+EAD1→ GAP2→ ZnR(fragment)+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ SLATT→	809	Vibrio alginolyticus	GCF_001273715.1	gammaproteobacteria
WP_053486428.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ CASPASE+EAD1→	826	Pseudomonas coronafaciens	GCA_001275735.1	gammaproteobacteria
WP_053572419.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	698	Caballeronia cordobensis	GCF_001278535.1	betaproteobacteria
WP_053856890.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ DO-GTPase2.1→ PSE→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ CASPASE+EAD1→	809	Halomonas	GCA_900099955.1	gammaproteobacteria
WP_055335602.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	871	Ralstonia solanacearum	GCF_001373335.1	betaproteobacteria
WP_056213067.1	GAP1-N1+GAP1-M+GAP1-C	GAP1-N1+GAP1-M+GAP1-C*→	487	Methylobacterium sp. Leaf94	GCF_001426045.1	alphaproteobacteria
WP_056265586.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP1-N1+GAP1-M+GAP1-C+EAD1*→ CASPASE+EAD1→	750	Methylobacterium sp. Leaf87	GCA_001422775.1	alphaproteobacteria
WP_056276317.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ PSE→ GAP1-N1+GAP1-M+GAP1-C*→	686	Hydrogenophaga sp. Root209	GCA_001428625.1	betaproteobacteria
WP_056690820.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ CASPASE+EAD1→	824	Sphingobium sp. Leaf26	GCA_001421665.1	alphaproteobacteria
WP_057298085.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	762	Pelomonas sp. Root1217	GCF_001425705.1	betaproteobacteria
WP_057416337.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ CASPASE+EAD1→	826	Pseudomonas syringae group genomosp. 3	GCA_001401405.1	gammaproteobacteria
WP_057443670.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	876	Pseudomonas amygdali	GCA_001401265.1	gammaproteobacteria
WP_057505037.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	871	Stenotrophomonas nitritireducens	GCA_001431425.1	gammaproteobacteria
WP_058029521.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	PNP_UDP_1+EAD1→ GAP2→ ZnR(fragment)+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ SLATT→	809	Pseudoalteromonas phenolica	GCA_001444405.1	gammaproteobacteria
WP_058248883.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ CASPASE+EAD1→	835	Tropicibacter naphthalenivorans	GCA_001458375.1	alphaproteobacteria
WP_058410945.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	674	Pseudomonas	GCA_001467145.1	gammaproteobacteria
WP_058428192.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ CASPASE+EAD1→	834	Pseudomonas syringae	GCA_001467105.1	gammaproteobacteria
WP_058819802.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	629	Salmonella enterica	GCA_004219785.1	gammaproteobacteria
WP_059570022.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	643	Burkholderia sp. TSV86	GCA_001522865.1	betaproteobacteria
WP_059729175.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	880	Burkholderia ubonensis	GCA_001522035.1	betaproteobacteria
WP_059733060.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	876	Burkholderia cepacia	GCA_001526205.1	betaproteobacteria

acc	architecture	operon	len	species	gca	taxend
WP_059864452.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	876	Burkholderia ubonensis	GCA_001528175.1	betaproteobacteria
WP_059931657.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	864	Burkholderia ubonensis	GCF_001528875.1	betaproteobacteria
WP_060016453.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	876	Burkholderia stagnalis	GCA_001527825.1	betaproteobacteria
WP_060087567.1	GAP1-M+GAP1-C	Calcineurin+GAPEAD1→||←?||DO-GTPase2.1→ DO-GTPase1→ GAP1-M+GAP1-C*→	792	Burkholderia ubonensis	GCA_001529865.1	betaproteobacteria
WP_060227644.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ CASPASE+EAD1→	827	Burkholderia ubonensis	GCA_001533325.1	betaproteobacteria
WP_060275707.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	871	Burkholderia ubonensis	GCA_001532865.1	betaproteobacteria
WP_060408983.1	GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-M+GAP1-C*→	786	Pseudomonas syringae	GCA_001535945.1	gammaproteobacteria
WP_060854171.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	700	Caballeronia cordobensis	GCA_001544575.2	betaproteobacteria
WP_061209303.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	672	Leptospira borgpetersenii	GCF_001568445.1	spirochaetes
WP_061218562.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	671	Leptospira weilii	GCF_001569365.1	spirochaetes
WP_061908297.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ CASPASE+EAD1→ CASPASE+??→	814	Devosia sp. Leaf420	GCA_001425445.1	alphaproteobacteria
WP_062959907.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ DO-GTPase2.1(fragment)→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	601	Thalassospira xiamenensis	GCA_003326775.1	alphaproteobacteria
WP_063151208.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	871	Enterobacteriaceae	GCF_900075065.1	gammaproteobacteria
WP_064170057.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	869	Klebsiella	GCA_002152295.1	gammaproteobacteria
WP_064791174.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	871	Enterobacter asburiae	GCA_001663525.1	gammaproteobacteria
WP_064992291.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	674	Mesorhizobium loti	GCA_001672365.1	alphaproteobacteria
WP_065204322.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	PNP_UDP_1+EAD1→ GAP2→ ZnR(fragment)+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ SLATT→	809	Shewanella sp. Alg231_23	GCF_900079515.1	gammaproteobacteria
WP_065832748.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ CASPASE+EAD1→	828	Pseudomonas syringae	GCA_001698815.1	gammaproteobacteria
WP_066124811.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	875	Bordetella ansorpii	GCA_900078705.1	betaproteobacteria
WP_066213797.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	880	Blastomonas sp. CCH5-A3	GCF_001556295.1	alphaproteobacteria
WP_066223696.1	GAP1-N1+GAP1-M+GAP1-C	GAP2→ PSE→ PSE→ GAP1-N1+GAP1-M+GAP1-C*→ EAD1→?→??+EAD1→ EAD1+Trypsin→	344	Formosa haliotis	GCF_001685485.1	bacteroidetes
WP_066271148.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ CASPASE+EAD1→	800	Hydrogenophaga palleronii	GCF_001571225.1	betaproteobacteria
WP_066306413.1	GAP1-N1+GAP1-M+GAP1-C	PNP_UDP_1+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	693	Flavobacterium sp. TAB 87	GCA_001529295.1	bacteroidetes
WP_066533121.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ ZnR(fragment)+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ CASPASE+EAD1→	822	Comamonas terrigena	-	betaproteobacteria
WP_066769098.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	887	Croceicoccus mobilis	GCF_001661965.1	alphaproteobacteria
WP_069091270.1	GAP1-N1+GAP1-M+GAP1-C	GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	880	Mesorhizobium sp. SEMIA 3007	GCA_001708695.1	alphaproteobacteria
WP_069212636.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	PNP_UDP_1+EAD1→ GAP2→ ZnR(fragment)+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ SLATT→	809	Vibrio cholerae	-	gammaproteobacteria
WP_069548605.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	PNP_UDP_1+EAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ SLATT→	807	Vibrio parahaemolyticus	GCA_001727475.1	gammaproteobacteria
WP_072408563.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ PNP_UDP_1+EAD1→	826	Chryseobacterium limigenitum	GCA_900114875.1	bacteroidetes
WP_074276944.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	649	Bradyrhizobium erythrophlei	GCA_900129675.1	alphaproteobacteria
WP_074277581.1	GAP1-M+GAP1-C	GAP1-M+GAP1-C*→	522	Bradyrhizobium erythrophlei	GCA_900129675.1	alphaproteobacteria
WP_074304590.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	917	Singulisphaera sp. GP187	GCA_900129635.1	planctomycetes
WP_074658816.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ PNP_UDP_1+EAD1→	829	Flavobacterium	GCA_002217275.1	bacteroidetes
WP_074907605.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ CASPASE+EAD1→	829	Pseudomonas syringae	GCA_900115275.1	gammaproteobacteria
WP_075907279.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ CASPASE+EAD1→	824	Actinomadura sp. CNU-125	GCA_001942465.1	actinobacteria
WP_075979084.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	215	Leptospira santarosai	GCA_001952675.1	spirochaetes
WP_076403769.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	867	Pseudomonas putida	GCF_900156185.1	gammaproteobacteria
WP_076658804.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	217	Leptospira santarosai	GCA_001981425.1	spirochaetes
WP_077839733.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	637	Clostridium beijerinckii	GCA_002006205.1	firmicutes
WP_078010983.1	GAP1-N1+GAP1-M+GAP1-C+PNP_UDP_1+EAD1	GAP2→ DO-GTPase2.1→ DO-GTPase1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+PNP_UDP_1+EAD1*→	1142	Hymenobacter sp. CRA2	GCA_002007105.1	bacteroidetes
WP_078130559.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ PNP_UDP_1+EAD1→	845	Leptospira alexanderi	GCF_002009845.1	spirochaetes
WP_078754774.1	GAP1-N1+GAP1-M+GAP1-C	GAP1-N1+GAP1-M+GAP1-C*→	606	Enterovibrio nigricans	GCA_002835505.1	gammaproteobacteria
WP_078789132.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	??+PNP_UDP_1+EAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→	815	Geobacter thiogenes	GCA_900167465.1	deltaproteobacteria
WP_079392583.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ CASPASE+EAD1→	832	Pseudomonas	GCA_002326205.1	gammaproteobacteria
WP_080161065.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	629	Salmonella enterica	GCA_004271805.1	gammaproteobacteria
WP_080291534.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	667	Burkholderia pseudomallei	GCA_003606245.1	betaproteobacteria
WP_080323218.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	872	Burkholderia cenocepacia	GCA_002071875.1	betaproteobacteria
WP_080324388.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ CASPASE+EAD1→	829	Burkholderia cenocepacia	GCA_002071905.1	betaproteobacteria
WP_080377390.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	650	Pseudomonas syringae	GCA_001293665.1	gammaproteobacteria
WP_080406895.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	667	Burkholderia ubonensis	GCF_001526225.1	betaproteobacteria
WP_080565882.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ CASPASE+EAD1→	828	Xanthomonas campestris	GCF_000221965.1	gammaproteobacteria
WP_080902476.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ CASPASE+EAD1→	834	Pseudomonas fluorescens	GCF_000834545.1	gammaproteobacteria

acc	architecture	operon	len	species	gca	taxend
WP_081333857.1	GAP1-N1+GAP1-M+GAP1-C+CASPASE	GAP2→||←?||GAP1-N1+GAP1-M+GAP1-C+CASPASE*→	921	Burkholderia stagnalis	GCF_001718955.1	betaproteobacteria
WP_081480398.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	879	Pseudomonas	GCA_003001535.1	gammaproteobacteria
WP_084435545.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ CASPASE+EAD1→	753	Sinorhizobium saheli	GCF_001651875.1	alphaproteobacteria
WP_085211717.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	PNP_UDP_1+EAD1→||←?||GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→	825	Methylomagnum ishizawai	GCA_900155475.1	gammaproteobacteria
WP_085423962.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	644	Rhizobium oryzae	GCA_900177415.1	alphaproteobacteria
WP_085946283.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ PSE→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	649	Aeromonas salmonicida	-	gammaproteobacteria
WP_086054884.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ DO-GTPase2.1(fragment)→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	653	Pseudoruegeria sp. SK021	GCA_002119405.1	alphaproteobacteria
WP_086156276.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	641	Rhizobium sp. Kim5	GCA_000172695.2	alphaproteobacteria
WP_086321643.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	PNP_UDP_1+EAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→	798	Acinetobacter baumannii	GCA_002143185.1	gammaproteobacteria
WP_088100321.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ CASPASE+EAD1→	822	Xanthomonas retroflexus	GCF_900143175.1	gammaproteobacteria
WP_089766267.1	GAP1-N1+GAP1-M+GAP1-C	TIR+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	720	Chitinophaga terrae Kim and Jung 2007	GCA_900107795.1	bacteroidetes
WP_090271101.1	GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ DO-GTPase2.1(fragment)→ DO-GTPase1→ GAP1-M+GAP1-C*→	542	Litorimicrobium taeanense	-	alphaproteobacteria
WP_090309635.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ CASPASE+EAD1→	829	Pseudomonas linyingensis	GCA_900109175.1	gammaproteobacteria
WP_090943024.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	637	Pelosinus propionicus	GCA_900114615.1	firmicutes
WP_090964306.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP1-N1+GAP1-M+GAP1-C+EAD1*→ CASPASE+EAD1→	748	Aureimonas phyllosphaerae	GCA_900113065.1	alphaproteobacteria
WP_091457793.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ CASPASE+EAD1→	822	Giesbergeria anulus	GCF_900111115.1	betaproteobacteria
WP_091458865.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	681	Giesbergeria anulus	GCA_900111115.1	betaproteobacteria
WP_091694811.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ EAD1+Trypsin→?→??+EAD1→	844	Algoriphagus locisalis	GCA_900116615.1	bacteroidetes
WP_091713433.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	682	Methylobacterium phyllostachyos	GCA_900103445.1	alphaproteobacteria
WP_091720743.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	689	Mitsuaria sp. PDC51	GCA_900113225.1	betaproteobacteria
WP_092089286.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	564	Bradyrhizobium sp. R5	GCF_900101405.1	alphaproteobacteria
WP_092194891.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	699	Blastococcus sp. DSM 46838	-	actinobacteria
WP_092438108.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ CASPASE+EAD1→	823	Collimonas sp. OK607	GCA_900111995.1	betaproteobacteria
WP_092579008.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	876	Achromobacter sp. NFACC18-2	GCA_900108985.1	betaproteobacteria
WP_092699236.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR(fragment)+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	664	Acidovorax soli	-	betaproteobacteria
WP_092700910.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	871	Rhodanobacter glycinis	GCA_900114325.1	gammaproteobacteria
WP_093103449.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	880	Variovorax sp. CF079	GCF_900101545.1	betaproteobacteria
WP_093387274.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	867	Pseudomonas sp. UC 17F4	GCF_900101695.1	gammaproteobacteria
WP_093401103.1	GAP1-N1+GAP1-M+GAP1-C	GAP1-N1+GAP1-M+GAP1-C*→	681	Sphingomonas sp. OK281	GCA_900115295.1	alphaproteobacteria
WP_095649279.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	871	Pseudomonas indica	GCA_002286725.1	gammaproteobacteria
WP_096141060.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP1-N1+GAP1-M+GAP1-C+EAD1*→ SLATT→	735	Shewanella algae	GCA_002318995.1	gammaproteobacteria
WP_096425621.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ CASPASE+EAD1→	827	Pseudomonas putida	GCA_002356095.1	gammaproteobacteria
WP_097522738.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	674	Sinorhizobium sp. BJ1	GCA_002531555.1	alphaproteobacteria
WP_097608923.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ DO-GTPase2.1→ PSE→ GAP1-N1+GAP1-M+GAP1-C*→	682	Rhizobium sp. M10	GCA_002531955.1	alphaproteobacteria
WP_099207057.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ GAP2→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	681	Xanthomonas citri	GCF_002688625.1	gammaproteobacteria
WP_099315960.1	GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ DO-GTPase2.1(fragment)→ DO-GTPase1→ GAP1-M+GAP1-C*→	521	Burkholderia sp. AU18528	GCA_002223215.2	betaproteobacteria
WP_099380024.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP1-N1+GAP1-M+GAP1-C+EAD1*→ CASPASE+EAD1→	748	Janthinobacterium sp. BJB426	GCF_002735705.1	betaproteobacteria
WP_099407274.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	655	Chitinimonas sp. BJB300	GCF_002735695.1	betaproteobacteria
WP_099766932.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→??+EAD1→ EAD1+Trypsin→	843	Chryseobacterium sp. 52	GCA_002754245.1	bacteroidetes
WP_100195995.1	GAP1-N1+GAP1-M+GAP1-C	AB_hydrolase+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	681	Pseudorhodobacter sp. MZDSW-24AT	GCA_002794355.1	alphaproteobacteria
WP_100278437.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ ZnR(fragment)+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ PNP_UDP_1+EAD1→	837	Mariprofundus aestuarium	GCA_002795805.1	zetaproteobacteria
WP_100554785.1	GAP1-N1+GAP1-M+GAP1-C	DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	787	Bradyrhizobium sp. UASWS1016	GCA_002256345.1	alphaproteobacteria
WP_102083185.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	PNP_UDP_1+EAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→	811	Psychrobacter sp. Choline-02u-9	GCA_001742065.1	gammaproteobacteria
WP_102837409.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	871	Pseudomonas stutzeri	GCA_002890895.1	gammaproteobacteria
WP_102873726.1	GAP1-N1+GAP1-M+GAP1-C	AB_hydrolase+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	681	Phaeobacter inhibens	GCA_002892225.1	alphaproteobacteria
WP_102883896.1	GAP1-N1+GAP1-M+GAP1-C	AB_hydrolase+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	681	Phaeobacter inhibens	GCA_002892085.1	alphaproteobacteria
WP_103025358.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	604	Vibrio campbellii	GCF_002893865.1	gammaproteobacteria
WP_103162222.1	GAP1-N1+GAP1-M+GAP1-C	GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	869	Pectobacterium carotovorum	GCA_002904025.1	gammaproteobacteria
WP_104015000.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	813	Aeromonas jandaei	GCA_002925765.1	gammaproteobacteria
WP_105260592.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ CASPASE+EAD1→	827	Rhodoferax sp. TS-BS-61-7	GCA_002943465.1	betaproteobacteria
WP_105807446.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	880	Burkholderia multivorans	GCA_002981255.1	betaproteobacteria
WP_106138897.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ PNP_UDP_1+EAD1→	786	Spirosoma oryzae	GCF_003002825.1	bacteroidetes

acc	architecture	operon	len	species	gca	taxend
WP_106139082.1	GAP1-N1+GAP1-M+GAP1-C+EAD1	ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C+EAD1*→ PNP_UDP_1+EAD1→	830	Spirosoma oryzae	GCA_003002825.1	bacteroidetes
WP_106448472.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ PSE→ GAP1-N1+GAP1-M+GAP1-C*→	684	Simplicispira sp. SC1-8	GCA_003008595.1	betaproteobacteria
WP_107607145.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ PSE→ PSE→ ZnR+DO-GTPase2.1→ DO-GTPase1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	238	Leptospira santarosai	GCF_001008325.2	spirochaetes
WP_108195516.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	611	Vibrio splendidus	GCA_003049865.1	gammaproteobacteria
WP_108311778.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ PSE→ GAP1-N1+GAP1-M+GAP1-C*→	687	Limnohabitans parvus	GCA_003063455.1	betaproteobacteria
WP_108419298.1	GAP1-N1+GAP1-M+GAP1-C	Calcineurin+GAPEAD1→ GAP2→ ZnR+DO-GTPase2.1→ DO-GTPase1→ GAP1-N1+GAP1-M+GAP1-C*→	871	Klebsiella aerogenes	GCF_003057255.1	gammaproteobacteria

GAP1-N2-type GTPase-centric systems

acc	architecture	operon	len	species	gca	taxond
ADB15798.1	GAP1-N2+GAP1-M+GAP1-C	ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→?+TM+?+beta-rich?|→ GYF+GYF+TM+TM+TM→	844	Pirellula staleyi DSM 6068	GCA_ 000025185.1	planctomycetes
ADB76255.1	GAP1-N2+GAP1-M+GAP1-C	Pkinase+TM→ TM→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→?→|n−7n−7|?→ Pkinase+low_complexity→	552	Gemmatimonas phototrophica GP2 strain 43160	GCA_ 000025345.1	actinobacteria
ADH12266.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	813	Streptomyces bingchenggensis BCW-1	GCA_ 000992385.1	actinobacteria
AFP36529.1	GAP1-N2+GAP1-M+GAP1-C	HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→?+DO-GTPase2.2→	866	Mycobacterium smegmatis MC2 155	GCA_ 000282395.1	actinobacteria
AGS49281.1	GAP1-N2+GAP1-M+GAP1-C	ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→?→ HSP70→ +WA(canonical)→ unknown+CASPASE→ HSP70→	762	uncultured bacterium emsapd2	.	bacteria
AJE68329.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→?+DO-GTPase2.2→	661	Corynebacterium glutamicum	GCA_ 000828015.1	actinobacteria
AJI77744.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→?+DO-GTPase2.2→ polar_leader+TM+TM+TM→	611	Corynebacterium singulare	GCA_ 000833575.1	actinobacteria
AKA68369.1	GAP1-N2+GAP1-M+GAP1-C	Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→ TM+vWA(canonical)+YrKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→	891	Clostridium scatologenes	GCA_ 000963575.1	firmicutes
AKN39604.1	GAP1-N2+GAP1-M+GAP1-C	Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→ TM+vWA(canonical)+YrKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→	891	Clostridium carboniditorans P7	GCA_ 001038625.1	firmicutes
AKN77220.1	GAP1-N2+GAP1-M+GAP1-C	TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM→ +WA(canonical)→ Pkinase+ZnR+beta-rich→	1007	Streptomyces sp. FHB53	GCA_ 001934005.1	actinobacteria
AJP34837.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	1007	Paenibacillus sp. HHB B 3084	GCA_ 001447315.1	firmicutes
ALP51108.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→?+DO-GTPase2.2→	661	Corynebacterium glutamicum	GCA_ 001447965.2	actinobacteria
AMA01136.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→?+DO-GTPase2.2→	661	Corynebacterium glutamicum	GCA_ 001518935.2	actinobacteria
AMV18226.1	GAP1-N2+GAP1-M+TM+GAP1-C	DO-GTPase2.2→ GAP1-N2+GAP1-M+TM+GAP1-C*→?+TM+?+beta-rich?|→ GYF+GYF+Trypsin→	871	Planctomyces sp. SH-PL14	GCA_ 001610835.1	planctomycetes
AMV18442.1	GAP1-N2+GAP1-M+TM+GAP1-C	ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+TM+GAP1-C*→?+TM+?+beta-rich?|→ GYF+GYF+Trypsin→ Pkinase+low_complexity+TM→	896	Planctomyces sp. SH-PL14	GCA_ 001610835.1	planctomycetes
ANB35409.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→	647	Corynebacterium cruzillactis	GCA_ 001643015.1	actinobacteria
APA96790.15	GAP1-N2+GAP1-M+GAP1-C	Pkinase+TM→?→ ZnR+DO-GTPase2.1→ GAP1-N2+GAP1-M+GAP1-C*→	742	Nocardia seriolae	GCA_ 001864585.1	actinobacteria
APB71256.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YrKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	1002	Paenibacillus polymyxa	GCA_ 001874405.2	firmicutes
APB76202.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YrKA-like+TM+??→ PSE→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	1002	Paenibacillus polymyxa	GCA_ 001874425.2	firmicutes
APS18487.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	821	Streptomyces sp. Tue 6075	GCA_ 001931635.1	actinobacteria
APT08387.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→?+DO-GTPase2.2→	661	Corynebacterium glutamicum	GCA_ 001936195.1	actinobacteria
ARI51644.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	882	Streptomyces sp. SS	GCA_ 002094995.1	actinobacteria
ARX88833.1	GAP1-N2+GAP1-M+GAP1-C	Pkinase→?→?→?→?→ TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→?→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→	764	Streptomyces albolavus	GCA_ 002189675.1	actinobacteria
AUG76307.1	GAP1-N2+GAP1-M+GAP1-C	PPIC→ Pkinase→?→?→?→ HSP70_domain_2+low_complexity+domain_betaX→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→	807	Kitasatospora sp. MMS16-BH015	GCA_ 002943525.1	actinobacteria
BAC00114.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→?+DO-GTPase2.2→	662	Corynebacterium glutamicum ATCC 13032	GCA_ 000011225.1	actinobacteria
BAF55637.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→?+DO-GTPase2.2→	662	Corynebacterium glutamicum R	GCA_ 000010225.1	actinobacteria
BAG18277.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	915	Streptomyces griseus subsp. griseus NBRC 13350	GCA_ 000010605.1	actinobacteria
BAH49624.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→?+DO-GTPase2.2→	851	Rhodococcus opacus B4	GCA_ 000010805.1	actinobacteria
BAI 97076.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→?+DO-GTPase2.2→	654	Corynebacterium glutamicum	GCA_ 002355155.1	actinobacteria
BAI 97215.1	GAP1-N2+GAP1-M+GAP1-C	GrpE→ HSP70→?+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→	805	Corynebacterium glutamicum	GCA_ 002355675.1	actinobacteria
BAI 24350.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→?+DO-GTPase2.2→	654	Corynebacterium glutamicum	GCA_ 002355675.1	actinobacteria
BAN48920.1	GAP1-N2+GAP1-M+GAP1-C	HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→	695	Actinomyces naeslundii	GCA_ 002352015.1	actinobacteria
CAF20743.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→?+DO-GTPase2.2→	654	Corynebacterium glutamicum ATCC 13032	GCA_ 000196335.1	actinobacteria
CCD27513.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→?→?+DO-GTPase2.2→	883	Tetrasphaera jenkinsii Ben 74	GCA_ 001046875.1	actinobacteria
CDB93702.1	GAP1-N2+GAP1-M+TM+GAP1-C	GAP1-N2+GAP1-M+TM+GAP1-C*→	713	Firmicutes bacterium CAG:41	GCA_ 000431615.1	firmicutes
CDC62438.1	GAP1-N2+GAP1-M+TM+GAP1-C	GAP1-N2+GAP1-M+TM+GAP1-C*→	699	Clostridium sp. CAG:448	GCA_ 000433415.1	firmicutes
CDE12586.1	GAP1-N2+GAP1-M+TM+GAP1-C	HSP70(frag)+vWA(canonical)→?→ DO-GTPase2.1→ GAP1-N2+GAP1-M+TM+GAP1-C*→	767	Ruminococcus sp. CAG:830	GCA_ 000437175.1	firmicutes

acc	architecture	operon	len	species	gca	taxend
CDE84522.1	GAP1-N2+GAP1-M+TM+GAP1-C	FHA-like?+ZnR+ZnR+DO-GTPase2.2-> GAP1-N2+GAP1-M+TM+GAP1-C*->	451	Corallomargarita sp. CAG:312	GCA_000438015.1	verrucomicrobia
CNG08901.1	GAP1-N2+GAP1-M+GAP1-C	TPR_containing_alpha_helical+Fibronectin-like_repeats-> ZnR+ZnR+DO-GTPase2.2-> GAP1-N2+GAP1-M+GAP1-C*-> TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM->	656	Mycobacterium tuberculosis	GCA_001160225.1	actinobacteria
CQD15063.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM-> TM++vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail-> Tubulin+alpha_helical+??+?? -> GAP_unknown1+TM+TM+GAP_unknown2-> HRDC-like?+Fibronectin-like_repeats-> GAP1-N2+GAP1-M+GAP1-C*-> beta-rich+vWA(canonical)-=??+DO-GTPase2.2-> polar_leader+TM+TM+TM->	532	Corynebacterium striatum	GCA_001261035.1	actinobacteria
EDK43704.1	GAP1-N2+GAP1-M+TM+GAP1-C	TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2-> TM++vWA(canonical)+YtKA-like+TM+??-> Tubulin+coiled_coil+??-> Tubulin+coiled_coil+HTH?+?? -> Fibronectin-like_repeats+??-> ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR+ GAP1-N2+GAP1-M+	353	Clostridium khuveri DSM 555	GCA_000016505.1	firmicutes
EEB63587.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM-> TM++vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail-> Tubulin+alpha_helical+??+?? -> GAP_unknown1+TM+TM+GAP_unknown2-> HRDC-like?+Fibronectin-like_repeats-> GAP1-N2+GAP1-M+GAP1-C*-> beta-rich+vWA(canonical)-=??+DO-GTPase2.2->	868	Corynebacterium amycolatum SK46	GCA_001736055.1	actinobacteria
EET86374.1	GAP1-N2+GAP1-M+GAP1-C	TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2-> TM++vWA(canonical)+YtKA-like+TM+??-> Tubulin+coiled_coil+??-> Tubulin+coiled_coil+HTH?+?? -> TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail-> Fibronectin-like_repeats+??-> ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR-> GAP1-N2+GAP1-M+GAP1-C*-> GAP1-N2+GAP1-M->	144	Clostridium carboxidivorans P7	GCA_000175595.1	firmicutes
EET86375.1	GAP1-M	TM++vWA(canonical)+YtKA-like+TM+??-> Tubulin+coiled_coil+??-> Tubulin+coiled_coil+HTH?+?? -> TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail-> Fibronectin-like_repeats+??-> ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR+ GAP1-N2+GAP1-M+GAP1-C*-> GAP1-M->	216	Clostridium carboxidivorans P7	GCA_000175595.1	firmicutes
EFE43745.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*->	1002	Streptomyces albus J1074	GCA_000156475.1	actinobacteria
EFL61271.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*->	785	Streptomyces sp. SPB78	GCA_000158855.1	actinobacteria
EFL18295.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*->	293	Streptomyces sp. C	GCA_000158895.1	actinobacteria
EFL28260.1	GAP1-N2+GAP1-M+GAP1-C	TPR_containing_alpha_helical+Fibronectin-like_repeats-> ZnR+ZnR+DO-GTPase2.2-> GAP1-N2+GAP1-M+GAP1-C*-> TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM-> vWA(canonical)-> PP2C-> Pkinase+ZnR+beta-rich->	725	Streptomyces hygroscopicus ATCC 53653	GCA_000158915.1	actinobacteria
EGV41882.1	GAP1-N2+GAP1-M+GAP1-C	TM+TM+TM-> TM++vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail-> Tubulin+alpha_helical+??+?? -> GAP_unknown1+TM+TM+GAP_unknown2-> HRDC-like?+Fibronectin-like_repeats-> GAP1-N2+GAP1-M+GAP1-C*-> beta-rich+vWA(canonical)-=??+DO-GTPase2.2->	661	Corynebacterium glutamicum S9114	GCA_000223415.2	actinobacteria
EHM28476.1	GAP1-N2+GAP1-M+GAP1-C	TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM-> vWA(canonical)-> PP2C-> Pkinase+ZnR+beta-rich-=|e-?e-?|GAP1-N2+GAP1-M+GAP1-C*->	805	Streptomyces sp. W007	GCA_000230075.2	actinobacteria
EHQ63001.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM++vWA(canonical)+YtKA-like+TM+??-> Tubulin+coiled_coil+??-> Tubulin+coiled_coil+HTH?+?? -> TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail-> Fibronectin-like_repeats+??-> ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR-> GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->	1034	Paenibacillus dendritiformis C454	GCA_000245555.2	firmicutes
EJZ04364.1	GAP1-N2+GAP1-M+GAP1-C	HRDC-like?+Fibronectin-like_repeats-> GAP1-N2+GAP1-M+GAP1-C*->	133	Mycobacterium fortuitum subsp. fortuitum DSM 46621 = ATCC 6841	GCA_000295655.1	actinobacteria
EPH39666.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*-> vWA(canonical)->	870	Streptomyces aurantiacus JA 4570	GCA_000414115.1	actinobacteria
EQS68984.1	GAP1-N2+GAP1-M+GAP1-C	TM+TM+TM+TM+TM+TM+DO-GTPase2.1-> GAP1-N2+GAP1-M+GAP1-C*-=?7-> TM_region+DO-GTPase1->	556	Thermoplasmatales archaeon Gpl	GCA_001856845.1	euryarchaeota
EQD81319.1	GAP1-N2+GAP1-M+GAP1-C	ZnR+ZnR+DO-GTPase2.2-> GAP1-N2+GAP1-M+GAP1-C*->	434	Saccharopolyspora erythraea D	GCA_000143385.1	actinobacteria
EST36721.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*-> TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+Jelly_roll+beta-sandwich-=|e-STAND_NTPase+TM+TM+TM+TM+TM+TM	371	Streptomyces roseochromogenus subsp. oscitans DS 12.976	GCA_000497445.1	actinobacteria
ETJ06992.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C!(frag)*->	492	Actinomyces urogenitalis DORA_12	GCA_000508425.1	actinobacteria
ETT33608.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM++vWA(canonical)+YtKA-like+TM+??-> Tubulin+coiled_coil+??-> Tubulin+coiled_coil+HTH?+?? -> TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail-> Fibronectin-like_repeats+??-> ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR-> GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->	796	Paenibacillus sp. FSL R7-269	GCA_000517865.1	firmicutes
ETT39033.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM++vWA(canonical)+YtKA-like+TM+??-> Tubulin+coiled_coil+??-> Tubulin+coiled_coil+HTH?+?? -> TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail-> Fibronectin-like_repeats+??-> ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR-> GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->	1067	Paenibacillus sp. FSL R7-689	GCA_000517905.1	firmicutes
ETT00645.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	Tubulin+coiled_coil+??-> Tubulin+coiled_coil+HTH?+?? -> TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail-> Fibronectin-like_repeats+??-> ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR-> GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->	837	Paenibacillus sp. FSL R7-277	GCA_000517965.1	firmicutes
ETZ98452.1	GAP1-M+GAP1-C	Tubulin+alpha_helical+??+?? -> GAP_unknown1+TM+TM+GAP_unknown2-> GAP_unknown1+TM+TM+GAP_unknown2-> HRDC-like?+Fibronectin-like_repeats+> HRDC-like?+Fibronectin-like_repeats-> GAP1-N2+GAP1-M+GAP1-C-> GAP1-M+GAP1-C*-=?+> beta-rich+vWA(canonical)-=??+DO-GTPase2.2->	598	Mycobacterium kansasii 824	GCA_000524095.1	actinobacteria
EVT47746.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*->	325	Dietzia sp. UCD-THP	GCA_000459585.1	actinobacteria
GAK49946.1	GAP1-N2+GAP1-M+low_complexity+TM+TM	DO-GTPase2.1-> GAP1-N2+GAP1-M+low_complexity+TM+TM*->	480	Candidatus Modulifexus flocculans	GCA_000739515.1	bacteria
GAS84505.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM++vWA(canonical)+YtKA-like+TM+??-> Tubulin+coiled_coil+??-> Tubulin+coiled_coil+HTH?+?? -> TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail-> Fibronectin-like_repeats+??-> ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR-> GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->	1062	Paenibacillus amylolyticus	GCA_001570725.1	firmicutes
GAY11658.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM++vWA(canonical)+YtKA-like+TM+??-> Tubulin+coiled_coil+??-> Tubulin+coiled_coil+HTH?+?? -> TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail-> Fibronectin-like_repeats+??-> ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR-> GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->	947	Paenibacillus sp. NAIST15-1	GCA_001894745.1	firmicutes
GAV86249.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM-> TM++vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail-> Tubulin+alpha_helical+??+?? -> GAP_unknown1+TM+TM+GAP_unknown2-> HRDC-like?+Fibronectin-like_repeats-> GAP1-N2+GAP1-M+GAP1-C*-> beta-rich+vWA(canonical)-=??+DO-GTPase2.2->	661	Corynebacterium glutamicum	GCA_002604915.1	actinobacteria
KAJ49549.1	GAP1-N2+GAP1-M	ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR-> GAP1-N2+GAP1-M*->	387	Clostridium tetanomorphum DSM 665	GCA_000647895.1	firmicutes
KAJ53559.1	GAP1-N2+GAP1-M	TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2-> TM++vWA(canonical)+YtKA-like+TM+??-> Tubulin+coiled_coil+??-> Tubulin+coiled_coil+HTH?+?? -> TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail-> Fibronectin-like_repeats+??-> ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR-> GAP1-N2+GAP1-M*->	387	Clostridium tetanomorphum DSM 665	GCA_000647895.1	firmicutes
KDQ04749.1	GAP1-M+GAP1-C	GrpE-> TPR_containing_alpha_helical+Fibronectin-like_repeats-> ZnR+ZnR+DO-GTPase2.2-=?-> GAP1-M+GAP1-C*-> TM+TM+TM+ZnR+ZnR+DO-GTPase2.2-=?-> HSP70-> vWA(canonical)->	701	Rhodococcus qingshengii	GCA_000698455.1	actinobacteria
KFI76917.1	GAP1-N2+GAP1-M+GAP1-C	TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2-> GrpE-> HSP70-> HSP70-> vWA(canonical)-> Dna1+DnaJ+ZnR+ZnR+coiled_coil+Fibronectin-like_repeats-> ZnR+ZnR+DO-GTPase2.2-> GAP1-N2+GAP1-M+GAP1-C*->	967	Bifidobacterium stellenboschense	GCA_000741755.1	actinobacteria
KGF17444.1	GAP1-N2+GAP1-M+GAP1-C	TM++vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail-> Tubulin+alpha_helical+??+?? -> GAP_unknown1+TM+TM+GAP_unknown2-> HRDC-like?+Fibronectin-like_repeats-> GAP1-N2+GAP1-M+GAP1-C*-=??+DO-GTPase2.2->	854	Corynebacterium fenneyi DNF00450	GCA_000758965.1	actinobacteria
KHD07856.1	GAP1-N2+GAP1-M+GAP1-C	ZnR+ZnR+DO-GTPase2.2-> GAP1-N2+GAP1-M+GAP1-C*-> TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2->	813	Candidatus Thiomargarita nelsonii	GCA_000785145.2	gammaproteobacteria
KHD08233.1	GAP1-N2+GAP1-M+GAP1-C	DO-GTPase1-=?-> GAP1-N2+GAP1-M+GAP1-C*-> DO-GTPase2?->	914	Candidatus Thiomargarita nelsonii	GCA_000785145.2	gammaproteobacteria
KHD11963.1	GAP1-N2+GAP1-M+GAP1-C	ZnR+ZnR+DO-GTPase2.2-> GAP1-N2+GAP1-M+GAP1-C*->	668	Candidatus Thiomargarita nelsonii	-	gammaproteobacteria
KHD12726.1	GAP1-N2+GAP1-M	DO-GTPase1-=?-> GAP1-N2+GAP1-M*->	187	Candidatus Thiomargarita nelsonii	-	gammaproteobacteria
KHD13072.1	GAP1-N2+GAP1-M+GAP1-C	ZnR+ZnR+DO-GTPase2.2-> GAP1-N2+GAP1-M+GAP1-C*->	662	Candidatus Thiomargarita nelsonii	-	gammaproteobacteria
KFI04207.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*->	206	Streptomyces sp. RSD-27	GCA_000817655.1	actinobacteria
KFT22394.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*->	812	Streptomyces sp. AcH 505	GCA_000818175.1	actinobacteria

acc	architecture	operon	len	species	gca	taxend
KIH72595.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM++WA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich++WA(canonical)→??+DO-GTPase2.2→	661	Corynebacterium glutamicum	GCA_000819915.1	actinobacteria
KIX33869.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	821	Streptomyces griseus		actinobacteria
KIX77715.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	135	Streptomyces sp. MBRL 601	GCA_000932205.1	actinobacteria
KJY25356.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	204	Streptomyces katrae	GCA_000960975.1	actinobacteria
KJY44605.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	273	Streptomyces sp. NRRL S-444	GCA_000960985.1	actinobacteria
KMK66000.1	GAP1-N2+GAP1-M+TM+GAP1-C	DO-GTPase2.2→ GAP1-N2+GAP1-M+TM+GAP1-C*→	551	Puniceibacterium sp. IMCC21224	GCA_001038505.1	alphaproteobacteria
KNS65951.1	GAP1-N2+GAP1-M+GAP1-C	TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ +WA(canonical)→ Pkinase+ZnR+beta-rich→	879	Streptomyces regneni	GCA_001047335.1	actinobacteria
KNB71604.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM++WA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM++WA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*	825	Brevibacillus reuszeri	GCA_001187725.1	firmicutes
KOGS3654.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	840	Streptomyces griseus subsp. rhodochrous	GCA_001270675.1	actinobacteria
KOP61911.1	GAP1-N2+GAP1-M+TM+GAP1-C	TM++WA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM++WA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*	1010	Bacillus sp. FJAT-18019	GCA_001275645.1	firmicutes
KOR29601.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	440	Achromatium sp. WMS3	GCA_001276615.1	gammaproteobacteria
KOR33350.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	839	Achromatium sp. WMS3	GCA_001276615.1	gammaproteobacteria
KOR82125.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM++WA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM++WA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*	1011	Bacillus sp. solani	GCA_001277545.1	firmicutes
KOS01186.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM++WA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM++WA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*	1006	Paenibacillus polyxyxa	GCA_001277855.1	firmicutes
KOU06955.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	840	Streptomyces sp. NRRL F-2295	GCA_001279425.1	actinobacteria
KOU48584.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	840	Streptomyces sp. SMG1522	GCA_001279735.1	actinobacteria
KOV83698.1	GAP1-N2+GAP1-M+GAP1-C	TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ +WA(canonical)→ Pkinase+ZnR+beta-rich→	780	Streptomyces sp. NRRL WC-3723	GCA_001280945.1	actinobacteria
KOY14601.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM++WA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM++WA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*	1078	Paenibacillus sp. A59	GCA_001280595.1	firmicutes
KOY55812.1	GAP1-N2+GAP1-M+GAP1-C	TPR_containing_alpha_helical+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM→ +WA(canonical)→ PP2C→ Pkinase+ZnR+beta-rich→	834	Streptomyces sp. XY332	GCA_001280885.1	actinobacteria
KPU18578.1	GAP1-N2+GAP1-M+GAP1-C	Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→	344	Actinobacteria bacterium OV450	GCA_001280555.1	actinobacteria
KPL06138.1	GAP1-N2+GAP1-M+TM+GAP1-C	ZnR+DO-GTPase2.1→ GAP1-N2+GAP1-M+TM+GAP1-C*→	393	candidate-division BRC1 bacterium SM23_51	GCA_001304075.1	bacteria
KUO19072.1	GAP1-N2+GAP1-M+GAP1-C	TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM→ +WA(canonical)→ PP2C→ Pkinase+ZnR+beta-rich→	1166	Streptomyces sp. HV15	GCA_001514305.1	actinobacteria
KXA29097.1	GAP1-N2+GAP1-M+GAP1-C	TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→?→ HSP70→ HSP70→+WA(canonical)→ Dnaf+Dnaf+ZnR+ZnR+coiled_coil+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→	884	Gardnerella vaginalis	GCA_001546485.1	actinobacteria
KXK18278.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	1057	Chloroflexi bacterium OLB15	GCA_001567085.1	chloroflexi
OAAA2476.1	GAP1-N2+GAP1-M+GAP1-C+ZnR+DO-GTPase2	GAP1-N2+GAP1-M+GAP1-C+ZnR+DO-GTPase2*→	998	Frankia sp. EI5c	GCA_001630563.1	actinobacteria
OAB50176.1	GAP1-N2+GAP1-M+TM+low_complexity	GAP1-N2+GAP1-M+TM+low_complexity*→	435	Planctomycetaceae bacterium SCGC AG-212-F19	GCA_001644415.1	planctomycetes
ODS34705.1	GAP1-N2+GAP1-M+GAP1-C	DO-GTPase2.1→ GAP1-N2+GAP1-M+GAP1-C*→	595	Candidatus Scidinchus rubra	GCA_001723765.1	planctomycetes
OFT5754.9.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM++WA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich++WA(canonical)→??+DO-GTPase2.2→ polar_leader+TM+TM+TM→	611	Corynebacterium sp. HMSC05E07	GCA_001807225.1	actinobacteria
OFU5206.5	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM++WA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich++WA(canonical)→??+DO-GTPase2.2→ polar_leader+TM+TM+TM→	1054	Corynebacterium sp. HMSC11E11	GCA_001807025.1	actinobacteria
OGV44577.1	GAP1-N2+GAP1-M+TM+GAP1-C	FHA-like+??+ZnR+ZnR+DO-GTPase2.2+??→ GAP1-N2+GAP1-M+TM+GAP1-C*→	747	Lentisphaerae bacterium GWF2_57_35	GCA_001804865.1	lentisphaerae
OGV69332.1	GAP1-N2+GAP1-M	GAP1-N2+GAP1-M*→??+TM+??+beta-rich??→	279	Lentisphaerae bacterium RIFOXYA12_64_32	GCA_001802335.1	lentisphaerae
OHB70404.1	GAP1-N2+GAP1-M+GAP1-C	FGS-fold_domain→ ZnR+DO-GTPase2.1→ GAP1-N2+GAP1-M+GAP1-C*→	472	Planctomycetes bacterium RBG_13_63_9	GCA_001828265.1	planctomycetes
OHB78921.1	GAP1-N2+GAP1-M+GAP1-C	FGS-fold_domain→ ZnR+DO-GTPase2.1→ GAP1-N2+GAP1-M+GAP1-C(frag)*→	318	Planctomycetes bacterium RBG_16_64_10	GCA_001828305.1	planctomycetes
OHB82388.1	GAP1-N2+GAP1-M+GAP1-C	ZnR+DO-GTPase2.1→ GAP1-N2+GAP1-M+GAP1-C*→	456	Planctomycetes bacterium RBG_16_64_12	GCA_001828335.1	planctomycetes
OHE60810.1	GAP1-N2+GAP1-M+TM+GAP1-C	GAP1-N2+GAP1-M+TM+GAP1-C*→	912	Verrucomicrobia bacterium GWF2_62_7	GCA_001831115.1	verrucomicrobia
OHV41104.1	GAP1-N2+GAP1-M+GAP1-C+ZnR+DO-GTPase2	GAP1-N2+GAP1-M+GAP1-C+ZnR+DO-GTPase2*→	984	Frankia sp. Cc1.17	GCA_001854655.1	actinobacteria
OJW24960.1	GAP1-N2+GAP1-M+GAP1-C	ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→	1040	Planctomycetes bacterium 71-10	GCA_001898385.1	planctomycetes
OJW26983.1	GAP1-N2+GAP1-M	GAP1-N2+GAP1-M*→	222	Planctomycetales bacterium 71-10	GCA_001898385.1	planctomycetes
OKB62124.1	GAP1-N2+GAP1-M+GAP1-C	HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C(frag)*→	396	Mycobacterium sp. SWR-M5	GCA_001905305.1	actinobacteria
OKI26354.1	GAP1-N2+GAP1-M+GAP1-C	HSP70→[|=-?|GrpE→ HSP70→ TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→	781	Saccharothrix sp. CE00851	GCA_001905065.1	actinobacteria
OKI7725.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	817	Streptomyces sp. TSRB0095	GCA_001905525.1	actinobacteria
OKJ17625.1	GAP1-N2+GAP1-M+GAP1-C	TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM→ +WA(canonical)→ PP2C→ Pkinase+ZnR+beta-rich→[|=-?+?=-?|]GAP1-N2+GAP1-M+GAP1-C*→	807	Streptomyces sp. CE00316	GCA_001905595.1	actinobacteria
OKJ37923.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	830	Streptomyces sp. CE02366	GCA_001905905.1	actinobacteria

acc	architecture	operon	len	species	gca	taxend
OKX84744.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→	661	Corynebacterium glutamicum	GCA_001912755.2	actinobacteria
OKX87375.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→	661	Corynebacterium glutamicum	GCA_001912725.1	actinobacteria
OLA86330.1	GAP1-N2+GAP1-M+TM+GAP1-C	FHA-like?+ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+TM+GAP1-C*→	443	Verrucomicrobia bacterium CAG:312_58_20	GCA_001917305.1	verrucomicrobia
OME85740.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YiKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	1046	Paenibacillus pabuli	GCA_001955985.1	firmicutes
OMF04519.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YiKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	1073	Paenibacillus amylolyticus	GCA_001956035.1	firmicutes
OMG48224.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	1139	Paenibacillus macerans	GCA_001956535.1	firmicutes
OMO95906.1	TM+TM+TM+vWA+TM+TM+TM+ZnR+GTPase+GAP1-N2+GAP1-M+GAP1-C+ATP_grasp+ATP_grasp+Rossmann-like+thioredoxin_fold	TM+TM+TM+vWA+TM+TM+TM+ZnR+GTPase+GAP1-N2+GAP1-M+GAP1-C+ATP_grasp+ATP_grasp+Rossmann-like+thioredoxin_fold*→	3618	Corynebacterium oilitorius	GCA_001974825.1	viridiplantae
ONI43537.1	GAP1-N2+GAP1-M+GAP1-C	vWA(canonical)→ PP2C→ Pkinase+ZnR+beta-rich→[i=?e-?e-?]GAP1-N2+GAP1-M+GAP1-C*→	807	Streptomyces sp. HI2014 011-1	GCA_001983595.1	actinobacteria
OQY57022.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→[i=HSP70c-GrpE	844	Beggiatoa sp. 4572_84	GCA_002885445.1	gammaproteobacteria
ORB87026.1	GAP1-N2+GAP1-M+GAP1-C	TM+DUF4190+TM→ TM+DUF4190+TM→ polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→	818	Mycobacterium kansasii	GCA_002868654.1	actinobacteria
ORB92406.1	GAP1-N2+GAP1-M+GAP1-C	TM+DUF4190+TM→ TM+DUF4190+TM→ polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→	818	Mycobacterium kansasii	GCA_002868855.1	actinobacteria
ORB97660.1	GAP1-N2+GAP1-M+GAP1-C	TM+DUF4190+TM→ TM+DUF4190+TM→ polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→	818	Mycobacterium kansasii	GCA_002869035.1	actinobacteria
ORC04457.1	GAP1-N2+GAP1-M+GAP1-C	TM+DUF4190+TM→ TM+DUF4190+TM→ polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→	734	Mycobacterium kansasii	GCA_002869935.1	actinobacteria
OSC60295.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	817	Streptomyces sp. BF-3	GCA_002916965.1	actinobacteria
OUT55991.1	GAP1-N2+GAP1-M+TM+GAP1-C	ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+TM+GAP1-C*→??+TM+??+beta-rich?!→ GYF+GYF+TM+TM+TM→	691	Rhodopirellula	GCA_002167455.1	planctomycetes
OUT61367.1	GAP1-N2+GAP1-M	FGS-fold_domain→ ZnR+DO-GTPase1.1→ GAP1-N2+GAP1-M*→	256	Rhodopirellula sp. TMED11	GCA_002167455.1	planctomycetes
OUT63273.1	GAP1-N2+GAP1-M+low_complexity+TM+TM	FHA-like?+ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+low_complexity+TM+TM*→	524	Verrucomicrobia bacterium TMED71	GCA_002170015.1	verrucomicrobia
OUS80014.1	GAP1-N2+GAP1-M+TM+beta-rich+??	FHA-like?+ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+TM+beta-rich+??*→??+TM+??→	1016	Verrucomicrobiaceae bacterium TMED76	GCA_002170435.1	verrucomicrobia
OWP54298.1	GAP1-N2+GAP1-M+GAP1-C	TM+TM+TM+TM+TM+TM+DO-GTPase2.1→ GAP1-N2+GAP1-M+GAP1-C*→??→ TM+GAP_unknown2+DO-GTPase1→	556	Cuniculiplasma sp. C_DKE	GCA_002204655.1	euryarchaeota
OXY86693.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	807	Streptomyces sp. ZR	GCA_002242735.1	actinobacteria
OYT35071.1	GAP1-N2+GAP1-M	GAP1-N2+GAP1-M*→	330	archaeon ex4484_74	GCA_002524715.1	archaea
OYV90204.1	??+GAP1-N2+GAP1-M+??+TM+TM	??+GAP1-N2+GAP1-M+??+TM+TM*→	1329	Planctomycetia bacterium 21-64-5	GCA_002279215.1	planctomycetes
OYW70936.1	GAP1-N2+GAP1-M+TM	FHA-like?+ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+TM*→	441	Verrucomicrobia bacterium 12-59-8	GCA_002279765.1	verrucomicrobia
OYW71544.1	GAP1-N2+GAP1-M+TM+GAP1-C	FHA-like?+ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+TM+GAP1-C*→	918	Verrucomicrobia bacterium 12-59-8	GCA_002279765.1	verrucomicrobia
OZQ64785.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	1079	Paenibacillus taichungensis	GCA_002664305.1	firmicutes
PAC68390.1	GAP1-N2+GAP1-M+GAP1-C	TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→ GrpE→ HSP70→ vWA(canonical)→ Dnaj+Dnaj+ZnR+ZnR+coiled_coil+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→	849	Bifidobacterium criceti	GCA_002796935.1	actinobacteria
PAW85721.1	GAP1-N2+GAP1-M+TM+GAP1-C	ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+TM+GAP1-C*→	713	Opitutae bacterium Tous-C2FEB	GCA_002834375.1	verrucomicrobia
PAZ04795.1	GAP1-N2+GAP1-M+TM+GAP1-C	FHA-like?+ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+TM+GAP1-C*→	713	Opitutae bacterium AMD-G3	GCA_002296585.1	verrucomicrobia
PAZ04443.1	GAP1-N2+GAP1-M+TM+GAP1-C	FHA-like?+ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+TM+GAP1-C*→	709	Opitutae bacterium AMD-G1	GCA_002296595.1	verrucomicrobia
PBS99131.1	GAP1-N2+GAP1-M+GAP1-C	FGS-fold_domain→ ZnR+DO-GTPase1.1→ GAP1-N2+GAP1-M+GAP1-C*→	464	Blastopirellula sp.	GCA_002733575.1	planctomycetes
PBX68802.1	GAP1-N2+GAP1-M+TM+GAP1-C	FHA-like?+ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+TM+GAP1-C*→	709	Opitutae bacterium	GCA_002737185.1	verrucomicrobia
PBX78035.1	GAP1-N2+GAP1-M+TM	ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+TM*→	359	Planctomycetaceae bacterium	GCA_002737585.1	planctomycetes
PBX79082.1	GAP1-N2+GAP1-M+TM+GAP1-C	FHA-like?+ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+TM+GAP1-C*→	709	Opitutae bacterium	GCA_002737215.1	verrucomicrobia
PBX79721.1	GAP1-N2+GAP1-M+TM+GAP1-C	FHA-like?+ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+TM+GAP1-C*→	711	Opitutae bacterium	GCA_002737235.1	verrucomicrobia
PBX79953.1	GAP1-N2+GAP1-M+TM+GAP1-C	FHA-like?+ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+TM+GAP1-C*→	710	Opitutae bacterium	GCA_002737255.1	verrucomicrobia
PIE36367.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	586	candidate division KSB3 bacterium	GCA_002748445.1	bacteria
PIG42998.1	GAP1-N2+GAP1-M+GAP1-C	TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM→?→vWA(canonical)→ PP2C→ Pkinase+ZnR+beta-rich→	857	Streptomyces sp. 61	GCA_002754535.1	actinobacteria
PIH58186.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YiKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	1056	Paenibacillus sp. LK1	GCA_002764015.1	firmicutes
PIS64671.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM+TM→ PSE→ PSE→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C(frag)*→?→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→ polar_leader+TM+TM+TM→	199	Corynebacterium striatum	GCA_002775095.1	actinobacteria
PIS66423.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ PSE→ PSE→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→ polar_leader+TM+TM+TM→	496	Corynebacterium striatum	GCA_002775105.1	actinobacteria
PJF21892.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	794	Chloroflexi bacterium	GCA_002794505.1	chloroflexi
PJF22367.1	GAP1-N2+GAP1-M+TM+GAP1-C	GAP1-N2+GAP1-M+TM+GAP1-C*→	560	Chloroflexi bacterium	GCA_002794505.1	chloroflexi
PJF23276.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→ Pkinase+helical_region+TM_region→	1045	Chloroflexi bacterium	GCA_002794505.1	chloroflexi
PJF38527.1	GAP1-N2+GAP1-M	GAP1-N2+GAP1-M*→	220	Chloroflexi bacterium	GCA_002794585.1	chloroflexi
PJF41071.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	915	Chloroflexi bacterium	GCA_002794595.1	chloroflexi

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PJF45650.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	819	Chloroflexi bacterium	GCA_002794585.1 chloroflexi	
PJT46684.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	789	Streptomyces alboflavus	GCA_002808645.1 actinobacteria	
PKB09303.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	622	Streptomyces sp. Ag109_G2-1	GCA_002813225.1 actinobacteria	
PKK14792.1	GAP1-N2+GAP1-M+GAP1-C	GrpE→ HSP70→ TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+DO-GTPase2.2+TM→	784	Thermomonospora sp. CIF 1	GCA_001896795.2 actinobacteria	
PKQ21987.3	GAP1-N2+GAP1-M+low_complexity	ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+low_complexity*→	403	Actinobacteria bacterium IIGW-Actinobacteria-5	GCA_002843035.1 actinobacteria	
PLS26070.1	GAP1-N2+GAP1-M+GAP1-C	TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→ GrpE→ HSP70→ HSP70+vWA(canonical)→ DnaJ+DnaJ+ZnR+ZnR+coiled_coil+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→	968	Bifidobacterium parmae	GCA_002860365.1 actinobacteria	
SHT88951.1	GAP1-N2+GAP1-M+GAP1-C	TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→	305	Streptomyces sp. DI166	GCA_900091315.1 actinobacteria	
SCD96045.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	694	Streptomyces sp. Bpilot5-43	GCA_900091875.1 actinobacteria	
SCE10320.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	239	Streptomyces sp. TverLS-915	GCA_900091755.1 actinobacteria	
SCE16867.1	GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C→ GAP1-M+GAP1-C*→	707	Streptomyces sp. Termitarium-T10T-6	GCA_900091795.1 actinobacteria	
SCE16889.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→ GAP1-N2+GAP1-M+GAP1-C→	126	Streptomyces sp. Termitarium-T10T-6	GCA_900091795.1 actinobacteria	
SCE26370.1	GAP1-M+GAP1-C	GAP1-M+GAP1-C*→	412	Streptomyces sp. DpondAA-F4a	GCA_900091715.1 actinobacteria	
SCE41829.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	789	Streptomyces sp. IgrMP-1	GCA_900091955.1 actinobacteria	
SCG07756.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	831	Streptomyces sp. Nonst-T6T-25b	GCA_900091965.1 actinobacteria	
SCK36440.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	807	Streptomyces sp. SoanMP-e8	GCA_900090155.1 actinobacteria	
SDO36788.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YiKA-like+TM+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	1062	Paenibacillus sp. CF095	GCA_900310225.1 firmicutes	
SDM18502.1	GAP1-N2+GAP1-M+GAP1-C	Pkinase+TM→ TM→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→?→[e-7s-?]?→ Pkinase+low_complexity→	554	Geodermatophilus siccatus	GCA_900103785.1 actinobacteria	
SDO47351.1	GAP1-N2+GAP1-M+GAP1-C	Pkinase+TM→ TM→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→?→[e-7s-?]?→ Pkinase+low_complexity→	553	Geodermatophilus sp. DSM 45219	GCA_900104025.1 actinobacteria	
SDO55550.1	GAP1-N2+GAP1-M+GAP1-C	Pkinase+TM→ TM→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→?→[e-7s-?]?→ Pkinase+low_complexity→	556	Geodermatophilus africanus	GCA_900107105.1 actinobacteria	
SEDM32605.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	813	Streptomyces griseus	GCA_900107676.2 actinobacteria	
SEE68325.1	GAP1-N2+GAP1-M+GAP1-C	TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM→?→ vWA(canonical)→ PP2C→ Pkinase+ZnR+beta-rich→	895	Streptomyces sp. 3213.3	GCA_900105265.1 actinobacteria	
SEF85005.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+Cadherin-like	TM+vWA(canonical)+YiKA-like+TM+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+Cadherin-like*	965	Paenibacillus sp. UNC490MF	GCA_900107675.1 firmicutes	
SEG04795.1	GAP1-N2+GAP1-M+GAP1-C	GrpE→ HSP70→ TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM→	791	Actinomadura echinospora	GCA_900108175.1 actinobacteria	
SEH00144.1	GAP1-N2+GAP1-M+GAP1-C	GrpE→ HSP70→ TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM→	755	Nonomuraea solani	GCA_900108335.1 actinobacteria	
SEK51062.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YiKA-like+TM+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	1059	Streptomyces sp. OK003	GCA_900109515.1 firmicutes	
SEO61395.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YiKA-like+TM+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	1058	Paenibacillus sp. OK076	GCA_900110055.1 firmicutes	
SES36605.1	GAP1-N2+GAP1-M	CASPASE+TPR_region→?→ GAP1-N2+GAP1-M*→	182	Actinokineospora terrae	GCA_900111175.1 actinobacteria	
SET23369.1	GAP1-N2+GAP1-M+GAP1-C	Pkinase+TM→ TM→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→?→[e-7s-?]?→ Pkinase+low_complexity→	552	Geodermatophilus poikilotrophus	GCA_900111455.1 actinobacteria	
SEU01591.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YiKA-like+TM+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	1013	Paenibacillus sp. NFB01	GCA_900111565.1 firmicutes	
SFL38747.1	GAP1-N2+GAP1-M+GAP1-C	Pkinase+TM→ TM→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→	564	Geodermatophilus ruber	GCA_900114385.1 actinobacteria	
SFN59968.1	GAP1-N2+GAP1-M+GAP1-C	GrpE→ HSP70→ TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM→	778	Actinomadura madurae	GCA_900115095.1 actinobacteria	
SHN70262.1	GAP1-N2+GAP1-M+GAP1-C	Pkinase+TM→ TM→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→?→[e-7s-?]?→ Pkinase+low_complexity→	552	Geodermatophilus obscurus	GCA_900143215.1 actinobacteria	
SHN49947.1	GAP1-N2+GAP1-M+GAP1-C	HSP70→ TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→	697	Mycobacteroides abscessus subsp. abscessus	GCA_900130335.1 actinobacteria	
SM365450.1	GAP1-N2+GAP1-M+GAP1-C	TM+TM+TM+TM+TM+DO-GTPase2.1→ GAP1-N2+GAP1-M+GAP1-C*→?? + TM_region+DO-GTPase1→	556	Cuniculiplasma divulgatum	GCA_900083515.1 euryarchaeota	
SN300381.1	GAP1-N2+GAP1-M+GAP1-C	DO-GTPase2.1+TM→ GAP1-N2+GAP1-M+GAP1-C*→	484	Singulisphaera sp. GP187	GCA_900129635.1 planctomycetes	
SO900030.1	GAP1-N2+GAP1-M+GAP1-C	TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→	674	Nocardiopsis sp. JB363	GCA_900143625.1 actinobacteria	
SJM004603.1	GAP1-N2+GAP1-M+GAP1-C	TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+?? → GAP_unknown1+TM+TM+GAP_unknown2+BHD2C-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)=??+DO-GTPase2.2→	654	Corynebacterium glutamicum	GCA_900150955.1 actinobacteria	
SLL02929.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	746	Mycobacteroides abscessus subsp. abscessus	GCA_900132645.1 actinobacteria	
SMF90090.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YiKA-like+TM+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	1009	Paenibacillus uliginis N3/975	GCA_900177425.1 firmicutes	
SNS88073.1	GAP1-N2+GAP1-M+GAP1-C	Pkinase+TM→ TM→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ Pkinase+low_complexity→	553	Geodermatophilus pulveris	GCA_900183875.1 actinobacteria	
SOC31163.1	GAP1-N2+GAP1-M+TM+GAP1-C+TM	Pkinase+TM_region→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+TM+GAP1-C+TM*→	652	Ornithinimicrobium pekingense	GCA_900229015.1 actinobacteria	
WP_002646734.1	GAP1-N2+GAP1-M+GAP1-C	GrpE→ HSP70→ HSP70+vWA(canonical)→ DnaJ+DnaJ+DZnR+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→? → TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→	858	Gimesia maris	GCA_000181475.1 planctomycetes	
WP_002684417.1	GAP1-N2+GAP1-M+TM+GAP1-C	GAP1-N2+GAP1-M+TM+GAP1-C→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+TM+GAP1-C*=??+TM+??+beta-rich??→ GYF+GYF+TM+TM+TM→	861	Gimesia maris	GCA_000181475.1 planctomycetes	
WP_002684419.1	GAP1-N2+GAP1-M+TM+GAP1-C	GAP1-N2+GAP1-M+TM+GAP1-C*→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+TM+GAP1-C→??+TM+??+beta-rich?? → GYF+GYF+TM+TM+TM→	873	Gimesia maris	GCA_000181475.1 planctomycetes	
WP_002655127.1	GAP1-N2+GAP1-M+GAP1-C	FGS-fold_ domain→ ZnR+DO-GTPase2.1→ GAP1-N2+GAP1-M+GAP1-C*→	459	Blastopirellula marina	GCA_000203125.1 planctomycetes	
WP_003334069.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YiKA-like+TM+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	833	Brevibacillus laterosporus	GCA_000219535.3 firmicutes	
WP_003342911.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YiKA-like+TM+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	833	Brevibacillus laterosporus	GCA_000237055.2 firmicutes	

acc	architecture	operon	len	species	gca	taxend
WP_003388640.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+WA(canonical)+YrKA-like+TM+??-> Tubulin+coiled_coil+??-> Tubulin+coiled_coil+HTH?+??-> TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail-> Fibronectin-like_repeats+?? -> ZnR+ZnR+DO-GTPase2:2+ZnR+ZnR-> GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->	898	Brevibacillus borstelensis	GCA_003853565.1 firmicutes
WP_003882914.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM-> TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail-> Tubulin+alpha_helical+??+?? -> GAP_unknown1+TM+TM+GAP_unknown2-> HRDC-like?+Fibronectin-like_repeats-> GAP1-N2+GAP1-M+GAP1-C*-> beta-rich+vWA(canonical)-->??+DO-GTPase2:2->	631	Corynebacterium	GCA_002243555.1 actinobacteria
WP_003883602.1	GAP1-N2+GAP1-M+GAP1-C	HRDC-like?+Fibronectin-like_repeats-> GAP1-N2+GAP1-M+GAP1-C*-> ??+DO-GTPase2:2->	520	Mycobacteriaceae	GCA_000403365.2 actinobacteria
WP_003884602.1	GAP1-M+GAP1-C	polar_leader+TM+TM+TM-> TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail-> Tubulin+alpha_helical+??+?? -> GAP_unknown1+TM+TM+GAP_unknown2+ PSE-> PSE-> HRDC-like?+Fibronectin-like_repeats+ PSE-> GAP1-M+GAP1-C*-> beta-rich+vWA(canonical)-->??+DO-GTPase2:2-> TM+DUF4190+TM+PknH_C->	699	Mycolicibacterium fortuitum	GCA_000290855.1 actinobacteria
WP_003891373.1	GAP1-N2+GAP1-M+GAP1-C	HRDC-like?+Fibronectin-like_repeats-> GAP1-N2+GAP1-M+GAP1-C*-> ZnR+ZnR+DO-GTPase2:2->	822	Mycolicibacterium smegmatis	actinobacteria
WP_003965489.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*->	813	Streptomyces sp. ACT-1	GCA_000177175.2 actinobacteria
WP_004714441.1	GAP1-N2+GAP1-M+GAP1-C	HSP70-> HSP70+vWA(canonical)-> DnaJ+DnaJ+ZnR+ZnR+coiled_coil+Fibronectin-like_repeats-> ZnR+ZnR+DO-GTPase2:2-> GAP1-N2+GAP1-M+GAP1-C*-->?-->? -> TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2:2+TPR_region->	836	Clostridium sp. ASF502	GCA_000342135.1 firmicutes
WP_004942138.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*->	838	Streptomyces mobaraensis	GCA_003424125.1 actinobacteria
WP_005191940.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM-> TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail-> Tubulin+alpha_helical+??+?? -> GAP_unknown1+TM+TM+GAP_unknown2-> HRDC-like?+Fibronectin-like_repeats-> GAP1-N2+GAP1-M+GAP1-C*-> beta-rich+vWA(canonical)-->??+DO-GTPase2:2->	901	Gordonia amarae	GCA_000413345.2 actinobacteria
WP_005352622.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM-> TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail-> Tubulin+alpha_helical+??+?? -> GAP_unknown1+TM+TM+GAP_unknown2-> HRDC-like?+Fibronectin-like_repeats-> GAP1-N2+GAP1-M+GAP1-C*-> beta-rich+vWA(canonical)-->??+DO-GTPase2:2->	913	Rhodococcus opacus	GCA_000509685.1 actinobacteria
WP_005304499.1	GAP1-N2+GAP1-M+GAP1-C	GrpE-> HSP70-> TPR_containing_alpha_helical+Fibronectin-like_repeats-> ZnR+ZnR+DO-GTPase2:2-> GAP1-N2+GAP1-M+GAP1-C*-> TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2:2->	668	Corynebacterium	GCA_000106595.1 actinobacteria
WP_005514168.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM-> TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail-> Tubulin+alpha_helical+??+?? -> GAP_unknown1+TM+TM+GAP_unknown2-> HRDC-like?+Fibronectin-like_repeats-> GAP1-N2+GAP1-M+GAP1-C*-> beta-rich+vWA(canonical)-->??+DO-GTPase2:2->	842	Rhodococcus baagii	GCA_001664155.2 actinobacteria
WP_005529233.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM-> TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail-> Tubulin+alpha_helical+??+?? -> GAP_unknown1+TM+TM+GAP_unknown2-> HRDC-like?+Fibronectin-like_repeats-> GAP1-N2+GAP1-M+GAP1-C*-> beta-rich+vWA(canonical)-->??+DO-GTPase2:2-> polar_leader+TM+TM+TM->	523	Corynebacterium matruchotii	GCA_000175275.1 actinobacteria
WP_005524888.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM-> TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail-> Tubulin+alpha_helical+??+?? -> GAP_unknown1+TM+TM+GAP_unknown2-> HRDC-like?+Fibronectin-like_repeats-> GAP1-N2+GAP1-M+GAP1-C*-> beta-rich+vWA(canonical)-->??+DO-GTPase2:2-> polar_leader+TM+TM+TM->	523	Corynebacterium matruchotii	GCA_000175375.1 actinobacteria
WP_005630910.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM-> TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail-> Tubulin+alpha_helical+??+?? -> GAP_unknown1+TM+TM+GAP_unknown2-> HRDC-like?+Fibronectin-like_repeats-> GAP1-N2+GAP1-M+GAP1-C*-> beta-rich+vWA(canonical)-->??+DO-GTPase2:2-> polar_leader+TM+TM+TM->	532	Corynebacterium striatum	GCA_001594015.1 actinobacteria
WP_005830175.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	Tubulin+coiled_coil+??-> PSE-> TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail-> Fibronectin-like_repeats+?? -> ZnR+ZnR+DO-GTPase2:2+ZnR+ZnR-> GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->	834	Brevibacillus agri	GCA_002283415.2 firmicutes
WP_005882244.1	TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail-> Tubulin+alpha_helical+??+?? -> GAP_unknown1+TM+TM+GAP_unknown2-> HRDC-like?+Fibronectin-like_repeats-> GAP1-N2+GAP1-M+GAP1-C*-> ??+DO-GTPase2:2-> ?-->?-->?-> TM+TM+TM+vWA(canonical)+TM+TM+TM+vWA(canonical)+TM	GAP1-N2+GAP1-M+GAP1-C*->	930	Brevibacterium mcbrellneri	GCA_002178455.1 firmicutes
WP_005982930.1	GAP1-N2+GAP1-M	GrpE-> HSP70-> TPR_containing_alpha_helical+Fibronectin-like_repeats-> ZnR+ZnR+DO-GTPase2:2-> GAP1-N2+GAP1-M+GAP1-C*-> TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2:2->	898	Actinoscyrtonema rutgersii	GCA_000298005.1 actinobacteria
WP_006128441.1	GAP1-N2+GAP1-M	GrpE-> HSP70-> TPR_containing_alpha_helical+Fibronectin-like_repeats-> ZnR+ZnR+DO-GTPase2:2-> GAP1-N2+GAP1-M+GAP1-C*-> ??-->?-->?-->?-> HSP70-> +WA(canonical)->	790	Streptomyces filamentosus	GCA_001456455.1 firmicutes
WP_006245243.1	GAP1-N2+GAP1-M+GAP1-C	GrpE-> HSP70-> TPR_containing_alpha_helical+Fibronectin-like_repeats-> ZnR+ZnR+DO-GTPase2:2-> GAP1-N2+GAP1-M+GAP1-C*-> TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2:2->	796	Mycolicibacterium tusciae	GCF_000233415.2 actinobacteria
WP_006284418.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YrKA-like+TM+??-> Tubulin+coiled_coil+??-> Tubulin+coiled_coil+HTH?+??-> TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail-> Fibronectin-like_repeats+?? -> ZnR+ZnR+DO-GTPase2:2+ZnR+ZnR-> GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->	956	Paenibacillus popilliae	GCA_003152235.1 firmicutes
WP_006602915.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*-> TM+TM+TM+ZnR+ZnR+DO-GTPase2:2->	812	Streptomyces tsukubaensis	GCF_000202155.1 actinobacteria
WP_006542074.1	GAP1-N2+GAP1-M+GAP1-C+ZnR+DO-GTPase2	GAP1-N2+GAP1-M+GAP1-C+ZnR+DO-GTPase2*->	970	Frankia sp. EUN1f	GCA_001172675.1 actinobacteria
WP_006548570.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM-> TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail-> Tubulin+alpha_helical+??+?? -> GAP_unknown1+TM+TM+GAP_unknown2-> HRDC-like?+Fibronectin-like_repeats-> GAP1-N2+GAP1-M+GAP1-C*-->?-->?-> DO-GTPase2:2->	891	Actinomyces urogenitalis	GCA_001506395.1 actinobacteria
WP_006552801.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM-> TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail-> Tubulin+alpha_helical+??+?? -> PSE-> HRDC-like?+Fibronectin-like_repeats-> GAP1-N2+GAP1-M+GAP1-C*-> beta-rich+vWA(canonical)-->??+DO-GTPase2:2->	909	Rhodococcus pyridinivorans	GCA_002286965.2 actinobacteria
WP_006626564.1	GAP1-N2+GAP1-M+GAP1-C	Fibronectin-like_repeats+?? -> ZnR+ZnR+DO-GTPase2:2-> GAP1-N2+GAP1-M+GAP1-C*-->?-->? -> TM+TM+TM+ZnR+ZnR+DO-GTPase2:2-> TM+vWA(canonical)+YrKA-like+TM+??-> Tubulin+coiled_coil+??-> Tubulin+coiled_coil+HTH?+??-> TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail-> PSE-> ZnR+ZnR+DO-GTPase2:2+ZnR+ZnR->	794	Clostridium carboniditorans	GCA_001735095.1 firmicutes
WP_007646888.1	GAP1-N2+GAP1-M	TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2:2-> TM+vWA(canonical)+YrKA-like+TM+??-> Tubulin+coiled_coil+??-> Tubulin+coiled_coil+HTH?+??-> TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail-> PSE-> ZnR+ZnR+DO-GTPase2:2+ZnR+ZnR-> GAP1-N2+GAP1-M*	369	Clostridium carboniditorans	GCA_001735045.1 firmicutes
WP_007083299.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YrKA-like+TM+??-> Tubulin+coiled_coil+??-> Tubulin+coiled_coil+ZnR+??-> TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail-> Fibronectin-like_repeats+?? -> ZnR+ZnR+DO-GTPase2:2+ZnR+ZnR-> GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->	828	Bacillus bataviensis	GCA_003307675.1 firmicutes
WP_007166449.1	GAP1-N2+GAP1-M+GAP1-C	TM+DUF4190+TM+ PknH_C+ polar_leader+TM+TM+TM-> TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail-> Tubulin+alpha_helical+??+?? -> GAP_unknown1+TM+TM+GAP_unknown2-> HRDC-like?+Fibronectin-like_repeats-> GAP1-N2+GAP1-M+GAP1-C(Tm)*-> beta-rich+vWA(canonical)-->??+DO-GTPase2:2->	364	Mycobacteria	GCA_000164135.1 actinobacteria
WP_007319238.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM-> TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail-> Tubulin+alpha_helical+??+?? -> GAP_unknown1+TM+TM+GAP_unknown2-> HRDC-like?+Fibronectin-like_repeats-> GAP1-N2+GAP1-M+GAP1-C*-> beta-rich+vWA(canonical)-->??+DO-GTPase2:2->	890	Gordonia effusa	GCA_002413035.2 actinobacteria
WP_007320125.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM-> TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail-> Tubulin+alpha_helical+??+?? -> GAP_unknown1+TM+TM+GAP_unknown2-> HRDC-like?+Fibronectin-like_repeats-> GAP1-N2+GAP1-M+GAP1-C*-> beta-rich+vWA(canonical)-->??+DO-GTPase2:2->	958	Gordonia aralii	GCA_002411265.2 actinobacteria
WP_007430267.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	Tubulin+coiled_coil+??-> PSE-> TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail-> Fibronectin-like_repeats+?? -> ZnR+ZnR+DO-GTPase2:2+ZnR+ZnR-> GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->	1000	Paenibacillus sp. Aloe-11	GCA_002457415.1 firmicutes
WP_007431903.1	GAP1-N2+GAP1-M	GAP1-N2+GAP1-M*	821	Streptomyces sp. W007	GCA_004139071.2 actinobacteria
WP_007724671.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YrKA-like+TM+??-> Tubulin+coiled_coil+??-> Tubulin+coiled_coil+HTH?+??-> TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail-> Fibronectin-like_repeats+?? -> ZnR+ZnR+DO-GTPase2:2+ZnR+ZnR-> GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->	831	Brevibacillus sp. BC25	GCA_002820075.1 firmicutes
WP_007793561.1	GAP1-N2+GAP1-M+GAP1-C	TM+DUF4190+TM+ TM+DUF4190+TM+ polar_leader+TM+TM+TM-> TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail-> Tubulin+alpha_helical+??+?? -> PSE-> PSE-> GAP1-N2+GAP1-M+GAP1-C*-> beta-rich+vWA(canonical)-->??+DO-GTPase2:2-> TM+DUF4190+TM+PknH_C-> TM+DUF4190+TM+PknH_C->	924	Brevibacterium colombiense	GCA_002221105.4 actinobacteria
WP_007793805.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YrKA-like+TM+??-> Tubulin+coiled_coil+??-> Tubulin+coiled_coil+HTH?+??-> TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail-> Fibronectin-like_repeats+?? -> ZnR+ZnR+DO-GTPase2:2+ZnR+ZnR-> GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->	834	Paenibacillus sp. CF112	GCA_002446435.1 firmicutes
WP_007820797.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*->	772	Streptomyces sp. Tu6071	GCA_002213655.1 actinobacteria
WP_009076374.1	GAP1-N2+GAP1-M+GAP1-C	FHA-like?+ZnR+ZnR+DO-GTPase2:2-> GAP1-N2+GAP1-M+GAP1-C*->	1000	Verrucomicrobia bacterium DG1235	GCA_001755954.1 verrucomicrobia
WP_009195826.1	GAP1-N2+GAP1-M+GAP1-C	ZnR+ZnR+DO-GTPase2:2-> GAP1-N2+GAP1-M+GAP1-C*-> TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2:2-> TM+beta-sandwich+NTF-like-> GrpE->	850	Microcystis sp. T1-4	GCA_002974335.1 cyanobacteria
WP_009379378.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM-> TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail-> Tubulin+alpha_helical+??+?? -> GAP_unknown1+TM+TM+GAP_unknown2-> HRDC-like?+Fibronectin-like_repeats-> GAP1-N2+GAP1-M+GAP1-C*-> beta-rich+vWA(canonical)-->??+DO-GTPase2:2->	866	Gordonia malaguae	GCA_003444135.1 actinobacteria
WP_009410972.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*->	789	Streptomyces	GCA_00299175.2 actinobacteria
WP_009714732.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM-> TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail-> Tubulin+alpha_helical+??+?? -> GAP_unknown1+TM+TM+GAP_unknown2-> HRDC-like?+Fibronectin-like_repeats-> GAP1-N2+GAP1-M+GAP1-C*-> beta-rich+vWA(canonical)-->??+DO-GTPase2:2->	904	Rhodococcus sp. AW25M09	GCA_000328955.1 actinobacteria
WP_009729950.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM-> TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail-> Tubulin+alpha_helical+??+?? -> GAP_unknown1+TM+TM+GAP_unknown2-> HRDC-like?+Fibronectin-like_repeats-> GAP1-N2+GAP1-M+GAP1-C*-->?-->?-> DO-GTPase2:2->	969	Actinomyces massiliensis	GCA_000296275.1 actinobacteria
WP_009747379.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM-> TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail-> Tubulin+alpha_helical+??+?? -> GAP_unknown1+TM+TM+GAP_unknown2-> HRDC-like?+Fibronectin-like_repeats-> GAP1-N2+GAP1-M+GAP1-C*-> beta-rich+vWA(canonical)-->??+DO-GTPase2:2->	913	Rhodococcus sp. JVH1	GCA_002736775.1 actinobacteria
WP_009267633.1	GAP1-N2+GAP1-M+GAP1-C	TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2:2-> GrpE-> HSP70-> HSP70+vWA(canonical)-> DnaJ+DnaJ+ZnR+ZnR+coiled_coil+Fibronectin-like_repeats-> ZnR+ZnR+DO-GTPase2:2-> GAP1-N2+GAP1-M+GAP1-C*-->?-->? -> TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2:2->	886	Peptoanaerobacter stomatis	GCA_002288095.2 firmicutes
WP_009306923.1	GAP1-N2+GAP1-M+GAP1-C	HSP70-> HSP70+vWA(canonical)-> DnaJ+DnaJ+ZnR+ZnR+coiled_coil+Fibronectin-like_repeats-> ZnR+ZnR+DO-GTPase2:2-> GAP1-N2+GAP1-M+GAP1-C*-->?-->? -> TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2:2->	838	Peptoanaerobacter stomatis	GCA_002950035.1 firmicutes
WP_009895527.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YrKA-like+TM+??-> Tubulin+coiled_coil+HTH?+??-> TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail-> Fibronectin-like_repeats+?? -> ZnR+ZnR+DO-GTPase2:2+ZnR+ZnR-> GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->	990	Paenibacillus sp. HGF5	GCA_003944555.2 firmicutes
WP_009929884.1	GAP1-N2+GAP1-M+GAP1-C	GrpE-> HSP70-> TPR_containing_alpha_helical+Fibronectin-like_repeats-> ZnR+ZnR+DO-GTPase2:2-> GAP1-N2+GAP1-M+GAP1-C*-> TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2:2-->?-->?-> HSP70-> +WA(canonical)->	818	Actinomyces sp. ICM47	GCA_002290635.1 actinobacteria
WP_009672117.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+Cadherin-like	TM+vWA(canonical)+YrKA-like+TM+??-> Tubulin+coiled_coil+??-> Tubulin+coiled_coil+HTH?+??-> TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail-> Fibronectin-like_repeats+?? -> ZnR+ZnR+DO-GTPase2:2+ZnR+ZnR-> GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+Cadherin-like*->	965	Paenibacillus	GCA_002124295.2 firmicutes
WP_009741053.1	GAP1-N2+GAP1-M+GAP1-C	GrpE-> HSP70-> TPR_containing_alpha_helical+Fibronectin-like_repeats-> ZnR+ZnR+DO-GTPase2:2-> GAP1-N2+GAP1-M+GAP1-C*-> TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2:2-->?-->? -> HSP70->	792	Frankia sp. QA3	GCA_000262465.1 actinobacteria

acc	architecture	operon	len	species	gca	taxend
WP_009748877.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ PSE→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*	920	Actinomyces sp. oral taxon 448	GCA_000220835.1	actinobacteria
WP_009953310.1	GAP1-N2+GAP1-M+GAP1-C	GrpE→ HSP70→ TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*	802	Saccharopolyspora erythraea	GCA_000062885.1	actinobacteria
WP_009497927.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*	787	Saccharopolyspora erythraea	GCA_000062885.1	actinobacteria
WP_010045066.1	GAP1-N2+GAP1-M+TM	GAP1-N2+GAP1-M+TM*	274	Gemmata obscuriglobus	GCA_003149495.1	planctomycetes
WP_010045922.1	GAP1-N2+GAP1-M+TM+low_complexity+TM	DO-GTPase2.1→?→ GAP1-N2+GAP1-M+TM+low_complexity+TM*	968	Gemmata obscuriglobus	GCA_003149495.1	planctomycetes
WP_010188424.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*	557	Corynebacterium sarimcoeum	GCA_000022905.1	actinobacteria
WP_010023793.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*	772	Streptomyces sp. SA3_actG	GCA_000179195.1	actinobacteria
WP_010346131.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*	999	Paenibacillus peoriae	GCF_000238685.1	firmicutes
WP_010493111.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+Cadherin-like	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+Cadherin-like*	936	Paenibacillus elgii	GCF_000213315.1	firmicutes
WP_010685460.1	GAP1-N2+GAP1-M+GAP1-C	ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+TM+GAP1-C*→??+TM+??+beta-rich?→ GYF+GYF+ZnR+TM+TM+TM→	875	Schlesnerin paludicola	GCF_000255605.1	planctomycetes
WP_010641232.1	GAP1-N2+GAP1-M	GrpE→ HSP70→ TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*	789	Streptomyces sp. S4		actinobacteria
WP_010696601.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*	800	Saccharopolyspora spinosa	GCA_002846275.1	actinobacteria
WP_010015330.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*	631	Corynebacterium glutamicum	GCF_000011325.1	actinobacteria
WP_010557145.1	GAP1-N2+GAP1-M+GAP1-C	HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→??+DO-GTPase2.2→	829	Mycobacterium	GCF_000157165.1	actinobacteria
WP_011594626.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*	913	Rhodococcus jostii	GCA_000014565.1	actinobacteria
WP_011726629.1	GAP1-N2+GAP1-M+GAP1-C	HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→??+DO-GTPase2.2→	922	Kribbella flavida	GCA_000423205.1	actinobacteria
WP_011775814.1	GAP1-N2+GAP1-M+TM+GAP1-C+TM+TM	PP2C→?→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+TM+GAP1-C+TM+TM→	763	Pasmatrihabacter aureocens	GCA_000014925.1	actinobacteria
WP_011854161.1	GAP1-N2+GAP1-M+GAP1-C	HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→??+DO-GTPase2.2→	829	Mycobacteriaceae	GCA_000610005.1	actinobacteria
WP_012036365.1	GAP1-N2+GAP1-M+GAP1-C	Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→ TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M→	896	Clostridium kluyveri	GCA_000036365.1	firmicutes
WP_012620487.1	GAP1-N2+GAP1-M	GAP1-N2+GAP1-M+GAP1-C→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→ TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M*	359	Clostridium kluyveri	GCA_000010265.1	firmicutes
WP_012835243.1	GAP1-N2+GAP1-M+GAP1-C	GrpE→ HSP70→ TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*	792	Thermononospora curvata	GCA_000023435.1	actinobacteria
WP_012852227.1	GAP1-N2+GAP1-M+GAP1-C	GrpE→ HSP70→ TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*	784	Thermononospora curvata	GCA_000023435.1	actinobacteria
WP_012913505.1	GAP1-N2+GAP1-M	FGS-fold_domain→ ZnR+DO-GTPase2.1→ GAP1-N2+GAP1-M*	246	Streptococcus gallolyticus	GCA_000025565.1	firmicutes
WP_013237251.1	GAP1-N2+GAP1-M+GAP1-C	Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??	868	Clostridium jiangnaihili	GCA_000143685.1	firmicutes
WP_013237261.1	GAP1-N2+GAP1-M	Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→*→*→*→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M*	351	Clostridium jiangnaihili	GCA_000143685.1	firmicutes
WP_013310112.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*	1002	Paenibacillus polymyxa	GCA_000146875.2	firmicutes
WP_013370937.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*	1009	Paenibacillus polymyxa	GCA_000146985.2	firmicutes
WP_013605745.1	GAP1-N2+GAP1-M	FGS-fold_domain→ ZnR+DO-GTPase2.1→ GAP1-N2+GAP1-M*	231	Clostridium pallida	GCA_000185415.1	planctomycetes
WP_013655639.1	GAP1-N2+GAP1-M+GAP1-C+TM+polar_tail+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+TM+polar_tail+beta-rich*	870	Cellulosilyticum lentocellum	GCA_000178835.2	firmicutes
WP_013901661.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+Cadherin-like	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+Cadherin-like*	921	Paenibacillus macilaginous	GCA_000259855.1	firmicutes
WP_014011376.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*	579	Corynebacterium variabile	GCA_000179205.2	actinobacteria
WP_014049755.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*	863	Streptomyces	GCA_000177195.2	actinobacteria
WP_014153312.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*	804	Streptomyces pratensis	GCA_000176115.2	actinobacteria
WP_014173128.1	GAP1-N2+GAP1-M+GAP1-C	ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→	815	Streptomyces	GCA_000092565.1	actinobacteria
WP_014283329.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*	1005	Paenibacillus terrae	GCA_002255585.1	firmicutes
WP_014005341.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+Cadherin-like	TM+vWA(canonical)+YtKA-like+TM+??→ PSE→ PSE→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+Cadherin-like*	921	Paenibacillus macilaginous	GCA_000259855.1	firmicutes
WP_014695319.1	GAP1-N2+GAP1-M+GAP1-C	GrpE→ HSP70→ TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*	740	Coprococcus	GCA_000239135.1	firmicutes
WP_014919933.1	GAP1-N2+GAP1-M+GAP1-C	TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*	868	Nocardiopsis alba	GCA_000294515.1	actinobacteria
WP_014962605.1	GAP1-N2+GAP1-M+TM+low_complexity	GAP1-N2+GAP1-M+TM+low_complexity*→?	602	Nitrosopumilus	GCA_000296555.1	Nitrososphaeota
WP_015245331.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*	1145	Singulisphaera acidiphila	GCA_002424515.3	planctomycetes
WP_015246829.1	GAP1-N2+GAP1-M	FGS-fold_domain→ ZnR+DO-GTPase2.1→ GAP1-N2+GAP1-M*	220	Singulisphaera acidiphila	GCA_002424515.3	planctomycetes
WP_015250492.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*	469	Singulisphaera acidiphila	GCA_002424515.3	planctomycetes
WP_015506605.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*	789	Streptomyces	GCA_000350225.1	actinobacteria
WP_015792688.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*	804	Streptomyces sp. PAMC 26508	GCA_000364805.1	actinobacteria
WP_015612204.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*	812	Streptomyces fulvisimus	GCA_000345945.1	actinobacteria
WP_015653149.3	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*	654	Corynebacterium callunae	GCA_000344785.1	actinobacteria
WP_015657008.1	GAP1-N2+GAP1-M+GAP1-C	TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C* → TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM→ vWA(canonical)→ PP2C→ Pkinase+ZnR+beta-rich→	832	Streptomyces davaonensis	GCA_000340325.1	actinobacteria
WP_015701655.1	GAP1-N2+GAP1-M+GAP1-C	TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→?→ HSP70→ HSP70→vWA(canonical)→?→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*	889	Treponema azotonutricium	GCA_000214355.1	spirochaetes
WP_015737595.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→?→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*	992	Paenibacillus sp. Y412MC10	GCA_000236685.1	firmicutes
WP_015903872.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*	832	Brevibacillus brevis	GCA_000068015.1	firmicutes
WP_016202160.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*	750	Bacillus neabonii	GCA_000401235.1	firmicutes
WP_016062300.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+Cadherin-like	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+Cadherin-like*	921	Paenibacillus macilaginous	GCA_000259855.2	firmicutes

acc	architecture	operon	len	species	gca	taxend
WP_016431979.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→ sWA(canonical)→ PP2C→ Pkinase+ZnR+beta-rich-u[]=-TPR_containing_alpha_helical+Fibronectin-like_repeats	785	Streptomyces sp. HGB0020	GCA_000413315.1	actinobacteria
WP_016730660.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+sWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH1+??→ TM+TM+TM+sWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	832	Bacillales	GCA_001184753.1	firmicutes
WP_016601154.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	Tubulin+coiled_coil+HTH1*→ TM+TM+TM+sWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*	549	Paenibacillus polymyxa	GCA_000507985.1	firmicutes
WP_016882979.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+ TM+ TM+sWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+sWA(canonical)→??+DO-GTPase2.2→	913	Rhodococcus sp. DK17	GCA_000283875.1	actinobacteria
WP_017193728.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM+ TM+ TM+sWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→?→??+DO-GTPase2.2→	909	Actinomyces massiliensis	GCA_000298963.1	actinobacteria
WP_017246635.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+sWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH1+??→ TM+TM+TM+sWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	832	Brevibacillus brevis	GCA_000296715.2	firmicutes
WP_017428408.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+sWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH1+??→ TM+TM+TM+sWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	549	Paenibacillus polymyxa	GCA_000307675.1	firmicutes
WP_017535628.1	GAP1-N2+GAP1-M+GAP1-C	TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→	868	Nocardiopsis alba	GCF_000341225.1	actinobacteria
WP_017542141.1	GAP1-N2+GAP1-M+GAP1-C	GrpE→ HSP70→ TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→??→	813	Nocardiopsis prasina	GCF_000341265.1	actinobacteria
WP_017565406.1	GAP1-N2+GAP1-M+GAP1-C	TPR_containing_alpha_helical+Fibronectin-like_repeats+extended_insert+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+ZnR+ZnR+DO-GTPase2.2→	943	Nocardiopsis synnemnatataformans	GCF_000564904.1	actinobacteria
WP_017569953.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	781	Nocardiopsis halotolerans	GCF_000341065.1	actinobacteria
WP_017576227.1	GAP1-N2+GAP1-M+GAP1-C	HSP70→ TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→	857	Nocardiopsis lunsenensis	GCF_000342905.1	actinobacteria
WP_017583227.1	GAP1-N2+GAP1-M+GAP1-C	GrpE→ HSP70→ TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→??→ HSP70→ sWA(canonical)→	790	Nocardiopsis tullifonsis	GCF_000349985.1	actinobacteria
WP_017589329.1	GAP1-N2+GAP1-M+GAP1-C	TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→	861	Nocardiopsis ganjahanensis	GCF_000349995.1	actinobacteria
WP_017606786.1	GAP1-N2+GAP1-M+GAP1-C	TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→	830	Nocardiopsis alkaliphila	GCF_000341005.1	actinobacteria
WP_017609151.1	GAP1-N2+GAP1-M+GAP1-C	HSP70→ PSE→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→	879	Nocardiopsis dejungensis	GCF_000341115.1	actinobacteria
WP_017814015.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+sWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH1+??→ TM+TM+TM+sWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	1138	Paenibacillus sp. A9	GCA_000346635.1	firmicutes
WP_018097235.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM+ TM+ TM+sWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+sWA(canonical)→??+DO-GTPase2.2→ polar_leader+TM+TM+TM+	583	Corynebacterium ciconiae	GCF_000372265.1	actinobacteria
WP_018023270.1	GAP1-N2+GAP1-M+GAP1-C	Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+sWA(canonical)→??+DO-GTPase2.2→ polar_leader+TM+TM+TM+	526	Corynebacterium ulceribovis	GCF_000372945.1	actinobacteria
WP_018100677.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM+ TM+sWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+sWA(canonical)→??+DO-GTPase2.2→ polar_leader+TM+TM+TM+	815	Streptomyces	GCF_000375275.1	actinobacteria
WP_018348503.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→ sWA(canonical)→ PSE→ Pkinase+ZnR+beta-rich→[]=-TPR_containing_alpha_helical+Fibronectin-like_repeats	792	Streptomyces vitaminophilus	GCA_001445053.1	actinobacteria
WP_018469179.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	789	Streptomyces sp. LaPyAH-202	GCA_003688775.1	actinobacteria
WP_018491644.1	GAP1-N2+GAP1-M	-	877	Streptomyces sp. CoaMP-sW	-	actinobacteria
WP_018514559.1	GAP1-N2+GAP1-M	-	859	Streptomyces sp. SoneMP-v10	-	actinobacteria
WP_018554808.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	859	Streptomyces sp. ATmAS-D23	GCF_000373645.1	actinobacteria
WP_018657913.1	GAP1-N2+GAP1-M+GAP1-C	GrpE→ HSP70→ TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM+→	818	Actinomadura flavalba	GCF_000374305.1	actinobacteria
WP_018671154.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+sWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH1+??→ TM+TM+TM+sWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	833	Brevibacillus laterosporus	GCA_002756795.1	firmicutes
WP_018680644.1	GAP1-N2+GAP1-M+GAP1-C	GrpE→ HSP70→ TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→ HSP70→ sWA(canonical)→	847	Actinokineospora enzanensis	GCF_000372445.1	actinobacteria
WP_018758407.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+sWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH1+??→ TM+TM+TM+sWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	956	Paenibacillus terrigena	GCF_003748451.1	firmicutes
WP_018837575.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+sWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH1+??→ TM+TM+TM+sWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	1000	Paenibacillus massiliensis	GCF_000372535.1	firmicutes
WP_018895729.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	789	Streptomyces sp. CNY228	GCF_003377545.1	actinobacteria
WP_018978693.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+sWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH1+??→ TM+TM+TM+sWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	1089	Saccharothrix kiseleuna	GCF_003374145.1	firmicutes
WP_019061048.1	GAP1-N2+GAP1-M+GAP1-C	GrpE→ HSP70→ TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+Jelly_roll+beta-sandwich→[]=-STAND_NTPase+TM+TM+TM+TM+TM+TM	512	Streptomyces prunicolor	GCF_003067365.1	actinobacteria
WP_019062737.1	GAP1-N2+GAP1-M	-	1082	Streptomyces prunicolor	-	actinobacteria
WP_019071485.1	GAP1-N2+GAP1-M+GAP1-C	TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM+→ sWA(canonical)→ PP2C→ Pkinase+ZnR+beta-rich→	920	Streptomyces lokutoneensis	GCF_003765645.1	actinobacteria
WP_019339896.1	GAP1-N2+GAP1-M	-	861	Streptomyces sp. AA1529	-	actinobacteria
WP_019422337.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail	TM+TM+TM+sWA+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C+polar_tail*→	1006	Paenibacillus sp. OSY-SE	GCF_000283315.1	firmicutes
WP_019513906.1	GAP1-N2+GAP1-M+GAP1-C	TM+DUF4190+TM→ TM+DUF4190+TM→ polar_leader+TM+TM+TM+ TM+sWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+sWA(canonical)→??+DO-GTPase2.2→ PSE→ TM+DUF4190+TM+PknH_C→ TM+DUF4190+TM+PknH_C→	840	Mycobacteriaceae	GCA_003137305.3	actinobacteria
WP_019606165.1	GAP1-N2+GAP1-M+GAP1-C	TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→	903	Nocardiopsis sp. CNS-639	GCF_000381605.1	actinobacteria
WP_019634286.1	GAP1-N2+GAP1-M+GAP1-C	GrpE→ HSP70→ TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM+→	775	Actinomadura atramentaria	GCF_003381885.1	actinobacteria
WP_019838417.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+sWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH1+??→ TM+TM+TM+sWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	1152	Streptomyces flavovirens	GCA_003381955.1	actinobacteria
WP_019687104.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+sWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH1+??→ TM+TM+TM+sWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	1009	Paenibacillus polymyxa	GCA_900445525.1	firmicutes
WP_019913815.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+sWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH1+??→ TM+TM+TM+sWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	1038	Paenibacillus sp. RW-567	GCF_003374185.1	firmicutes
WP_020384555.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM+ TM+sWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+sWA(canonical)→??+DO-GTPase2.2→ TM+TM+TM→	526	Corynebacterium doosanense	GCA_000767055.1	actinobacteria
WP_020440145.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM+ TM+sWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+sWA(canonical)→??+DO-GTPase2.2→ TM+TM+TM→	613	Corynebacterium terpenotabidum	GCA_000418365.1	actinobacteria
WP_020464398.1	GAP1-N2+GAP1-M+GAP1-C	HSP70→ TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→	887	Frankia sp. EAN1pec	GCA_000418005.1	actinobacteria
WP_020471914.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	831	Zavarzinella formosa	GCF_000255705.1	planctomycetes
WP_020503925.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	1131	Lamprocystis purpurea	GCF_003379525.1	gammaproteobacteria
WP_020509485.1	GAP1-N2+GAP1-M+GAP1-C	HSP70→[]=-?/[]GrpE→ HSP70→ TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→	817	Actinoplanes globisporus	GCF_003379645.1	actinobacteria
WP_020603718.1	GAP1-N2+GAP1-M+GAP1-C	PP2C→ Pkinase→?→?→?→ HSP70_domain_2+low_complexity+domain_beta3→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→	816	Streptomyces sp. CNY243	GCF_003737165.1	actinobacteria
WP_020617137.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+sWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH1+??→ TM+TM+TM+sWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→?→ ZnR+ZnR+DO-GTPase2.2→ ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	1061	Paenibacillus daejeonensis	GCF_003378385.1	firmicutes
WP_020629738.1	GAP1-N2+GAP1-M+GAP1-C	GrpE→ HSP70→ TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→?→ HSP70→ sWA(canonical)→[]=-?/=-?/=- HSP70	816	Amycolatopsis alba	GCA_002234585.1	actinobacteria

acc	architecture	operon	len	species	gca	taxend
WP_020679048.1	GAP1:N2+GAP1:M+GAP1:C	PP2C-> Pkinase-=7->7-=7-> HSP70_domain_2+low_complexity+domain_betaX-> ZnR+ZnR+DO-GTPase2:2-> GAP1:N2+GAP1:M+GAP1:C*-> TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2:2->	816	Streptomyces sp. CNQ766	GCF_000377105.1	actinobacteria
WP_020679138.1	GAP1:N2+GAP1:M+GAP1:C	PP2C-> Pkinase-=7->7-=7-> HSP70_domain_2+low_complexity+domain_betaX-> ZnR+ZnR+DO-GTPase2:2-> GAP1:N2+GAP1:M+GAP1:C*-> TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2:2->	816	Streptomyces sp. CNS335	GCF_000377125.1	actinobacteria
WP_020933024.1	GAP1:N2+GAP1:M+GAP1:C	polar_leader+TM+TM+TM-> TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich-lr_tail-> Tubulin+alpha_helical+??+??-> GAP_unknown1+TM+TM+GAP_unknown2-> HRDC-like?+Fibronectin-like_repeats-> GAP1:N2+GAP1:M+GAP1:C* -> beta-rich+vWA(canonical)-=7?+DO-GTPase2:2-> TM+TM+TM->	901	Corynebacterium maris	GCF_000432645.1	actinobacteria
WP_020492943.1	GAP1:N2+GAP1:M		967	Streptomyces collinus	GCF_000444875.1	actinobacteria
WP_021930295.1	GAP1:N2+GAP1:M+GAP1:C	Dnaj+DnaJ+ZnR+ZnR+coil+Fibronectin-like_repeats-> ZnR+ZnR+DO-GTPase2:2(frag)-=7-> GAP1:N2+GAP1:M+GAP1:C*-> TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2:2+TM+beta-sandwich+NTF-like-> GrpE-> HSP70-=7->7-=7-> HSP70+vWA(canonical)->	840	Cryptosphaerra watsonii	GCA_001039615.1	cyanobacteria
WP_025386058.1	GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YrKA-like+TM+??-> Tubulin+coiled_coil+??-> Tubulin+coiled_coil+HTH1+??-> TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail-> Fibronectin-like_repeats+??-> ZnR+ZnR+DO-GTPase2:2+ZnR+ZnR-> GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich*->	833	Brevibacillus laterosporus	GCA_000472325.2	firmicutes
WP_021627243.1	GAP1:N2+GAP1:M+GAP1:C	Fibronectin-like_repeats+??-> ZnR+ZnR+DO-GTPase2:2-> GAP1:N2+GAP1:M+GAP1:C*-> TM+vWA(canonical)+YrKA-like+TM+??-> Tubulin+coiled_coil+??-> PSE-> TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail-> Fibronectin-like_repeats+??->	868	Clostridium autoethanogenum	GCA_000484505.1	firmicutes
WP_021627385.1	GAP1:N2+GAP1:M+GAP1:C	Tubulin+coiled_coil+??-> PSE-> TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail-> Fibronectin-like_repeats+??-=7->7-=7-> ZnR+ZnR+DO-GTPase2:2+ZnR+ZnR-> GAP1:N2+GAP1:M*->	351	Clostridium autoethanogenum	GCA_000484505.1	firmicutes
WP_023373055.1	GAP1:N2+GAP1:M+GAP1:C	TM+DUF4190+TM-> TM+DUF4190+TM-> polar_leader+TM+TM+TM-> TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lr_tail-> Tubulin+alpha_helical+??+??-> GAP_unknown1+TM+TM+GAP_unknown2-> HRDC-like?+Fibronectin-like_repeats-> GAP1:N2+GAP1:M+GAP1:C*-> beta-rich+vWA(canonical)-=7?+DO-GTPase2:2->	819	Mycobacterium kansasii	GCA_000157895.2	actinobacteria
WP_024164015.1	GAP1:N2+GAP1:M+GAP1:C	GAP1:N2+GAP1:M+GAP1:C*->	789	Streptomyces sp. PVA 94-07	GCA_000495755.1	actinobacteria
WP_024214102.1	GAP1:N2+GAP1:M+GAP1:C	GAP1:N2+GAP1:M+GAP1:C*->	789	Streptomyces sp. GBA 94-10	GCA_000495635.1	actinobacteria
WP_023375045.1	GAP1:N2+GAP1:M+GAP1:C	GAP1:N2+GAP1:M+GAP1:C*-> PPP2C-> Pkinase+Zn2h+beta-rich-=||=-TPR_containing_alpha_helical+Fibronectin-like_repeats	865	Streptomyces niveus	GCA_000757645.1	actinobacteria
WP_023552702.1	GAP1:N2+GAP1:M+GAP1:C	Pkinase-=7->7-=7-> HSP70_domain_2+low_complexity+domain_betaX-> ZnR+ZnR+DO-GTPase2:2-> GAP1:N2+GAP1:M+GAP1:C*-> TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2:2->	815	Streptomyces roseochromogenus	GCA_000497445.1	actinobacteria
WP_023559271.1	GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YrKA-like+TM+??-> Tubulin+coiled_coil+??-> Tubulin+coiled_coil+HTH1+??-> TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail-> Fibronectin-like_repeats+??-> ZnR+ZnR+DO-GTPase2:2+ZnR+ZnR-> GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich*->	836	Streptococcus pneumoniae	GCA_000509271.1	firmicutes
WP_023921833.1	GAP1:N2+GAP1:M+GAP1:C	??-=7+HTH7+GrpE-> HSP70-> Dnaj+DnaJ+ZnR+Fibronectin-like_repeats-> ZnR+ZnR+DO-GTPase2:2-> GAP1:N2+GAP1:M+GAP1:C*-> TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2:2->	861	Ruminococcus lactaris	GCA_000567785.1	firmicutes
WP_023960422.1	GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich	Tubulin+coiled_coil+??-> PSE-> TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail-> Fibronectin-like_repeats+??-> ZnR+ZnR+DO-GTPase2:2+ZnR+ZnR-> GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich*->	889	Paenibacillus sp. JCM 10914	GCA_000613225.1	firmicutes
WP_023988392.1	GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YrKA-like+TM+??-> Tubulin+coiled_coil+??-> Tubulin+coiled_coil+HTH1+??-> TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail-> Fibronectin-like_repeats+??-> ZnR+ZnR+DO-GTPase2:2+ZnR+ZnR-> GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich*->	1002	Paenibacillus polymyxa	GCA_000507205.2	firmicutes
WP_023995839.1	GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YrKA-like+TM+??-> Tubulin+coiled_coil+??-> Tubulin+coiled_coil+HTH1+??-> TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail-> Fibronectin-like_repeats+??-> ZnR+ZnR+DO-GTPase2:2+ZnR+ZnR-> GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich*->	953	Bacillus vireti	GCA_000508325.2	firmicutes
WP_024164121.1	GAP1:N2+GAP1:M+GAP1:C	GAP1:N2+GAP1:M+GAP1:C*->	829	Streptomyces filamentosus	GCA_000156056.2	actinobacteria
WP_024391768.1	GAP1:N2+GAP1:M+GAP1:C	HSP70-=7-> ZnR+ZnR+DO-GTPase2:2-> GAP1:N2+GAP1:M+GAP1:C*->	697	Streptococcus suis	GCF_000440555.1	firmicutes
WP_024692035.1	GAP1:N2+GAP1:M+GAP1:C	GAP1:N2+GAP1:M+GAP1:C*->	735	Streptomyces sp. AW19M42	GCF_000493035.1	actinobacteria
WP_026327788.1	GAP1:N2+GAP1:M+GAP1:C+polar_tail	TM+TM+TM+vWA+TM+TM+polar_tail-> Fibronectin-like_repeats+??-> ZnR+ZnR+DO-GTPase2:2-> GAP1:N2+GAP1:M+GAP1:C+polar_tail*->	1079	Paenibacillus	GCA_000499205.1	firmicutes
WP_026867251.1	GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YrKA-like+TM+??-> Tubulin+coiled_coil+??-> Tubulin+coiled_coil+HTH1+??-> TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail-> Fibronectin-like_repeats+??-> ZnR+ZnR+DO-GTPase2:2+ZnR+ZnR-> GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich*->	920	Paenibacillus borstelensis	GCA_000611215.1	firmicutes
WP_025333415.1	GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YrKA-like+TM+??-> Tubulin+coiled_coil+??-> Tubulin+coiled_coil+HTH1+??-> TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail-> Fibronectin-like_repeats+??-> ZnR+ZnR+DO-GTPase2:2+ZnR+ZnR-> GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich*->	1025	Paenibacillus sabinae	GCA_000612505.1	firmicutes
WP_025672161.1	GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich	Tubulin+coiled_coil+??-> Tubulin+coiled_coil+HTH1+??-> TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail-> Fibronectin-like_repeats+??-> ZnR+ZnR+DO-GTPase2:2+ZnR+ZnR-> GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich*->	1000	Paenibacillus massiliensis	GCF_000724105.1	firmicutes
WP_025679141.1	GAP1:N2+GAP1:M+GAP1:C+polar_tail	Tubulin+coiled_coil+??-> Tubulin+coiled_coil+HTH1+??-> TM+TM+TM+vWA+TM+TM+TM+polar_tail-> Fibronectin-like_repeats+??-> ZnR+ZnR+DO-GTPase2:2-> GAP1:N2+GAP1:M+GAP1:C+polar_tail*->	1009	Paenibacillus polymyxa	GCF_000520795.1	firmicutes
WP_026052328.1	GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YrKA-like+TM+??-> Tubulin+coiled_coil+??-> Tubulin+coiled_coil+HTH1+??-> TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail-> Fibronectin-like_repeats+??-> ZnR+ZnR+DO-GTPase2:2+ZnR+ZnR-> GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich*->	1006	Paenibacillus sp. 1-49	GCF_000520815.1	firmicutes
WP_026526095.1	GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich	TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail-> Fibronectin-like_repeats+??-> ZnR+ZnR+DO-GTPase2:2+ZnR+ZnR-> GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich*->	750	Paenibacillus ferrytiluse	GCF_000526095.1	firmicutes
WP_025717315.1	GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YrKA-like+TM+??-> Tubulin+coiled_coil+??-> Tubulin+coiled_coil+HTH1+??-> TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail-> Fibronectin-like_repeats+??-> ZnR+ZnR+DO-GTPase2:2+ZnR+ZnR-> GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich*->	1019	Paenibacillus sp. 1-18	GCF_000527515.1	firmicutes
WP_025717575.1	GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YrKA-like+TM+??-> Tubulin+coiled_coil+??-> Tubulin+coiled_coil+HTH1+??-> TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail-> Fibronectin-like_repeats+??-> ZnR+ZnR+DO-GTPase2:2+ZnR+ZnR-> GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich*->	1002	Paenibacillus polymyxa	GCF_000527575.1	firmicutes
WP_025848105.1	GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YrKA-like+TM+??-> Tubulin+coiled_coil+??-> Tubulin+coiled_coil+HTH1+??-> TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail-> Fibronectin-like_repeats+??-> ZnR+ZnR+DO-GTPase2:2+ZnR+ZnR-> GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich*->	834	Brevibacillus agri	GCF_000621125.1	firmicutes
WP_025868117.1	GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+Cadherin-like	TM+vWA(canonical)+YrKA-like+TM+??-> Tubulin+coiled_coil+??-> Tubulin+coiled_coil+HTH1+??-> TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail-> Fibronectin-like_repeats+??-> ZnR+ZnR+DO-GTPase2:2+ZnR+ZnR-> GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+Cadherin-like*->	955	Paenibacillus chitinolyticus	GCF_000622225.1	firmicutes
WP_026400369.1	GAP1:N2+GAP1:M+GAP1:C	GrpE-> HSP70-> TPR_containing_alpha_helical+Fibronectin-like_repeats-> ZnR+ZnR+DO-GTPase2:2-> GAP1:N2+GAP1:M+GAP1:C*-> TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2:2+TM->	810	Actinomadura rifamycini	GCF_000425065.1	actinobacteria
WP_026806792.1	GAP1:N2+GAP1:M+GAP1:C	GrpE-> HSP70-=7?+Fibronectin-> ZnR+ZnR+DO-GTPase2:2-> GAP1:N2+GAP1:M+GAP1:C*-> TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2:2->	808	Actinomycetospora dentalis	GCF_000425085.1	actinobacteria
WP_026414948.1	GAP1:N2+GAP1:M+GAP1:C	GrpE-> HSP70-> TPR_containing_alpha_helical+Fibronectin-like_repeats-> ZnR+ZnR+DO-GTPase2:2-> GAP1:N2+GAP1:M+GAP1:C*->	767	Actinomadura oligospora	GCF_000518265.1	actinobacteria
WP_026423378.1	GAP1:N2+GAP1:M+GAP1:C+TM+beta-rich	vWA(canonical)+beta-rich+low_complexity-=7->7-> Tubulin+alpha_helical+??-=7?+TM+TM+TM+TM+??-> Pkinase+TM-> ZnR+ZnR+DO-GTPase2:2-> GAP1:N2+GAP1:M+GAP1:C+TM+beta-rich*->	605	Actinokineospora inagensis	GCF_000682865.1	actinobacteria
WP_026557695.1	GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YrKA-like+TM+??-> Tubulin+coiled_coil+??-> Tubulin+coiled_coil+HTH1+??-> TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail-> Fibronectin-like_repeats+??-> ZnR+ZnR+DO-GTPase2:2+ZnR+ZnR-> GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich*->	834	Bacillus sp. SAP2.1	GCF_000792695.1	firmicutes
WP_026576603.1	GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YrKA-like+TM+??-> Tubulin+coiled_coil+??-> Tubulin+coiled_coil+HTH1+??-> Fibronectin-like_repeats+??-> ZnR+ZnR+DO-GTPase2:2+ZnR+ZnR-> GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich*->	947	Bacillus sp. UNC411MFS	GCF_000868805.1	firmicutes
WP_027034143.1	GAP1:N2+GAP1:M+GAP1:C	polar_leader+TM+TM+TM-> TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lr_tail-> Tubulin+alpha_helical+??+??-> GAP_unknown1+TM+TM+GAP_unknown2-> HRDC-like?+Fibronectin-like_repeats-> GAP1:N2+GAP1:M+GAP1:C*-> beta-rich+vWA(canonical)-=7?+DO-GTPase2:2->	708	Corynebacterium freiburgense	GCF_000932145.1	actinobacteria
WP_027019792.1	GAP1:N2+GAP1:M+GAP1:C	polar_leader+TM+TM+TM+=||=-?[]TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lr_tail-> Tubulin+alpha_helical+??+??-> GAP_unknown1+TM+TM+GAP_unknown2-> HRDC-like?+Fibronectin-like_repeats-> GAP1:N2+GAP1:M+GAP1:C*-> beta-rich+vWA(canonical)-=7?+DO-GTPase2:2->	816	Corynebacterium sputi	GCF_000427865.1	actinobacteria
WP_027344197.1	GAP1:N2+GAP1:M+GAP1:C	TPR_containing_alpha_helical+Fibronectin-like_repeats-> ZnR+ZnR+DO-GTPase2:2-> GAP1:N2+GAP1:M+GAP1:C*-> TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2:2->	790	Hamadaea tenuomeda	GCF_000429845.1	actinobacteria
WP_027623024.1	GAP1:N2+GAP1:M+GAP1:C	Fibronectin-like_repeats+??-> ZnR+ZnR+DO-GTPase2:2-> GAP1:N2+GAP1:M+GAP1:C*-> TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2:2-> TM+vWA(canonical)+YrKA-like+TM+??-> Tubulin+coiled_coil+??-> Tubulin+coiled_coil+HTH1+??-> TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail-> Fibronectin-like_repeats+??-> ZnR+ZnR+DO-GTPase2:2+ZnR+ZnR->	888	Clostridium hadense	GCF_000619945.1	firmicutes
WP_027740791.1	GAP1:N2+GAP1:M+GAP1:C	PP2C-> Pkinase-=7->7-=7-> HSP70_domain_2+low_complexity+domain_betaX-> ZnR+ZnR+DO-GTPase2:2-> GAP1:N2+GAP1:M+GAP1:C*-> TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2:2->	816	Streptomyces sp. CNT321	GCF_000514995.1	actinobacteria
WP_027752538.1	GAP1:N2+GAP1:M+GAP1:C	PP2C-> Pkinase-=7->7-=7-> HSP70_domain_2+low_complexity+domain_betaX-> ZnR+ZnR+DO-GTPase2:2-> GAP1:N2+GAP1:M+GAP1:C*-> TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2:2->	814	Streptomyces sp. CNR099	GCF_000514715.1	actinobacteria
WP_027761039.1	GAP1:N2+GAP1:M+GAP1:C	PP2C-> Pkinase-=7->7-=7-> HSP70_domain_2+low_complexity+domain_betaX-> ZnR+ZnR+DO-GTPase2:2-> GAP1:N2+GAP1:M+GAP1:C*-> TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2:2->	861	Streptomyces sp. CNT318	GCF_000524765.1	actinobacteria
WP_027766703.1	GAP1:N2+GAP1:M+GAP1:C	PP2C-> Pkinase-=7->7-=7-> HSP70_domain_2+low_complexity+domain_betaX-> ZnR+ZnR+DO-GTPase2:2-> GAP1:N2+GAP1:M+GAP1:C*-> TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2:2->	816	Streptomyces sp. CNQ865	GCF_000620805.1	actinobacteria
WP_027871381.1	GAP1:N2+GAP1:M+low_complexity+TM+TM	TM+vWA(canonical)+YrKA-like+IG-like+TM+??-> Tubulin+coiled_coil+??-=7->7-> ZnR+insert+ZnR+DO-GTPase2:2-> GAP1:N2+GAP1:M+low_complexity+TM+TM*->	517	[Eubacterium] ventriosum	GCF_000621585.1	firmicutes
WP_028286059.1	GAP1:N2+GAP1:M+GAP1:C	TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2:2-> GrpE-> HSP70-> HSP70+vWA(canonical)-=7-> ZnR+ZnR+DO-GTPase2:2-> GAP1:N2+GAP1:M+GAP1:C*->	709	Selenomonas sp. AE3003	GCF_000686945.1	firmicutes
WP_028418123.1	GAP1:N2+GAP1:M+GAP1:C	GAP1:N2+GAP1:M+GAP1:C*->	877	Streptomyces sp. SoWiqMP-sa22h	GCF_000647875.1	actinobacteria
WP_028442687.1	GAP1:N2+GAP1:M+GAP1:C	GAP1:N2+GAP1:M+GAP1:C*->	803	Streptomyces	GCA_900091745.1	actinobacteria

acc	architecture	operon	len	species	gca	taxend
WP_028507262.1	GAP1-N2+GAP1-M+GAP1-C	TM+=WA(canonical)+YtKA-like+IG-like+TM+?7→ Tubulin+coiled_coil+?7–+?7–+?7→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C*→7–+7–+7→ Tubulin+coiled_coil+?7→	853	Ruminococcaceae bacterium AB4001	GCF_000621765.1	firmicutes
WP_028510139.1	GAP1-N2+GAP1-M+GAP1-C	HSP70→+?→ HSP70(frag)+=WA(canonical)→+?→ ZnR+ZnR+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→+?→ GAP1-N2+GAP1-M+GAP1-C*→	898	Ruminococcus sp. NK3A76	GCF_000686125.1	firmicutes
WP_028510938.1	GAP1-N2+GAP1-M+GAP1-C	GrpE→ HSP70→ HSP70+=WA(canonical)→7→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→	920	Ruminococcus sp. NK3A76	GCF_000686125.1	firmicutes
WP_028521017.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+=WA(canonical)+YtKA-like+TM+?7→ TM+TM+TM+=WA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+?7→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	1002	Paenibacillus	GCA_900116035.1	firmicutes
WP_028547019.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+=WA(canonical)+YtKA-like+TM+?7→ Tubulin+coiled_coil+?7→ Tubulin+coiled_coil+HTH7+?7→ TM+TM+TM+=WA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+?7→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	966	Paenibacillus taiwanensis	GCF_000425125.1	firmicutes
WP_028630929.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM+ TM+=WA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+?7+?7→ GAP_unknown1+TM+TM+GAP_unknown2→+ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→+?7+DO-GTPase2.2→	716	Nocardioides sp. URHA0032	GCF_000620645.1	actinobacteria
WP_029110494.1	GAP1-N2+GAP1-M+GAP1-C	HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→7+DO-GTPase2.2→	819	Mycobacterium sp. URHD0025	GCF_000426065.1	actinobacteria
WP_029822797.1	GAP1-N2+GAP1-M	TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→ TM+=WA(canonical)+YtKA-like+TM+?7→ Tubulin+coiled_coil+?7→ Tubulin+coiled_coil+HTH7+?7→ TM+TM+TM+=WA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+?7→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M*	368	Clostridium scatologenes	GCA_000968275.1	firmicutes
WP_029668928.1	GAP1-N2+GAP1-M+GAP1-C	TM+DUF4190+TM+=polar_leader+TM+TM+TM+ PSE→ Tubulin+alpha_helical+?7+?7→ GAP_unknown1+TM+TM+GAP_unknown2→+ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+=WA(canonical)→?7+DO-GTPase2.2→ TM+DUF4190+TM+PknH_C→ TM+DUF4190+TM+PknH_C→ TM+DUF4190+TM+PknH_C→	837	Mycobacterium sp. UM_WWY	GCF_000455145.1	actinobacteria
WP_029519151.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+=WA(canonical)+YtKA-like+TM+?7→ Tubulin+coiled_coil+?7→ Tubulin+coiled_coil+HTH7+?7→ TM+TM+TM+=WA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+?7→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	1005	Paenibacillus polymyxa	GCA_003941845.1	firmicutes
WP_030127205.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	804	Streptomyces	GCF_000710815.1	actinobacteria
WP_030172535.1	GAP1-N2+GAP1-M+GAP1-C	GrpE→ HSP70→ TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→TM→	612	Spirillospora albida	GCF_000718255.1	actinobacteria
WP_030353718.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	791	Streptomyces scopuliridis	GCA_003073355.1	actinobacteria
WP_030360297.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	970	Streptomyces	GCF_000716675.1	actinobacteria
WP_030366192.1	GAP1-N2+GAP1-M+GAP1-C	TPR_containing_alpha_helical+Fibronectin-like_repeats→ PSE→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM→ +WA(canonical)→ PP2C→ Pkinase+ZnR+beta-rich→	810	Streptomyces sp. NRRL S-241	GCF_000717925.1	actinobacteria
WP_030442497.1	GAP1-N2+GAP1-M+TM+GAP1-C	ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+TM+GAP1-C*→	726	Actinoplanes subtropicus	GCF_000721705.1	actinobacteria
WP_030455901.1	GAP1-N2+GAP1-M+GAP1-C+TM+low_complexity+TM	+WA(canonical)→ DO-GTPase1→ GAP1-N2+GAP1-M+GAP1-C+TM+low_complexity+TM*→	749	Herbidosporа cretacea	GCF_000719065.1	actinobacteria
WP_030466420.1	GAP1-N2+GAP1-M+sLATT+sLATT	+WA(canonical)+beta-rich+low_complexity→ Tubulin+alpha_helical+?7+?7→?7+TM+TM+TM+TM+?7→ Pkinase+TM→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+sLATT+sLATT*	653	GCF_000974415.1	actinobacteria	
WP_030466670.1	GAP1-N2+GAP1-M+GAP1-C	TM+=WA(canonical)+TM→ HSP70→+?7+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→|=> GrpE	736	Lechevalieria aerocolonigenes	GCF_000974445.1	actinobacteria
WP_030472835.1	GAP1-N2+GAP1-M+GAP1-C	TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM→ +WA(canonical)→ PP2C→ Pkinase+ZnR+beta-rich→	850	Streptomyces cyanofuscatus	GCF_000718835.1	actinobacteria
WP_030626361.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	803	Streptomyces	GCF_000720535.1	actinobacteria
WP_030637205.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	804	Streptomyces flavovirens	GCF_000720355.1	actinobacteria
WP_030670494.1	GAP1-N2+GAP1-M+GAP1-C	GrpE→ HSP70→ TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+Jelly_roll+beta-sandwich→|=>STAND_NTPase+TM+TM+TM+TM+TM+TM+TM	476	Streptomyces cellulosae	GCF_000721105.1	actinobacteria
WP_030687752.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→ +WA(canonical)→ PP2C→ Pkinase+ZnR+beta-rich→	817	Streptomyces sp. NRRL B-1347	GCF_000720325.1	actinobacteria
WP_030699417.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	789	Streptomyces griseus	GCF_000719495.1	actinobacteria
WP_030702758.1	GAP1-N2+GAP1-M	GAP1-N2+GAP1-M*	808	Streptomyces griseus		actinobacteria
WP_030709003.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	826	Streptomyces griseus	GCA_003989035.1	actinobacteria
WP_030719916.1	GAP1-N2+GAP1-M+GAP1-C	TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ PSE→ +WA(canonical)→ PP2C→ Pkinase+ZnR+beta-rich→	814	Streptomyces sp. NRRL S-237	GCF_000718305.1	actinobacteria
WP_030765365.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→|→ PSE|+WA(canonical)→ PP2C→ Pkinase+ZnR+beta-rich→	814	Streptomyces sp. NRRL S-275	GCF_000719655.1	actinobacteria
WP_030766999.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	789	Streptomyces griseus	GCF_000719435.1	actinobacteria
WP_030778616.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→ +WA(canonical)→ PP2C→ Pkinase+ZnR+beta-rich→|→ TPR_containing_alpha_helical+Fibronectin-like_repeats	840	Streptomyces sp. NRRL S-920	GCF_000717945.1	actinobacteria
WP_030804300.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	830	Streptomyces medioluni	GCF_000721685.1	actinobacteria
WP_030878231.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C* → PSE→?→|→ TPR_containing_alpha_helical+Fibronectin-like_repeats	792	Streptomyces sp. NRRL S-1868	GCF_000721305.1	actinobacteria
WP_030879622.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	804	Streptomyces sp. NRRL B-24051	GCF_000720405.1	actinobacteria
WP_030885101.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C* → PSE→?→|→ TPR_containing_alpha_helical+Fibronectin-like_repeats	792	Streptomyces sp. NRRL F-5053	GCF_000721445.1	actinobacteria
WP_030900888.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	853	Streptomyces sp. NRRL F-5126	GCF_000721265.1	actinobacteria
WP_030902783.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→|→ PSE|+WA(canonical)→ PP2C→ Pkinase+ZnR+beta-rich→	814	Streptomyces sp. NRRL S-115	GCF_000720795.1	actinobacteria
WP_030917034.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	802	Streptomyces sp. NRRL B-24720	GCF_000721715.1	actinobacteria
WP_030974850.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	806	Streptomyces sp. NRRL S-1824	GCF_000719575.1	actinobacteria
WP_030998194.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	777	Streptomyces sp. NRRL F-5630	GCF_000719475.1	actinobacteria
WP_031064156.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	803	Streptomyces sp. NRRL WC-3549	GCF_000721935.1	actinobacteria
WP_031076043.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	804	Streptomyces	GCA_001294345.1	actinobacteria
WP_031176954.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	789	Streptomyces sp. NRRL B-3253	GCF_000725635.1	actinobacteria
WP_031192232.1	GAP1-N2+GAP1-M+GAP1-C	TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ PSE→ +WA(canonical)→ PP2C→ Pkinase+ZnR+beta-rich→	880	Streptomyces	GCF_000725655.1	actinobacteria
WP_031192409.1	GAP1-N2+GAP1-M+GAP1-C	Pkinase→?→?→?→ HSP70_domain_2+low_complexity+domain_betaX→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→	814	Streptomyces	GCF_000716675.1	actinobacteria
WP_031412702.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+=WA(canonical)+YtKA-like+TM+?7→ Tubulin+coiled_coil+?7→ Tubulin+coiled_coil+HTH7+?7→ TM+TM+TM+=WA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+?7→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	833	Brevibacillus laterosporus		firmicutes
WP_031463423.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+=WA(canonical)+YtKA-like+TM+?7→ Tubulin+coiled_coil+?7→ Tubulin+coiled_coil+HTH7+?7→ TM+TM+TM+=WA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+?7→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	1009	Paenibacillus polymyxa	GCF_000735775.1	firmicutes
WP_031498745.1	GAP1-N2+GAP1-M+GAP1-C	TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM→ +WA(canonical)→ PP2C→ Pkinase+ZnR+beta-rich→	953	Streptomyces bicolor	GCF_000725465.1	actinobacteria
WP_031549005.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	746	Bacillus	GCF_001059885.1	firmicutes
WP_031932515.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+=WA(canonical)+YtKA-like+TM+?7→ Tubulin+coiled_coil+?7→ Tubulin+coiled_coil+HTH7+?7→ TM+TM+TM+=WA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+?7→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	920	Brevibacillus borstelensis	GCF_000738785.1	firmicutes
WP_032079599.1	GAP1-N2+GAP1-M	TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→ TM+=WA(canonical)+YtKA-like+TM+?7→ Tubulin+coiled_coil+?7→ Tubulin+coiled_coil+HTH7+?7→ TM+TM+TM+=WA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+?7→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M*	369	Clostridium drakei	GCA_003906175.1	firmicutes

acc	architecture	operon	len	species	gca	taxend
WP_032748152.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	830	Streptomyces globisporus	GCA_000261345.2	actinobacteria
WP_032786924.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	826	Streptomyces sp. JS01	GCA_000743295.1	actinobacteria
WP_032791831.1	GAP1-N2+GAP1-M+GAP1-C	ZnR+ZnR+DO-GTPase2.2→ PSE→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM→ vWA(canonical)→ PP2C→ Pkinase+ZnR+beta-rich→[(=?+?)]GAP1-N2+GAP1-M+GAP1-C*→	833	Streptomyces sp. W007		actinobacteria
WP_032917154.1	GAP1-N2+GAP1-M+GAP1-C	TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM→ vWA(canonical)→ PP2C→ Pkinase+ZnR+beta-rich→	820	Streptomyces rimosus	GCF_000720725.1	actinobacteria
WP_033090710.1	GAP1-N2+GAP1-M+GAP1-C	Pkinase+TM→ ZnR+DO-GTPase2.1→ GAP1-N2+GAP1-M+GAP1-C*→	696	Nocardia seriolae	GCA_002356035.1	actinobacteria
WP_032217060.1	GAP1-N2+GAP1-M+GAP1-C	TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ PSE→ vWA(canonical)→ PP2C→ Pkinase+ZnR+beta-rich→	814	Streptomyces virginiae	GCF_000716685.1	actinobacteria
WP_032281611.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	789	Streptomyces griseus	GCF_000717375.1	actinobacteria
WP_032281599.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	814	Streptomyces sp. NRRL F-525	GCF_000716605.1	actinobacteria
WP_033001491.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	806	Streptomyces atroolivaceus	GCF_000717025.1	actinobacteria
WP_033023584.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	806	Streptomyces zerevisiae	GCF_000716605.1	actinobacteria
WP_033395526.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→[=:HSP70_domain_1	782	Dactylosporangium aurantiacum	GCF_000716715.1	actinobacteria
WP_033495525.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	751	Saccharothrix sp. NRRL B-16314	GCF_000716545.1	actinobacteria
WP_033945349.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	789	Streptomyces sp. CNQ431	GCF_000797385.1	actinobacteria
WP_034263571.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM1+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→?→??+DO-GTPase2.2→	891	Actinomyces urogenitalis	GCA_000758745.1	actinobacteria
WP_034382650.1	GAP1-N2+GAP1-M+GAP1-C	GrpE→ HSP70→ TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM→	729	Herbidospora cretacea	GCF_000719065.1	actinobacteria
WP_034402972.1	GAP1-N2+GAP1-M+GAP1-C	HSP70+vWA(canonical)→ DnaJ+DnaJ+ZnR+ZnR+coiled_coil+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*	725	Conexibacter woesei DSM 14670	GCA_000022715.1	nitrospirae/ectomicrobia group palauensis
WP_034447882.1	GAP1-N2+GAP1-M+GAP1-C	TM+vWA(canonical)+YtKA-like+H-like+TM+??→ Tubulin+coiled_coil+??→?→?→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C*→?→?→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+??→	810	Butyrivibrio sp. AE2032	GCF_000762965.1	firmicutes
WP_034527772.1	GAP1-N2+GAP1-M+GAP1-C	TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→ GrpE→ HSP70→ HSP70+vWA(canonical)→ DnaJ+DnaJ+ZnR+ZnR+coiled_coil+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*	968	Bifidobacterium stellenboschense	GCF_000741785.1	actinobacteria
WP_035113596.1	GAP1-N2+GAP1-M+GAP1-C	Tubulin+alpha_helical+??+??→+ GAP_unknown1+TM+TM+GAP_unknown2+ HRDC-like?+Fibronectin-like_repeats→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→?→?→?→DO-GTPase2.2→	393	Corynebacterium auriscanis	GCA_000767255.1	actinobacteria
WP_035144553.1	GAP1-N2+GAP1-M+GAP1-C	Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→ TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→	888	Clostridium tetanomorphum	GCA_000427695.1	firmicutes
WP_035375609.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	853	Fervidicella metallireducens	GCA_000601455.1	firmicutes
WP_035452571.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	685	Bacillus sp. JCM 19045	GCA_000372571.1	firmicutes
WP_035441099.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	618	Bacillus sp. JCM 19046	GCA_000376345.1	firmicutes
WP_035847344.1	GAP1-N2+GAP1-M+GAP1-C	TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM→ vWA(canonical)→ PP2C→ Pkinase+ZnR+beta-rich→	659	Kitasatospora azatica	GCF_000744785.1	actinobacteria
WP_036437168.1	GAP1-N2+GAP1-M+GAP1-C	Pkinase+TM→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→	559	Modestobacter caceresii	GCA_000764485.1	actinobacteria
WP_036506376.1	GAP1-N2+GAP1-M+GAP1-C	HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→?→DO-GTPase2.2→	819	Mycolicibacterium farcinogenes	GCA_000723385.1	actinobacteria
WP_036430020.1	GAP1-N2+GAP1-M+GAP1-C	TM+DUF4190+TM→ polar_leader+TM+TM+TM→ PSE→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→?→DO-GTPase2.2→ TM+DUF4190+TM+PkinH_C→ TM+DUF4190+TM+PkinH_C→	836	Gordoniibacter magnetiense	GCA_000612825.1	actinobacteria
WP_036443731.1	GAP1-N2+GAP1-M+GAP1-C	HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→?→DO-GTPase2.2→	819	Mycolicibacterium	GCA_000612885.1	actinobacteria
WP_036556971.2	GAP1-N2+GAP1-M+GAP1-C	Pkinase+TM→ ZnR+DO-GTPase2.1→ GAP1-N2+GAP1-M+GAP1-C*→	696	Nocardia seriolae	GCF_000546715.2	actinobacteria
WP_036663727.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	992	Paenibacillus sp. FSL H8-457	GCA_000517945.1	firmicutes
WP_036695219.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	972	Paenibacillus	GCA_000517945.1	firmicutes
WP_036684993.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+Cadherin-like	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+Cadherin-like*	936	Paenibacillus tyrfis	GCA_000722545.1	firmicutes
WP_037285335.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail	Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C+polar_tail→	1075	Saccharothrix mecitovska	GCF_000635365.1	firmicutes
WP_037629188.1	GAP1-N2+GAP1-M+GAP1-C	TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ PSE→ vWA(canonical)→ PP2C→ Pkinase+ZnR+beta-rich→	880	Streptomyces	GCF_000716535.1	actinobacteria
WP_037664202.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→ vWA(canonical)→	763	Streptomyces atratmiacus	GCF_000414115.1	actinobacteria
WP_037687653.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	737	Streptomyces lavendulae	GCA_002845835.1	actinobacteria
WP_037016615.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	805	Streptomyces atratus	GCF_000745675.1	actinobacteria
WP_037154715.1	GAP1-N2+GAP1-M+GAP1-C	TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM→ vWA(canonical)→ PP2C→ Pkinase+ZnR+beta-rich→	968	Streptomyces mirabilis	GCF_000745715.1	actinobacteria
WP_037741390.1	GAP1-N2+GAP1-M+GAP1-C	TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM→ vWA(canonical)→ PP2C→ Pkinase+ZnR+beta-rich→	939	Streptomyces mirabilis	GCF_000746385.1	actinobacteria
WP_037748429.1	GAP1-N2+GAP1-M+GAP1-C	PP2C→ Pkinase→?→?→?→ HSP70_domain_2+low_complexity+domain_betaX→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→	816	Streptomyces sp. CNQ-525	GCA_004212925.1	actinobacteria
WP_037831065.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	804	Streptomyces sp. NRRL S-325	GCF_000721505.1	actinobacteria
WP_037842916.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	789	Streptomyces sp. NRRL F-6628	GCF_000721455.1	actinobacteria
WP_037885477.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	803	Streptomyces sp. NTK 937	GCA_000698495.1	actinobacteria
WP_037931882.1	GAP1-N2+GAP1-M+GAP1-C	TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ PSE→ vWA(canonical)→ PP2C→ Pkinase+ZnR+beta-rich→	880	Streptomyces sp. NRRL WC-3744	GCF_000717895.1	actinobacteria
WP_037933696.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	772	Streptomyces	GCF_000691485.1	actinobacteria
WP_038563339.1	GAP1-N2+GAP1-M+GAP1-C	Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→?→DO-GTPase2.2→ TM+DUF4190+TM+PkinH_C→ TM+DUF4190+TM+PkinH_C→	828	Mycobacteriaceae	GCA_000416365.2	actinobacteria
WP_039273583.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	1005	Paenibacillus polymyxa	GCA_000718835.1	firmicutes
WP_039326609.1	GAP1-N2+GAP1-M+GAP1-C	HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→?→DO-GTPase2.2→	819	Mycolicibacterium setense	GCA_000805375.1	actinobacteria
WP_039696565.1	GAP1-N2+GAP1-M+GAP1-C	HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→?→DO-GTPase2.2→	819	Mycolicibacterium setense	GCF_000805375.1	actinobacteria
WP_039754556.1	GAP1-N2+GAP1-M+GAP1-C	Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→?→?→DO-GTPase2.2→	919	Actinomyces oris	GCF_000180155.1	actinobacteria
WP_039879046.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→[(=:?)]TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	1111	Paenibacillus sp. FSL R7-0273	GCA_000758625.1	firmicutes

acc	architecture	operon	len	species	gca	taxend
WP_040101454.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail	Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C+polar_tail"→	1009	Paenibacillus polymyxa	GCA_000819665.1	firmicutes
WP_040195297.1	GAP1-N2+GAP1-M+TM+GAP1-C+TM	ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+TM+GAP1-C+TM"→	776	Candidatus Soleaferrea massiliensis	GCF_000820765.1	firmicutes
WP_040333054.1	GAP1-N2+GAP1-M+TM+GAP1-C	GAP1-N2+GAP1-M+TM+GAP1-C"→[/c+Pkinase	611	Butyricicoccus pullicaecorum	GCF_900143195.1	firmicutes
WP_040961565.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C"→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→	863	Corynebacterium amycolatum	GCF_000173655.1	actinobacteria
WP_040373124.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ PSE→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich"→	868	Bacillus psychrosaccharolyticus	GCF_000305495.1	firmicutes
WP_040705664.1	GAP1-N2+GAP1-M+GAP1-C	GrpE→ HSP70→ TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C"→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→?→ HSP70→ +WA(canonical)→	855	Nocardia takedensis	GCF_000398695.1	actinobacteria
WP_040816614.1	GAP1-N2+GAP1-M+GAP1-C	Pkinase→TM→ ZnR+DO-GTPase2.1→ GAP1-N2+GAP1-M+GAP1-C"→	705	Nocardia concava	GCF_000398815.1	actinobacteria
WP_040860755.1	GAP1-N2+GAP1-M+GAP1-C	Pkinase→TM→ ZnR+DO-GTPase2.1→ GAP1-N2+GAP1-M+GAP1-C"→	742	Nocardia nilgiriensis	GCF_000398655.1	actinobacteria
WP_041021553.1	GAP1-N2+GAP1-M+GAP1-C	Pkinase+TM→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C"→[/c+?c+?][?]→ Pkinase+low_complexity→	555	Geodermatophilus obscurus	GCF_000025345.1	actinobacteria
WP_041992698.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C"→	824	Streptomyces sp. AcH 505	GCF_000818175.1	actinobacteria
WP_042296274.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+Cadherin-like	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+Cadherin-like"→	965	Paenibacillus chitinolyticus	GCF_001417005.1	firmicutes
WP_042284210.1	GAP1-N2+GAP1-M+GAP1-C	TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C"→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→	868	Nocardiopsis alba	GCF_000710955.1	actinobacteria
WP_042495823.1	GAP1-N2+GAP1-M	GAP1-N2+GAP1-M	808	Streptomyces griseus	-	actinobacteria
WP_043193346.1	GAP1-N2+GAP1-M+GAP1-C	TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C"→ PSE→ +vWA(canonical)→ PP2C→ Pkinase+ZnR+beta-rich→	880	Streptomyces sp. NRRL WC-3725	GCF_000720295.1	actinobacteria
WP_043623715.1	GAP1-N2+GAP1-M+GAP1-C	TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C"→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM→?→ vWA(canonical)→ PP2C→ Pkinase+ZnR+beta-rich→	820	Streptomyces sp. NRRL F-5193	GCF_000423715.1	actinobacteria
WP_043454546.1	GAP1-N2+GAP1-M+GAP1-C	TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C"→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM→ +vWA(canonical)→ PP2C→ Pkinase+ZnR+beta-rich→	870	Streptomyces fulvoluteus	GCF_000718165.1	actinobacteria
WP_043002539.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C"→	808	Streptomyces bingchenggensis	GCF_000093285.1	actinobacteria
WP_043524316.1	GAP1-N2+GAP1-M+TM+GAP1-C	DO-GTPase1→ GAP1-N2+GAP1-M+TM+GAP1-C"→?→?→ TM+vWA(canonical)+TM+low_complexity→ CASPASE+low_complexity→ TPR_region+CASPASE→	572	Streptomyces atabensis	GCA_000750585.1	actinobacteria
WP_043030432.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich"→	725	Bacillus sp. EB01	GCF_000613125.1	firmicutes
WP_041818195.1	GAP1-N2+GAP1-M+GAP1-C	ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C"→?→TM+?+beta-rich?→ GYF+GYF+TM+TM+TM→	815	Pseudoalteromonas piscicida strain JL-2	GCF_000183925.1	gammaproteobacteria
WP_041486087.1	GAP1-N2+GAP1-M+GAP1-C	TM+DUF4190+TM→ TM+DUF4190+TM→ polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C"→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→ TM+DUF4190+TM+PknH_C→ TM+DUF4190+TM+PknH_C→ TM+DUF4190+TM+PknH_C→ TM+DUF4190+TM+PknH_C→	829	Mycobacterium colombiense	CGA_000661085.1	actinobacteria
WP_044514372.1	GAP1-N2+GAP1-M+GAP1-C	HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C"→??+DO-GTPase2.2→	819	Mycolicibacterium septicum	GCF_000455325.1	actinobacteria
WP_044669174.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich"→	1028	Corynebacterium ternse	GCA_900015435.1	firmicutes
WP_044785686.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich"→	1009	Paenibacillus polymyxa	GCA_000943535.1	firmicutes
WP_045017275.1	GAP1-N2+GAP1-M+SLATT+SLATT	vWA(canonical)+beta-rich+low_complexity→ Tubulin+alpha_helical+??+??→ TM+TM+TM+TM+??→ Pkinase+TM+ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+SLATT+SLATT"→	650	Lechevalieria aerocolonigenes	GCA_000952955.1	actinobacteria
WP_045754520.1	GAP1-N2+GAP1-M+GAP1-C	TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C"→	796	Actinoplanes rectilinentus	GCF_000962825.1	actinobacteria
WP_046202033.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→?→? GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C"→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→	626	Corynebacterium kroppenstedtii	GCA_002817755.1	actinobacteria
WP_046202154.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C"→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→	626	Corynebacterium kroppenstedtii	GCF_000721855.1	actinobacteria
WP_046213785.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich"→	1125	Paenibacillus wulumuqiensis	GCF_000971965.1	firmicutes
WP_046293718.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich"→	1141	Paenibacillus dauci	GCF_000971985.1	firmicutes
WP_046260777.1	GAP1-N2+GAP1-M+GAP1-C	TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C"→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM→ +vWA(canonical)→ PP2C→ Pkinase+ZnR+beta-rich→	918	Streptomyces sp. WM6386	GCA_000972385.1	actinobacteria
WP_046496261.1	GAP1-N2+GAP1-M	GAP1-N2+GAP1-M	845	Streptomyces odonnellii	-	actinobacteria
WP_046704194.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C"→ +vWA(canonical)→ PP2C→ Pkinase+ZnR+beta-rich→	811	Streptomyces europaseicabiei	GCF_000988945.1	actinobacteria
WP_047016408.1	GAP1-N2+GAP1-M+GAP1-C	HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C"→??+DO-GTPase2.2→	819	Mycolicibacterium	GCA_001012795.1	actinobacteria
WP_047076691.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich"→	832	Bacillus furmeaus	GCA_006540145.1	firmicutes
WP_047141722.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C"→	789	Streptomyces sp. KE1	GCA_001014595.1	actinobacteria
WP_047179414.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C"→	833	Streptomyces sp. MNU77	-	actinobacteria
WP_047464182.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C"→	789	Streptomyces sp. M10	GCF_000806535.1	actinobacteria
WP_047840705.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich"→	1069	Paenibacillus sp. VT-400	GCA_000378915.1	firmicutes
WP_047871140.1	GAP1-N2+GAP1-M+GAP1-C	TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C"→	883	Nocardiopsis sp. RV163	GCF_001029525.1	actinobacteria
WP_047936961.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich"→	746	Bacillus circulans	GCA_001029955.1	firmicutes
WP_048035300.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich"→	832	Brevibacillus brevis	GCA_001039275.2	firmicutes
WP_048037372.1	GAP1-N2+GAP1-M+GAP1-C	TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→ GrpE→ HSP70→ HSP70+vWA(canonical)→ DnaJ+DnaJ+ZnR+ZnR+coiled_coil+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C"→	882	Methanosaeta mazei	GCA_000979065.1	euryarchaeota
WP_048041778.1	GAP1-N2+GAP1-M+GAP1-C	TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→ GrpE→ HSP70→ HSP70+vWA(canonical)→ DnaJ+DnaJ+ZnR+ZnR+coiled_coil+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C"→	882	Methanosaeta mazei	GCA_000979035.1	euryarchaeota
WP_048398625.1	GAP1-N2	GAP1-N2+GAP1-M+GAP1-C	569	Candidatus Achromatium palustre	-	gammaproteobacteria
WP_048482846.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C"→	613	Methylobacterium aquaticum	GCF_000172255.1	alphaproteobacteria
WP_048760431.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C"→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→	862	Corynebacterium vitaerumins	GC_001054325.1	actinobacteria
WP_049152802.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C"→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→ polar_leader+TM+TM+TM→	555	Corynebacterium surimsuensis	GC_001054325.1	actinobacteria
WP_049714333.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C"→	921	Streptomyces castingaensis	GCF_001187435.1	actinobacteria
WP_049740646.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich"→	840	Brevibacillus reuseri	GC_000540225.1	firmicutes

acc	architecture	operon	len	species	gca	taxend
WP_049744098.1	GAP1-N2+GAP1-M+GAP1-C	HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→??+DO-GTPase2.2→	817	Mycolicibacterium goodii	GCA_001187505.1 actinobacteria	
WP_048895018.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail	Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C+polar_tail*→	1072	Paenibacillus antibioticophila	GCF_000455265.1 firmicutes	
WP_049068941.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	780	Streptomyces wadayamensis	GCF_000988945.1 actinobacteria	
WP_050249621.1	GAP1-N2+GAP1-M+GAP1-C	GrpE→ HSP70→ [[→ ?]HSP70++WA(canonical)→ DnaJ+DnaJ+ZnR+ZnR+coiled_coil→Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ + TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM+PDZ+PDZ→	785	Verrucomicrobium sp. BvORR034	GCF_000739635.1 verrucomicrobia	
WP_050054884.1	GAP1-N2+GAP1-M+GAP1-C	GrpE→ HSP70→ TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ + TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→??→ HSP70→ +WA(canonical)→	791	Pseudarthrobacter sicvitoleoran	GCF_001046895.1 actinobacteria	
WP_050434801.1	GAP1-N2+GAP1-M+GAP1-C	TM+vWA(canonical)+YtKA-like+EG-like+TM+??→ Tubulin+coiled_coil→??→?→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C*→??+Pkinase→?→ Tubulin+coiled_coil→??→ Tubulin+coiled_coil→??→	831	Olsenella sp. oral taxon 807	GCF_001189515.2 actinobacteria	
WP_050537186.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*	827	Streptomyces europaeiscabiei	GCF_001190025.1 actinobacteria	
WP_050588178.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	607	Streptomyces sp. HCCB10043	GCF_000498935.1 actinobacteria	
WP_050970382.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail	TM+TM+TM+vWA+TM+TM+TM+polar_tail→ Fibronectin-like_repeats→??→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C+polar_tail→	1022	Paenibacillus dendritiformis	GCF_000245555.1 firmicutes	
WP_051546995.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)→TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	1064	Paenibacillus sp. PAMC 26794	GCF_000316035.1 firmicutes	
WP_052125300.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich+lc_tail	TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→[[→ ?]Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ + beta-rich+vWA(canonical)→??+DO-GTPase2.2→	909	Granulicoccus phenolivorans	GCF_000423085.1 actinobacteria	
WP_052127245.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil→??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)→TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	865	Paenibacillus assamensis	GCF_000372415.1 firmicutes	
WP_052235971.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil→??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)→TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	977	Paenibacillus pinihumi	GCF_000422505.1 firmicutes	
WP_052860015.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil→??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)→TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	1000	Paenibacillus panacisoli	GCF_000429085.1 firmicutes	
WP_053876085.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	777	Saccharopolyspora rectivirgula	GCF_000497205.1 actinobacteria	
WP_053416694.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich+lc_tail	TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ + beta-rich+vWA(canonical)→??+DO-GTPase2.2→	1068	Paenibacillus sp. FSL H7-689	GCF_000517905.1 firmicutes	
WP_051447278.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail	Tubulin+coiled_coil→??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C+polar_tail*→	1068	Paenibacillus sp. FSL H7-689	GCF_000517905.1 firmicutes	
WP_051403334.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil→??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)→TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	1002	Paenibacillus	GCA_00162305.1 firmicutes	
WP_051478561.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	Tubulin+coiled_coil→??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)→TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail*→	830	Paenibacillus sp. FSL R7-277	GCF_000519765.1 firmicutes	
WP_051488884.1	GAP1-M+GAP1-C	TM+DUF4190+TM→ TM+DUF4190+TM→polar_leader+TM+TM+TM→ PSE→ PSE→ GAP_unknown1+TM+TM+GAP_unknown2→ GAP_unknown1+TM+TM+GAP_unknown2→ PSE→ GAP1-M+GAP1-C*→ GAP1-N2+GAP1-M+GAP1-C→?→ beta-rich+vWA(canonical)→	150	Mycobacterium kansasii	GCF_000524095.1 actinobacteria	
WP_051605895.1	GAP1-M+GAP1-C	TM+DUF4190+TM→ TM+DUF4190+TM→polar_leader+TM+TM+TM→ PSE→ PSE→ GAP_unknown1+TM+TM+GAP_unknown2→ GAP_unknown1+TM+TM+GAP_unknown2→ PSE→ GAP1-M+GAP1-C→ GAP1-M+GAP1-C*→?→ beta-rich+vWA(canonical)→	614	Mycobacterium kansasii	GCF_000524095.1 actinobacteria	
WP_051491151.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil→??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)→TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	998	Paenibacillus	GCA_000517925.1 firmicutes	
WP_051603765.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil→??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)→TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	780	Paenibacillus sp. FSL R7-269	GCF_000517965.1 firmicutes	
WP_051541673.1	GAP1-N2+GAP1-M	TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→ TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil→??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)→TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M*→	389	Clostridium lundense	GCF_000619945.1 firmicutes	
WP_051606670.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+Cadherin-like	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil→??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)→TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+Cadherin-like*→	972	Streptomyces sp. UNC431MF	GCF_000620635.1 actinobacteria	
WP_051707761.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	777	Saccharopolyspora rectivirgula	GCF_000710755.1 actinobacteria	
WP_051716428.1	GAP1-N2+GAP1-M+GAP1-C	ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→?→ vWA(canonical)→ PPIC→ Pkinase+ZnR+beta-rich→	828	Streptomyces sp. NRRL F-5727	GCF_000719555.1 actinobacteria	
WP_051736663.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→	968	Rhodococcus	GCF_000960315.1 actinobacteria	
WP_051735507.1	GAP1-N2+GAP1-M+GAP1-C	PPPC→ Pkinase=+?→+?→+ HSP70_domain_2=low_complexity+domain_betaX= ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ PSE→[[=:TPR_region=CASPASE	815	Streptomyces sp. NRRL B-3229	GCF_000719505.1 actinobacteria	
WP_051739950.1	GAP1-N2+GAP1-M+GAP1-C	GrpE→ HSP70→ TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ + TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→?→ HSP70→ +WA(canonical)→?→[[=:[[=:HSP70=:unknown=CASPASE	671	Amycolatopsis rifamycinica	GCF_000605025.1 actinobacteria	
WP_051742302.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	837	Streptomyces xylophagus	GCF_000716435.1 actinobacteria	
WP_051767773.1	GAP1-N2+GAP1-M+GAP1-C	TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ + TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM→?→ +WA(canonical)→ PPPC→ Pkinase+ZnR+beta-rich→	823	Micrococcus papuae	actinobacteria	
WP_051807387.1	GAP1-N2+GAP1-M+GAP1-C	TPR_region=CASPASE[GrpE→ HSP70→ TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ + TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→	792	Actinoplanes auratinus	GCF_000721705.1 actinobacteria	
WP_051926186.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil→??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)→TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	1144	Paenibacillus macerans	GCA_000730575.1 firmicutes	
WP_052026186.1	GAP1-N2+GAP1-M	Tubulin+coiled_coil→??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)→TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ PSE→ GAP1-N2+GAP1-M*→	250	Paenibacillus pini	GCA_000763005.1 firmicutes	
WP_052038875.1	GAP1-N2+GAP1-M+GAP1-C	GrpE→ HSP70→ TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ + TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→?→?→ HSP70→ +WA(canonical)→	667	Actinomycos sp. S4-C9	GCF_000758775.1 actinobacteria	
WP_052045588.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ + beta-rich+vWA(canonical)→??+DO-GTPase2.2→	984	Rhodococcus	GCA_002258815.1 actinobacteria	
WP_052054083.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→[[→ ?]HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ + beta-rich+vWA(canonical)→??+DO-GTPase2.2→ polar_leader+TM+TM+TM→	850	Corynebacterium flmeyi	GCF_000758965.1 actinobacteria	
WP_052063015.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ + beta-rich+vWA(canonical)→??+DO-GTPase2.2→	904	Rhodococcus fascians	GCF_000759215.1 actinobacteria	
WP_052087819.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil→??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)→TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	977	Paenibacillus wynnii	GCF_000757885.1 firmicutes	
WP_052093525.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil→??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)→TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	1048	Paenibacillus sp. FSL H7-0357	GCF_000758525.1 firmicutes	
WP_052096292.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil→??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)→TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	998	Paenibacillus odorifer	GCF_000758725.1 firmicutes	
WP_052098204.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil→??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)→TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	1027	Paenibacillus sediffer	GCF_000758865.1 firmicutes	
WP_052149961.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil→??→ PSE→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	1061	Paenibacillus sp. P1XP2	GCA_000758385.1 firmicutes	
WP_052019635.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→?→ ZnR+DO-GTPase2.2→?→[[=:?=:?→ HSP70	326	Corynebacterium riegelii	GCA_001383715.1 actinobacteria	
WP_052031816.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→ polar_leader+TM+TM+TM→	559	Corynebacterium minutissimum	GCA_900478045.1 actinobacteria	
WP_052339668.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil→??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)→TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	911	Gordibacterium massiliense	GCF_000455485.1 firmicutes	
WP_052352262.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil→??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)→TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	903	Bacillus diefenzmanii	GCF_000612865.1 firmicutes	
WP_052533844.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil→??→ Tubulin+coiled_coil+HTH?+??→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	728	Bacillus	GCF_000613625.1 firmicutes	
WP_052880983.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil→??→ Tubulin+coiled_coil+HTH?+??→[[→ ?]TM+TM+TM+vWA(canonical)→TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	1088	Paenibacillus camerounensis	GCF_000723885.1 firmicutes	
WP_052404160.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil→??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)→TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	986	Paenibacillus sp. FSL H7-0737	GCF_000758545.1 firmicutes	
WP_052410072.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil→??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)→TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	1028	Paenibacillus durus	GCF_000756615.1 firmicutes	

acc	architecture	operon	len	species	gca	taxend
WP_052414459.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM→vWA(canonical)+YiKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	994	Paenibacillus sp. FSI, RI-0345	GCF_000758585.1	firmicutes
WP_052415693.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM→vWA(canonical)+YiKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	1027	Paenibacillus graminis	GCF_000758705.1	firmicutes
WP_052415985.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM→vWA(canonical)+YiKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	1075	Paenibacillus sp. FSI, RI-0912	GCF_000758605.1	firmicutes
WP_052418904.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM→vWA(canonical)+YiKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	1087	Paenibacillus sp. FSI, RI-0331	GCF_000758645.1	firmicutes
WP_052425573.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM→vWA(canonical)+YiKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	1070	Paenibacillus sp. FSI, P4-0081	GCF_000758565.1	firmicutes
WP_052424850.1	GAP1-N2+GAP1-M+TM+GAP1-C	DO-GTPase1→ GAP1-N2+GAP1-M+TM+GAP1-C*→?→ TM+vWA(canonical)+TM→low_complexity→	839	Streptomyces fulvoviolaceus	GCF_000718165.1	actinobacteria
WP_052429335.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM→vWA(canonical)+YiKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	1036	Paenibacillus borealis	GCF_000758665.1	firmicutes
WP_052433373.1	GAP1-N2+GAP1-M+GAP1-C	TPR_containing_alpha_helical+Fibronectin-like_repeats+→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+DO-GTPase2→ vWA(canonical)→ PPIC→ Pkinase+ZnR+beta-rich→	672	Streptacidiphilus carbonis	GCF_000787275.1	actinobacteria
WP_052437512.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→ polar_leader+TM+TM+TM→	456	Corynebacterium humireducens	GCA_000819415.1	actinobacteria
WP_052439737.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	811	Streptomyces sp. 150FB	GCF_000818195.1	actinobacteria
WP_052438866.1	GAP1-N2+GAP1-M+GAP1-C	GrpE→ HSP70→ TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→	814	Micromonospora carbonacea	GCF_000876225.1	actinobacteria
WP_052521158.1	GAP1-N2+GAP1-M+TM	GAP1-N2+GAP1-M+TM*→	273	Geminata sp. SH-PL17	GCA_001510831.1	cyanobacteriota
WP_052649326.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM→vWA(canonical)+YiKA-like+TM+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	1011	Paenibacillus vortex	GCF_001934115.1	firmicutes
WP_052676055.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM→vWA(canonical)+YiKA-like+TM+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	1011	Paenibacillus sp. IHBB 10380	GCF_001931115.1	firmicutes
WP_052737023.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM→vWA(canonical)+YiKA-like+TM+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	1065	Paenibacillus algorfontisola	GCA_900112925.1	firmicutes
WP_052737154.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM→vWA(canonical)+YiKA-like+TM+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	1057	Paenibacillus tengchongensis	GCA_900081545.1	firmicutes
WP_052755973.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM→vWA(canonical)+YiKA-like+TM+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	1030	Paenibacillus durus	GCF_000993825.1	firmicutes
WP_052776211.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM→vWA(canonical)+YiKA-like+TM+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	1006	Paenibacillus sp. IHB B 3415	GCF_000802655.1	firmicutes
WP_052834596.1	GAP1-N2+GAP1-M+low_complexity+TM+TM	polar_leader+TM+TM+TM→ TM→vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+low_complexity→TM+TM*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→ polar_leader+TM+TM+TM→	311	Oceanobacillus mesledae	GCA_001029836.1	firmicutes
WP_052800323.1	GAP1-N2+GAP1-M+GAP1-C	ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→	973	Thermogemmatispora	GCF_000702505.1	chloroflexi
WP_052947460.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM→vWA(canonical)+YiKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail(frag)→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	800	Anaerunibacillus tyrosinisolvens	GCF_001015555.1	firmicutes
WP_052959545.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM→vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→ polar_leader+TM+TM+TM→	496	Corynebacterium striatum	GCF_000382645.1	actinobacteria
WP_053048988.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM→vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→ polar_leader+TM+TM+TM→	535	Corynebacterium striatum	GCA_001602751.1	actinobacteria
WP_053049270.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→ polar_leader+TM+TM+TM→	535	Corynebacterium striatum	GCF_001058455.1	actinobacteria
WP_053088001.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM→vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→ polar_leader+TM+TM+TM→	535	Corynebacterium striatum	GCF_001058455.1	actinobacteria
WP_053177183.1	GAP1-N2+GAP1-M+GAP1-C	TPR_containing_alpha_helical+Fibronectin-like_repeats→ PSE→ GAP1-N2+GAP1-M+GAP1-C*→ PSE→ vWA(canonical)→ PP2C→ Pkinase+ZnR+beta-rich→	821	Streptomyces virginiae	GCA_001270565.1	actinobacteria
WP_053211995.1	GAP1-N2+GAP1-M+GAP1-C	TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ PSE→ vWA(canonical)→ PP2C→ Pkinase+ZnR+beta-rich→	880	Streptomyces antibioticus	GCA_001270635.1	actinobacteria
WP_053240737.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	883	Clostridium sp. DMHC 10	GCA_001270375.1	firmicutes
WP_053241473.1	GAP1-N2+GAP1-M+GAP1-C	Fibronectin-like_repeats+??→ PSE→ GAP1-N2+GAP1-M+GAP1-C(frag)*→ GAP1-N2+GAP1-M→?→ TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→ TM→vWA(canonical)+YiKA-like+TM+??→ PSE→?→ Tubulin+coiled_coil+HTH?+??→	86	Clostridium sp. DMHC 10	GCA_001270375.1	firmicutes
WP_053241474.1	GAP1-N2+GAP1-M	Fibronectin-like_repeats+??→ PSE→ GAP1-N2+GAP1-M+GAP1-C(frag)→ GAP1-N2+GAP1-M*→?→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→ TM+vWA(canonical)+YiKA-like+TM+??→ PSE→?→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→	224	Clostridium sp. DMHC 10	GCA_001270375.1	firmicutes
WP_053241935.1	GAP1-N2+GAP1-M	TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→ TM+vWA(canonical)+YiKA-like+TM+??→ PSE→?→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M*→	182	Clostridium sp. DMHC 10	GCA_001270375.1	firmicutes
WP_053325329.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM→vWA(canonical)+YiKA-like+TM+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M*→	1002	Paenibacillus peoriae	GCA_001272655.2	firmicutes
WP_053372393.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM→vWA(canonical)+YiKA-like+TM+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	995	Bacillus sp. FJAT-27812	GCF_001273065.1	firmicutes
WP_053478937.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM→vWA(canonical)+YiKA-like+TM+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	908	Bacillus sp. FJAT-21945	GCF_001275655.1	firmicutes
WP_053491363.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail	Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C+polar_tail*→	1022	Bacillus sp. FJAT-18019	GCF_001275655.1	firmicutes
WP_053587543.1	GAP1-N2+GAP1-M+GAP1-C	TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM→ vWA(canonical)→ PPIC→ Pkinase+ZnR+beta-rich→	865	Streptomyces sp. CFMR 7	GCA_001278095.1	actinobacteria
WP_053587611.1	GAP1-N2+GAP1-M+GAP1-C	TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM→ vWA(canonical)→ PP2C→ Pkinase+ZnR+beta-rich→|(→|*→?→?→?)|GAP1-N2+GAP1-M+GAP1-C*→	894	Streptomyces sp. CFMR 7	GCA_001278095.1	actinobacteria
WP_053652987.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→ HSP70→ GAP1-N2+GAP1-M+GAP1-C*→ Fibronectin→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→	808	Actinomyces sp. oral taxon 414	GCF_001278845.1	actinobacteria
WP_053585921.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	polar_leader+TM+TM+TM→ TM→vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→?→?→|(→?|Pkinase+TM+Septum_form→	901	Actinomyces sp. oral taxon 414	GCA_001278845.1	actinobacteria
WP_053619235.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	895	Nocardiopsis sp. NRRL B-16309	GCF_001279585.1	actinobacteria
WP_053734164.1	GAP1-N2+GAP1-M+GAP1-C	TM→vWA(canonical)+TM→ HSP70→?→?→Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→|(→ GrpE	747	Nocardia sp. NRRL S-836	GCF_001279525.1	actinobacteria
WP_053742290.1	GAP1-N2+GAP1-M+GAP1-C+TM+beta-rich	vWA(canonical)+beta-rich+low_complexity→?→?→ Tubulin+alpha_helical+??+??→ TM+TM+TM+TM→ Pkinase+TM→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C+TM+beta-rich*→?→|(→?|Pkinase+TM+Septum_form→	667	Nocardia sp. NRRL S-836	GCF_001279525.1	actinobacteria
WP_053777217.1	GAP1-N2+GAP1-M+GAP1-C	Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C(frag)*→?→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→	367	Gordonia sp. NB4-19Y	GCF_000347295.2	actinobacteria
WP_053782292.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail	TM+TM+TM+vWA+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C+polar_tail*→	1079	Paenibacillus sp. A59	GCF_001280595.1	firmicutes
WP_054027553.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM→vWA(canonical)+YiKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	979	Bacillus sp. FJAT-28004	GCF_001280845.1	firmicutes
WP_054245673.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM→vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→	913	Rhodococcus jostii	GCF_001292845.1	actinobacteria
WP_054293506.1	GAP1-N2+GAP1-M	Pkinase+TM→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M*→	400	Kibdelosporangium phytohabitans	GCA_001302585.1	actinobacteria
WP_054404307.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM→vWA(canonical)+YiKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	1023	Paenibacillus solani	GCF_001277345.1	firmicutes
WP_054569407.1	GAP1-N2+GAP1-M+GAP1-C+ZnR+DO-GTPase2	GAP1-N2+GAP1-M+GAP1-C+ZnR+DO-GTPase2*→	964	Tsukamurella sp. R43	GCA_001306605.1	actinobacteria
WP_054600667.1	GAP1-N2+GAP1-M+GAP1-C	HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→?→DO-GTPase2.2→	820	Mycolicibacterium fortuitum	GCA_001307545.1	actinobacteria
WP_054601302.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM→vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→ TM+DUF4190+TM+PknH_C→ TM+DUF4190+TM+PknH_C→	828	Mycolicibacterium fortuitum	GCA_001307545.1	actinobacteria

acc	architecture	operon	len	species	gca	taxend
WP_054706231.1	GAP1:N2+GAP1-M+GAP1-C	Tubulin+coiled_coil+HTH?+?7→ TM+TM+TM+WA+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2→ GAP1:N2+GAP1-M+GAP1-C*	660	Paenibacillus pinihumi	GCF_003312305.1	firmicutes
WP_054716519.1	GAP1:N2+GAP1-M+GAP1-C	GrpE→ HSP70→ DnaJ+DnaJ+ZnR+coiled_coil+Fibronectin-like_repeats+→ ZnR+ZnR+DO-GTPase2.2→ GAP1:N2+GAP1-M+GAP1-C*→?→ TM+TM+ZnR+ZnR+DO-GTPase2.2+TM+SH3→ FGS-fold_domain→	815	Martiniellum fragile	GCF_003310955.1	bacteroidetes
WP_054792602.1	GAP1:N2+GAP1-M+GAP1-C	GAP1:N2+GAP1-M+GAP1-C(frag)*→	128	Bacillus sp. JCM 19035	GCF_003310595.1	firmicutes
WP_054748701.1	GAP1:N2+GAP1-M+GAP1-C	GAP1:N2+GAP1-M+GAP1-C→	842	Oxobacter pfennigii	GCA_003317355.1	firmicutes
WP_054735715.1	GAP1:N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+?→ TM+TM+TM+WA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1:N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*	901	Oxobacter pfennigii	GCA_003317355.1	firmicutes
WP_054938831.1	GAP1:N2+GAP1-M	TM+WA(canonical)+YtKA-like+TM+??→ PSE→ PSE→ Tubulin+coiled_coil+HTH?+?→ TM+TM+TM+WA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1:N2+GAP1-M*→ GAP1:N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich→	206	Paenibacillus ihuae	GCF_003368795.1	firmicutes
WP_054939922.1	GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+WA(canonical)+YtKA-like+TM+??→ PSE→ PSE→ Tubulin+coiled_coil+HTH?+?→ TM+TM+TM+WA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1:N2+GAP1-M*→ GAP1:N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich→	864	Paenibacillus ihuae	GCF_003368795.1	firmicutes
WP_054971920.1	GAP1:N2+GAP1-M+GAP1-C+polar_tail+TM+Cadherin-like	TM+WA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+?→ TM+TM+TM+WA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1:N2+GAP1-M+GAP1-C+polar_tail+TM+Cadherin-like*	933	Paenibacillus sp. A3	GCA_003390685.1	firmicutes
WP_055106677.1	GAP1:N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+WA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+?→ TM+TM+TM+WA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1:N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*	1114	Paenibacillus ihumii	GCF_004403875.1	firmicutes
WP_055317479.1	GAP1:N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+WA(canonical)+Fibronectin-like_repeats+TM+beta-rich+le_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1:N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→ TM+DUF4190+TM+PknH_C→ TM+DUF4190+TM+PknH_C→	828	Mycolicibacterium peregrinum	GCA_002102415.1	actinobacteria
WP_055119701.1	GAP1:N2+GAP1-M+GAP1-C	HRDC-like?+Fibronectin-like_repeats→ GAP1:N2+GAP1-M+GAP1-C*→??+DO-GTPase2.2→	828	Mycolicibacterium peregrinum	GCA_002102345.1	actinobacteria
WP_055161845.1	GAP1:N2+GAP1-M+GAP1-C	GAP1:N2+GAP1-M+GAP1-C*→ vWA(canonical)→ PPIC→ Pkinase+ZnR+beta-rich→||→ TPR_containing_alpha_helical+Fibronectin-like_repeats	811	Streptomyces kanamycinus	GCF_004104275.1	actinobacteria
WP_055702748.1	GAP1:N2+GAP1-M+GAP1-C	GAP1:N2+GAP1-M+GAP1-C*→ vWA(canonical)→ PPIC→ Pkinase+ZnR+beta-rich→	806	Streptomyces silaceus	GCF_004197415.1	actinobacteria
WP_055712604.1	GAP1:N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+WA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+?→ TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1:N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*	819	Brevibacillus choshinensis	GCF_000349035.1	firmicutes
WP_056032652.1	GAP1:N2+GAP1-M+GAP1-C+polar_tail	Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+?→ TM+TM+TM+WA+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2→ GAP1:N2+GAP1-M+GAP1-C+polar_tail*	1067	Paenibacillus sp. Leaf72	GCA_004128585.1	firmicutes
WP_056489197.1	GAP1:N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+WA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+?→ TM+TM+TM+WA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1:N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*	932	Paenibacillus sp. Leaf182	GCA_004128585.1	firmicutes
WP_056641465.1	GAP1:N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+WA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+?→ HRDC-like?+Fibronectin-like_repeats→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1:N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*	996	Paenibacillus sp. Soil522	GCA_004128245.1	firmicutes
WP_056682743.1	GAP1:N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+WA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+?→ TM+TM+TM+WA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1:N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*	908	Bacillus solani	GCA_004129595.1	firmicutes
WP_056958357.1	GAP1:N2+GAP1-M+GAP1-C	GAP1:N2+GAP1-M+GAP1-C*→	827	Streptomyces	GCA_004126325.1	actinobacteria
WP_056702032.1	GAP1:N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+WA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+?→ TM+TM+TM+WA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1:N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*	1059	Paenibacillus sp. Root52	GCA_004126866.1	firmicutes
WP_056722968.1	GAP1:N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+WA(canonical)+Fibronectin-like_repeats+TM+beta-rich+le_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1:N2+GAP1-M+GAP1-C*→?→ GAP1:N2+GAP1-M+GAP1-C*	706	Nocardioides sp. Root190	GCA_004128565.1	actinobacteria
WP_056791870.1	GAP1:N2+GAP1-M+GAP1-C	GAP1:N2+GAP1-M+GAP1-C*	801	Streptomyces	GCA_004129615.1	actinobacteria
WP_056963515.1	GAP1:N2+GAP1-M+GAP1-C	GAP1:N2+GAP1-M+GAP1-C*	827	Streptomyces amlatus	GCF_004134155.1	actinobacteria
WP_057506601.1	GAP1:N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+WA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+?→ TM+TM+TM+WA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1:N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*	908	Bacillus praedii	GCF_004149605.1	firmicutes
WP_057642968.1	GAP1:N2+GAP1-M+GAP1-C	HRDC-like?+Fibronectin-like_repeats→ GAP1:N2+GAP1-M+GAP1-C*→?→ DO-GTPase2.2→	822	Mycobacterium smegmatis	GCA_004157595.1	actinobacteria
WP_058301504.1	GAP1:N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+WA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+?→ TM+TM+TM+WA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1:N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*	911	Gorillibacterium timonense	GCF_004157415.1	firmicutes
WP_058554030.1	GAP1:N2+GAP1-M+GAP1-C	GrpE→ HSP70→ HSP70+WA(canonical)→?→ ZnR+ZnR+DO-GTPase2.2→ GAP1:N2+GAP1-M+GAP1-C*→?→ TIR→ TM+ZnR+ZnR+DO-GTPase2.2+PBGA+PBGA→	859	Thisbacoccus sp. ML1	GCF_004091955.1	gammaproteobacteria
WP_058624998.1	GAP1:N2+GAP1-M+GAP1-C	GrpE→ HSP70→ TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1:N2+GAP1-M+GAP1-C* → TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→	670	Corynebacterium testaceum	GCA_001470635.1	actinobacteria
WP_058710444.1	GAP1:N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+WA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+?→ TM+TM+TM+WA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1:N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*	1009	Paenibacillus	GCA_002872435.1	firmicutes
WP_058929585.1	GAP1:N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+WA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+?→ TM+TM+TM+WA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1:N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*	1009	Paenibacillus	GCA_002872435.1	firmicutes
WP_059013430.1	GAP1:N2+GAP1-M+GAP1-C	GAP1:N2+GAP1-M+GAP1-C*→	460	Streptomyces specialis	GCF_004293375.1	actinobacteria
WP_059036548.1	GAP1:N2+GAP1-M+GAP1-C	Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1:N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→	862	Gordonia desulfuricans	GCF_004365495.1	actinobacteria
WP_059061848.1	GAP1:N2+GAP1-M+GAP1-C	GrpE→ HSP70→ TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1:N2+GAP1-M+GAP1-C* → TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→?→?→ HSP70→ vWA(canonical)→	677	Leuconostoc sp. G161	GCA_004182305.1	actinobacteria
WP_059049966.1	GAP1:N2+GAP1-M+GAP1-C	HRDC-like?+Fibronectin-like_repeats→ GAP1:N2+GAP1-M+GAP1-C*→?→ DO-GTPase2.2→	624	Streptomyces sp. GA-2829	GCA_004499965.1	actinobacteria
WP_059063061.1	GAP1:N2+GAP1-M+GAP1-C	HRDC-like?+Fibronectin-like_repeats→ GAP1:N2+GAP1-M+GAP1-C*→?→ DO-GTPase2.2→	830	Mycobacterium sp. IS-1742	GCA_004500125.1	actinobacteria
WP_059064059.1	GAP1:N2+GAP1-M+GAP1-C	HRDC-like?+Fibronectin-like_repeats→ GAP1:N2+GAP1-M+GAP1-C*→?→ DO-GTPase2.2→	830	Mycobacterium sp. IS-1496	GCA_004499995.1	actinobacteria
WP_059213934.1	GAP1:N2+GAP1-M+GAP1-C	GAP1:N2+GAP1-M+GAP1-C*	780	Streptomyces griseus	GCA_005369565.1	actinobacteria
WP_059253638.1	GAP1:N2+GAP1-M+GAP1-C	TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1:N2+GAP1-M+GAP1-C* → TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM+ vWA(canonical)→ PPIC→ Pkinase+ZnR+beta-rich→	941	Streptomyces reticuli	GCA_005118815.1	actinobacteria
WP_059312175.1	GAP1:N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+?→ TM+TM+TM+WA+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1:N2+GAP1-M*→	363	Paenibacillus borvis	GCF_003121715.2	firmicutes
WP_060625106.1	GAP1:N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+WA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+?→ TM+TM+TM+WA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1:N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*	998	Paenibacillus ehrei	GCA_003012825.2	firmicutes
WP_060635379.1	GAP1:N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+WA(canonical)+Fibronectin-like_repeats+TM+beta-rich+le_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1:N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→	969	Rhodococcus pyridinivorans	GCA_003143525.1	actinobacteria
WP_060729914.1	GAP1:N2+GAP1-M+GAP1-C	TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1:N2+GAP1-M+GAP1-C* → TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM+ vWA(canonical)→ PPIC→ Pkinase+ZnR+beta-rich→	820	Streptomyces albus	GCF_001541145.1	actinobacteria
WP_060842402.1	GAP1:N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+WA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+?→ TM+TM+TM+WA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1:N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*	1028	Paenibacillus rigoagondasis	GCF_001546065.1	firmicutes
WP_060893378.1	GAP1:N2+GAP1-M+GAP1-C	GAP1:N2+GAP1-M+GAP1-C* → vWA(canonical)→ PPIC→ Pkinase+ZnR+beta-rich→	811	Streptomyces europaeisabiei	GCF_001550375.1	actinobacteria
WP_060895036.1	GAP1:N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+WA(canonical)+Fibronectin-like_repeats+TM+beta-rich+le_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1:N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→	673	Corynebacterium kroppenstedtii	GCA_001552955.1	actinobacteria
WP_060957505.1	GAP1:N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+le_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1:N2+GAP1-M+GAP1-C*→?→ DO-GTPase2.2→	933	Actinomyces cris	GCA_001552935.1	actinobacteria
WP_061043383.1	GAP1:N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+WA(canonical)+Fibronectin-like_repeats+TM+beta-rich+le_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1:N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→	925	Rhodococcus sp. SC4	GCA_001555475.1	actinobacteria
WP_061083832.1	GAP1:N2+GAP1-M+GAP1-C	TPR_containing_alpha_helical+Fibronectin-like_repeats+extended_insert+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1:N2+GAP1-M+GAP1-C* → TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→	902	Nocardiopsis dassonvillei	actinobacteria	
WP_061265397.1	GAP1:N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+le_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1:N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→ TM+DUF4190+TM+PknH_C→ TM+DUF4190+TM+PknH_C→	828	Mycolicibacterium fortuitum	GCA_001570465.1	actinobacteria
WP_061265617.1	GAP1:N2+GAP1-M+GAP1-C	HRDC-like?+Fibronectin-like_repeats→ GAP1:N2+GAP1-M+GAP1-C*→??+DO-GTPase2.2→	828	Mycolicibacterium fortuitum	GCA_001570465.1	actinobacteria
WP_061294805.1	GAP1:N2+GAP1-M+GAP1-C	GrpE→ HSP70→ TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1:N2+GAP1-M+GAP1-C* → TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM→	721	Herbidospora cretacea	GCF_001570605.1	actinobacteria
WP_061300064.1	GAP1:N2+GAP1-M+GAP1-C+TM+low_complexity+TM	vWA(canonical)→ DO-GTPase1→ GAP1:N2+GAP1-M+GAP1-C+TM+low_complexity+TM*→	765	Herbidospora cretacea	GCF_001570605.1	actinobacteria

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WP_061403385.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*?->	789	Streptomyces albus	GCA_001537385.1	actinobacteria
WP_061069039.1	GAP1-N2+GAP1-M+GAP1-C	TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail-> Tubulin+alpha_helical+??+??-> GAP_unknown1+TM+TM+GAP_unknown2-> HRDC-like?+Fibronectin-like_repeats-> GAP1-N2+GAP1-M+GAP1-C*-> beta-rich+vWA(canonical)->??+DO-GTPase2.2->	925	Rhodococcus sp. LB1	GCA_001834455.1	actinobacteria
WP_017986933.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->	746	Bacillus circulans	GCA_900445325.1	firmicutes
WP_001831359.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail	Tubulin+coiled_coil+??-> Tubulin+coiled_coil+HTH?+??-> TM+TM+TM+vWA+TM+TM+TM+polar_tail-> Fibronectin-like_repeats+??-> ZnR+ZnR+DO-GTPase2.2-> GAP1-N2+GAP1-M+GAP1-C+polar_tail*->	1013	Paenibacillus polymyxa	GCA_001593085.1	firmicutes
WP_061933079.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM+ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail-> Tubulin+alpha_helical+??+??-> GAP_unknown1+TM+TM+GAP_unknown2-> HRDC-like?+Fibronectin-like_repeats-> GAP1-N2+GAP1-M+GAP1-C*-> beta-rich+vWA(canonical)->??+DO-GTPase2.2-> polar_leader+TM+TM+TM->	515	Corynebacterium	GCA_001579275.1	actinobacteria
WP_063036226.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM+ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail-> Tubulin+alpha_helical+??+??-> GAP_unknown1+TM+TM+GAP_unknown2-> HRDC-like?+Fibronectin-like_repeats-> GAP1-N2+GAP1-M+GAP1-C*-> beta-rich+vWA(canonical)->??+DO-GTPase2.2-> polar_leader+TM+TM+TM->	519	Corynebacterium simulans	GCA_001586215.1	actinobacteria
WP_063042647.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM+ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail-> Tubulin+alpha_helical+??+??-> GAP_unknown1+TM+TM+GAP_unknown2-> HRDC-like?+Fibronectin-like_repeats-> GAP1-N2+GAP1-M+GAP1-C*-> beta-rich+vWA(canonical)->??+DO-GTPase2.2-> polar_leader+TM+TM+TM->	515	Corynebacterium simulans	GCA_001586235.1	actinobacteria
WP_021494333.1	GAP1-N2+GAP1-M+GAP1-C	TPR_containing_alpha_helical+Fibronectin-like_repeats+ ZnR+ZnR+DO-GTPase2.2-> GAP1-N2+GAP1-M+GAP1-C*-> TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM+ vWA(canonical)-> PP2C-> Pkinase+ZnR+beta-rich->	959	Streptomyces curacoi	GCA_001513975.1	actinobacteria
WP_002215611.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YrkA-like+TM+??-> Tubulin+coiled_coil+??-> Tubulin+coiled_coil+HTH?+??-> TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail-> Fibronectin-like_repeats+??-> ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR-> GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->	1077	Paenibacillus pabuli	GCA_001514495.1	firmicutes
WP_003519655.1	GAP1-N2+GAP1-M+GAP1-C	GrpE-> HSP70-> TPR_containing_alpha_helical+Fibronectin-like_repeats-> ZnR+ZnR+DO-GTPase2.2-> GAP1-N2+GAP1-M+TM+GAP1-C*->	733	Herbidospora sakaraetensis	GCA_001570525.1	actinobacteria
WP_023317280.1	GAP1-N2+GAP1-M+GAP1-C+TM+low_complexity+TM	vWA(canonical)-> DO-GTPase1-> GAP1-N2+GAP1-M+GAP1-C+TM+low_complexity+TM*->	753	Herbidospora sakaraetensis	GCA_001570525.1	actinobacteria
WP_023370252.1	GAP1-N2+GAP1-M+GAP1-C	GrpE-> HSP70-> TPR_containing_alpha_helical+Fibronectin-like_repeats+ ZnR+ZnR+DO-GTPase2.2-> GAP1-N2+GAP1-M+GAP1-C*-> TM+TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM->	725	Herbidospora sakaraetensis	GCA_001570525.1	actinobacteria
WP_023493315.1	GAP1-N2+GAP1-M+GAP1-C+TM+low_complexity+TM	vWA(canonical)-> DO-GTPase1-> GAP1-N2+GAP1-M+GAP1-C+TM+low_complexity+TM*->	750	Herbidospora yilanensis	GCA_001570565.1	actinobacteria
WP_023570212.1	GAP1-N2+GAP1-M+GAP1-C	GrpE-> HSP70-> TPR_containing_alpha_helical+Fibronectin-like_repeats+ ZnR+ZnR+DO-GTPase2.2-> GAP1-N2+GAP1-M+GAP1-C*-> TM+TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM->	725	Herbidospora yilanensis	GCA_001570565.1	actinobacteria
WP_024409995.1	GAP1-N2+GAP1-M+GAP1-C+TM+low_complexity+TM	vWA(canonical)-> DO-GTPase1-> GAP1-N2+GAP1-M+GAP1-C+TM+low_complexity+TM*->	744	Herbidospora daliensis	GCA_001570585.1	actinobacteria
WP_024433533.1	GAP1-N2+GAP1-M+GAP1-C	GrpE-> HSP70-> TPR_containing_alpha_helical+Fibronectin-like_repeats+ ZnR+ZnR+DO-GTPase2.2-> GAP1-N2+GAP1-M+GAP1-C*-> TM+TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM->	725	Herbidospora daliensis	GCA_001570585.1	actinobacteria
WP_052195551.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YrkA-like+TM+??-> Tubulin+coiled_coil+HTH?+??-> Tubulin+coiled_coil+HTH?+??-> TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail-> Fibronectin-like_repeats+??-> ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR-> GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->	1037	Paenibacillus jilunlii	GCA_001546055.1	firmicutes
WP_025302145.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM+ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail-> Tubulin+alpha_helical+??+??-> GAP_unknown1+TM+TM+GAP_unknown2-> HRDC-like?+Fibronectin-like_repeats-> GAP1-N2+GAP1-M+GAP1-C*-> beta-rich+vWA(canonical)->??+DO-GTPase2.2->	965	Lysinimicrobium rhizosphaerae	GCA_009071455.1	firmicutes
WP_022775649.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*-> vWA(canonical)-> PP2C-> Pkinase+ZnR+beta-rich-->[x-> TPR_containing_alpha_helical+Fibronectin-like_repeats	790	Streptomyces sp. NRRL S-1521	GCA_001507605.1	actinobacteria
WP_022795562.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM+ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail-> Tubulin+alpha_helical+??+??-> GAP_unknown1+TM+TM+GAP_unknown2-> HRDC-like?+Fibronectin-like_repeats-> GAP1-N2+GAP1-M+GAP1-C*-> beta-rich+vWA(canonical)->??+DO-GTPase2.2->	913	Williamsia muralis	GCA_003643525.1	actinobacteria
WP_026294042.1	GAP1-N2+GAP1-M+GAP1-C	TM+DUF4190+TM+polar_leader+TM+TM+TM+ PSE-> Tubulin+alpha_helical+??+??-> GAP_unknown1+TM+TM+GAP_unknown2-> HRDC-like?+Fibronectin-like_repeats-> GAP1-N2+GAP1-M+GAP1-C*-> beta-rich+vWA(canonical)->??+DO-GTPase2.2-> TM+DUF4190+TM+PknH_C-> TM+DUF4190+TM+PknH_C-> TM+DUF4190+TM+PknH_C->	837	Mycobacterium brisbanense	GCA_003594025.1	actinobacteria
WP_028368883.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YrkA-like+TM+??-> Tubulin+coiled_coil+??-> Tubulin+coiled_coil+HTH?+??-> TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail-> Fibronectin-like_repeats+??-> ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR-> GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->	1061	Paenibacillus amylolyticus	GCA_001570725.1	firmicutes
WP_063610973.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+Cadherin-like	TM+vWA(canonical)+YrkA-like+TM+??-> Tubulin+coiled_coil+HTH?+??-> Tubulin+coiled_coil+HTH?+??-> TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail-> Fibronectin-like_repeats+??-> ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR-> GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+Cadherin-like*->	936	Paenibacillus cisgli	GCA_001610775.1	firmicutes
WP_023127291.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YrkA-like+TM+??-> Tubulin+coiled_coil+??-> Tubulin+coiled_coil+HTH?+??-> TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail-> Fibronectin-like_repeats+??-> ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR-> GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->	1009	Paenibacillus jamilae	GCA_001619755.1	firmicutes
WP_023127312.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YrkA-like+TM+??-> Tubulin+coiled_coil+??-> Tubulin+coiled_coil+HTH?+??-> TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail-> Fibronectin-like_repeats+??-> ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR-> GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->	836	Paenibacillus parabevis	GCA_001619812.1	firmicutes
WP_023477831.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YrkA-like+TM+??-> Tubulin+coiled_coil+??-> Tubulin+coiled_coil+HTH?+??-> TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail-> Fibronectin-like_repeats+??-> ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR-> GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->	1002	Paenibacillus glucanolyticus	GCA_001638025.1	firmicutes
WP_003579561.1	GAP1-N2+GAP1-M+GAP1-C	Fibronectin-like_repeats+??-> PSE-+? -> ZnR+ZnR+DO-GTPase2.2-> GAP1-N2+GAP1-M+GAP1-C*-> TM+vWA(canonical)+YrkA-like+TM+??-> Tubulin+coiled_coil+??-> Tubulin+coiled_coil+HTH?+??-> TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail-> Fibronectin-like_repeats+??->	870	Clostridium ljungdahlii	GCA_001638045.1	firmicutes
WP_063555605.1	GAP1-N2+GAP1-M	TM+TM+TM+TM+polar_tail-> Fibronectin-like_repeats+??-+?-+?-+?-+ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR-> GAP1-N2+GAP1-M*->	351	Clostridium ljungdahlii	GCA_001638065.1	firmicutes
WP_035660009.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	Tubulin+coiled_coil+HTH?+??-> TM+TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail-> Fibronectin-like_repeats+??-> ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR-> GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->	1056	Paenibacillus sp. O199	GCA_001636635.1	firmicutes
WP_036013863.1	GAP1-N2+GAP1-M+GAP1-C	Fibronectin-like_repeats+??-> ZnR+ZnR+DO-GTPase2.2-> GAP1-N2+GAP1-M+GAP1-C*-> TM+vWA(canonical)+YrkA-like+TM+??-> Tubulin+coiled_coil+HTH?+??-> TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail-> Fibronectin-like_repeats+??->	868	Clostridium cuskatii	GCA_001638365.1	firmicutes
WP_036013941.1	GAP1-N2+GAP1-M	TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail-> Fibronectin-like_repeats+??-+?-+?-+?-+ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR-> GAP1-N2+GAP1-M*->	351	Clostridium cuskatii	GCA_001638385.1	firmicutes
WP_037260015.1	GAP1-N2+GAP1-M+GAP1-C	TPR_containing_alpha_helical+Fibronectin-like_repeats-+? -> ZnR+ZnR+DO-GTPase2.2-> GAP1-N2+GAP1-M+GAP1-C*-> TM+TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM-> vWA(canonical)-> PP2C-> Pkinase+ZnR+beta-rich->	823	Streptomyces sp. RG22	GCA_001650215.1	actinobacteria
WP_037692856.1	GAP1-N2+GAP1-M+GAP1-C	TPR_containing_alpha_helical+Fibronectin-like_repeats+ ZnR+ZnR+DO-GTPase2.2-> GAP1-N2+GAP1-M+GAP1-C*-> TM+TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM+ vWA(canonical)-> PP2C-> Pkinase+ZnR+beta-rich->	936	Streptomyces auranticus	GCA_001418335.1	actinobacteria
WP_039586962.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM+ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail-> Tubulin+alpha_helical+??+??-> GAP_unknown1+TM+TM+GAP_unknown2-> HRDC-like?+Fibronectin-like_repeats-> GAP1-N2+GAP1-M+GAP1-C*-> beta-rich+vWA(canonical)->??+DO-GTPase2.2-> ?-+[|x-> ?-+-?-> HSP70-> GrpE	336	Corynebacterium alermanniae	GCA_001586235.1	actinobacteria
WP_039738310.1	GAP1-N2+GAP1-M+GAP1-C	GrpE-> HSP70-> TPR_containing_alpha_helical+Fibronectin-like_repeats+ ZnR+ZnR+DO-GTPase2.2-> GAP1-N2+GAP1-M+GAP1-C*-> TM+TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2-+? -> HSP70-> vWA(canonical)->	806	Dietzia cinnamea	GCA_001643175.1	actinobacteria
WP_040182298.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YrkA-like+TM+??-> Tubulin+coiled_coil+??-> Tubulin+coiled_coil+HTH?+??-> TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail-> Fibronectin-like_repeats+??-> ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR-> GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->	833	Brevibacillus sp. SKDU10	GCA_001652205.1	firmicutes
WP_040663183.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM+ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail-> Tubulin+alpha_helical+??+??-> GAP_unknown1+TM+TM+GAP_unknown2-> HRDC-like?+Fibronectin-like_repeats-> GAP1-N2+GAP1-M+GAP1-C*-> beta-rich+vWA(canonical)->??+DO-GTPase2.2->	899	Rhodococcus opacus	GCA_900450725.1	actinobacteria
WP_042003137.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YrkA-like+TM+??-> Tubulin+coiled_coil+??-> Tubulin+coiled_coil+HTH?+??-> TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail-> Fibronectin-like_repeats+??-> ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR-> GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*->	832	Brevibacillus brevis	GCA_001649505.1	firmicutes
WP_044154745.1	GAP1-N2+GAP1-M+GAP1-C	TM+TM+TM+ZnR+ZnR+DO-GTPase2.2-+? -> HSP70-> vWA(canonical)-> Dna4+Dna3-ZnR+ZnR+DO-GTPase2.2-> GAP1-N2+GAP1-M+GAP1-C*->	914	Gardnerella vaginalis	GCA_001654145.1	actinobacteria
WP_064914835.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail	TM+TM+TM+vWA+TM+TM+TM+polar_tail-> Fibronectin-like_repeats+??-> ZnR+ZnR+DO-GTPase2.2-> GAP1-N2+GAP1-M+GAP1-C+polar_tail*->	1058	Paenibacillus sp. AB87	GCA_001659845.1	firmicutes
WP_065789597.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail	Tubulin+coiled_coil+HTH?+??-> Tubulin+coiled_coil+HTH?+??-> TM+TM+TM+vWA+TM+TM+TM+polar_tail-> Fibronectin-like_repeats+??-> ZnR+ZnR+DO-GTPase2.2-> GAP1-N2+GAP1-M+GAP1-C+polar_tail*->	1009	Paenibacillus polymyxa	GCA_001659895.1	firmicutes
WP_064850367.1	GAP1-N2+GAP1-M+GAP1-C	HRDC-like?+Fibronectin-like_repeats-> GAP1-N2+GAP1-M+GAP1-C*-> ??+DO-GTPase2.2->	820	Mycobacterium fortuitum	GCA_001665455.1	actinobacteria
WP_064851658.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM+ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail-> Tubulin+alpha_helical+??+??-> GAP_unknown1+TM+TM+GAP_unknown2-> HRDC-like?+Fibronectin-like_repeats-> GAP1-N2+GAP1-M+GAP1-C*-> beta-rich+vWA(canonical)->??+DO-GTPase2.2-> TM+DUF4190+TM+PknH_C-> TM+DUF4190+TM+PknH_C->	828	Mycobacterium fortuitum	GCA_001665455.1	actinobacteria
WP_064865881.1	GAP1-N2+GAP1-M+GAP1-C	HRDC-like?+Fibronectin-like_repeats-> GAP1-N2+GAP1-M+GAP1-C*-> ??+DO-GTPase2.2->	820	Mycobacterium fortuitum	GCA_001665415.1	actinobacteria
WP_064899012.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM+ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail-> Tubulin+alpha_helical+??+??-> GAP_unknown1+TM+TM+GAP_unknown2-> HRDC-like?+Fibronectin-like_repeats-> GAP1-N2+GAP1-M+GAP1-C*-> beta-rich+vWA(canonical)->??+DO-GTPase2.2-> TM+DUF4190+TM+PknH_C->	828	Mycobacterium fortuitum	GCA_001665415.1	actinobacteria
WP_064875995.1	GAP1-N2+GAP1-M+GAP1-C	HRDC-like?+Fibronectin-like_repeats-> GAP1-N2+GAP1-M+GAP1-C*-> ??+DO-GTPase2.2->	820	Mycobacterium setense	GCA_001665415.1	actinobacteria
WP_064872881.1	GAP1-N2+GAP1-M+GAP1-C	HRDC-like?+Fibronectin-like_repeats-> GAP1-N2+GAP1-M+GAP1-C*-> ??+DO-GTPase2.2->	829	Mycobacterium sp. 852013-50142_SCH4511227	GCA_001665825.1	actinobacteria
WP_064878447.1	GAP1-N2+GAP1-M+GAP1-C	TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail-> Tubulin+alpha_helical+??+??-> GAP_unknown1+TM+TM+GAP_unknown2-> HRDC-like?+Fibronectin-like_repeats-> GAP1-N2+GAP1-M+GAP1-C*-> beta-rich+vWA(canonical)->??+DO-GTPase2.2-> TM+DUF4190+TM+PknH_C->	828	Mycobacterium peregrinum	GCA_001665625.1	actinobacteria
WP_064878636.1	GAP1-N2+GAP1-M+GAP1-C	HRDC-like?+Fibronectin-like_repeats-> GAP1-N2+GAP1-M+GAP1-C*-> ??+DO-GTPase2.2->	820	Mycobacterium peregrinum	GCA_001665625.1	actinobacteria
WP_064894838.1	GAP1-N2+GAP1-M+GAP1-C	HRDC-like?+Fibronectin-like_repeats-> GAP1-N2+GAP1-M+GAP1-C*-> ??+DO-GTPase2.2->	819	Mycobacterium conceptionense	GCA_001665335.1	actinobacteria
WP_064900244.1	GAP1-N2+GAP1-M+GAP1-C	HRDC-like?+Fibronectin-like_repeats-> GAP1-N2+GAP1-M+GAP1-C*-> ??+DO-GTPase2.2->	820	Mycobacterium fortuitum	GCA_001665315.1	actinobacteria

acc	architecture	operon	len	species	gca	taxend
WP_064901077.1	GAP1:N2+GAP1:M+GAP1:C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+?? → GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1:N2+GAP1:M+GAP1:C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→ TM+DUF4190+TM+PknH_C→	828	Mycolicibacterium fortuitum	GCA_001605315.1	actinobacteria
WP_064912096.1	GAP1:N2+GAP1:M+GAP1:C	HRDC-like?+Fibronectin-like_repeats→ GAP1:N2+GAP1:M+GAP1:C*→??+DO-GTPase2.2→	820	Mycolicibacterium fortuitum	GCA_001606795.1	actinobacteria
WP_064919053.1	GAP1:N2+GAP1:M+GAP1:C	HRDC-like?+Fibronectin-like_repeats→ GAP1:N2+GAP1:M+GAP1:C*→??+DO-GTPase2.2→	820	Mycobacterium sp. 852002-10279_SCH5584320	GCA_001607465.1	actinobacteria
WP_064924697.1	GAP1:N2+GAP1:M+GAP1:C	HRDC-like?+Fibronectin-like_repeats→ GAP1:N2+GAP1:M+GAP1:C*→??+DO-GTPase2.2→	820	Mycobacterium fortuitum	GCA_001606985.1	actinobacteria
WP_064932157.1	GAP1:N2+GAP1:M+GAP1:C	TM+[lc_insert+]+WA(canonical)+Fibronectin-like_repeats+TM+??+lc_tail→ Tubulin+alpha_helical+??+?? → GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1:N2+GAP1:M+GAP1:C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→ TM+DUF4190+TM+PknH_C→	828	Mycolicibacterium peregrinum	GCA_001605785.1	actinobacteria
WP_064932165.1	GAP1:N2+GAP1:M+GAP1:C	HRDC-like?+Fibronectin-like_repeats→ GAP1:N2+GAP1:M+GAP1:C*→??+DO-GTPase2.2→	828	Mycolicibacterium peregrinum	GCA_001605785.1	actinobacteria
WP_064948402.1	GAP1:N2+GAP1:M+GAP1:C	TM+DUF4190+TM→ polar_leader+TM+TM+TM+ PSE→ Tubulin+alpha_helical+??+?? → GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1:N2+GAP1:M+GAP1:C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→ TM+DUF4190+TM+PknH_C→ TM+DUF4190+TM+PknH_C→ TM+DUF4190+TM+PknH_C→	828	Mycobacterium sp. 852013-50091_SCH5140082	GCA_001606568.1	actinobacteria
WP_064957532.1	GAP1:N2+GAP1:M+GAP1:C	HRDC-like?+Fibronectin-like_repeats→ GAP1:N2+GAP1:M+GAP1:C*→??+DO-GTPase2.2→	820	Mycobacterium peregrinum	GCA_001607305.1	actinobacteria
WP_064958874.1	GAP1:N2+GAP1:M+GAP1:C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+?? → GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1:N2+GAP1:M+GAP1:C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→ TM+DUF4190+TM+PknH_C→ TM+DUF4190+TM+PknH_C→ TM+DUF4190+TM+PknH_C→	828	Mycobacterium peregrinum	GCA_001607305.1	actinobacteria
WP_064963228.1	GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YrKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+?? → TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich*→	1009	Bacillus polyxyna	GCA_001609285.1	actinobacteria
WP_065021493.1	GAP1:N2+GAP1:M+GAP1:C	HRDC-like?+Fibronectin-like_repeats→ GAP1:N2+GAP1:M+GAP1:C*→??+DO-GTPase2.2→	820	Mycolicibacterium fortuitum	GCA_001627855.1	actinobacteria
WP_065030253.1	GAP1:N2+GAP1:M+GAP1:C	TM+DUF4190+TM→ TM+DUF4190+TM→ polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+?? → GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1:N2+GAP1:M+GAP1:C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→ TM+DUF4190+TM+PknH_C→ TM+DUF4190+TM+PknH_C→ TM+DUF4190+TM+PknH_C→ TM+DUF4190+TM+PknH_C→	828	Mycobacterium colombiense	GCA_001627855.1	actinobacteria
WP_065052210.1	GAP1:N2+GAP1:M+GAP1:C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+?? → GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1:N2+GAP1:M+GAP1:C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→ TM+DUF4190+TM+PknH_C→ TM+DUF4190+TM+PknH_C→	828	Mycobacterium fortuitum	GCA_001673325.1	actinobacteria
WP_065052315.1	GAP1:N2+GAP1:M+GAP1:C	HRDC-like?+Fibronectin-like_repeats→ GAP1:N2+GAP1:M+GAP1:C*→??+DO-GTPase2.2→	820	Mycolicibacterium fortuitum	GCA_001673325.1	actinobacteria
WP_065063115.1	GAP1:N2+GAP1:M+GAP1:C	HRDC-like?+Fibronectin-like_repeats→ GAP1:N2+GAP1:M+GAP1:C*→??+DO-GTPase2.2→	819	Mycolicibacterium conceptionense	GCA_001673263.1	actinobacteria
WP_065063837.1	GAP1:N2+GAP1:M+GAP1:C	GrpE→ HSP70→ TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1:N2+GAP1:M+GAP1:C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→ HSP70→ +WA(canonical)→	892	Mycolicibacterium conceptionense	GCA_001673263.1	actinobacteria
WP_065069046.1	GAP1:N2+GAP1:M+GAP1:C	HRDC-like?+Fibronectin-like_repeats→ GAP1:N2+GAP1:M+GAP1:C*→??+DO-GTPase2.2→	820	Mycolicibacterium fortuitum	GCA_001672845.1	actinobacteria
WP_065069245.1	GAP1:N2+GAP1:M+GAP1:C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+?? → GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1:N2+GAP1:M+GAP1:C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→ TM+DUF4190+TM+PknH_C→ TM+DUF4190+TM+PknH_C→	828	Mycolicibacterium fortuitum	GCA_001672845.1	actinobacteria
WP_065070880.1	GAP1:N2+GAP1:M+GAP1:C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+?? → GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1:N2+GAP1:M+GAP1:C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→ TM+DUF4190+TM+PknH_C→	828	Mycolicibacterium fortuitum	GCA_001673275.1	actinobacteria
WP_065072527.1	GAP1:N2+GAP1:M+GAP1:C	HRDC-like?+Fibronectin-like_repeats→ GAP1:N2+GAP1:M+GAP1:C*→??+DO-GTPase2.2→	820	Mycolicibacterium fortuitum	GCA_001673275.1	actinobacteria
WP_065075085.1	GAP1:N2+GAP1:M+GAP1:C	Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2→ GAP1:N2+GAP1:M+GAP1:C*→ TM+vWA(canonical)+YrKA-like+TM+??→ Tubulin+coiled_coil+?? → Tubulin+coiled_coil+HTH?+?? → TM+TM+TM+TM+WA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+?? →	868	Clostridium ragsdalei	GCA_001675165.1	firmicutes
WP_065075106.1	GAP1:N2+GAP1:M+GAP1:C	TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→+?→+?→+?→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1:N2+GAP1:M*→	351	Clostridium ragsdalei	GCA_001675165.1	firmicutes
WP_065147874.1	GAP1:N2+GAP1:M+GAP1:C	HRDC-like?+Fibronectin-like_repeats→ GAP1:N2+GAP1:M+GAP1:C*→??+DO-GTPase2.2→	820	Mycolicibacterium fortuitum	GCA_001673485.1	actinobacteria
WP_065148828.1	GAP1:N2+GAP1:M+GAP1:C	GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1:N2+GAP1:M+GAP1:C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→ TM+DUF4190+TM+PknH_C→	828	Mycolicibacterium fortuitum	GCA_001673485.1	actinobacteria
WP_065204605.1	GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YrKA-like+TM+??→ Tubulin+coiled_coil+HTH?+?? → TM+TM+TM+TM+WA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ PSE→ GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich*→	976	Mycobacterium sp. K81	GCA_001684005.1	firmicutes
WP_065361675.1	GAP1:N2+GAP1:M+GAP1:C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+?? → GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1:N2+GAP1:M+GAP1:C*→??+DO-GTPase2.2→	933	Actinomyces oris	GCA_001682715.1	actinobacteria
WP_065368265.1	GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YrKA-like+TM+??→ Tubulin+coiled_coil+?? → Tubulin+coiled_coil+HTH?+?? → TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich*→	985	Bacillus sp. FJAT-26390	GCA_001685265.1	firmicutes
WP_065458973.1	GAP1:N2+GAP1:M+GAP1:C	HRDC-like?+Fibronectin-like_repeats→ GAP1:N2+GAP1:M+GAP1:C*→??+DO-GTPase2.2→	819	Mycolicibacterium vulneris	GCA_001686835.1	actinobacteria
WP_065509705.1	GAP1:N2+GAP1:M+GAP1:C	HRDC-like?+Fibronectin-like_repeats→ GAP1:N2+GAP1:M+GAP1:C*→??+DO-GTPase2.2→	819	Mycolicibacterium vulneris	GCA_001686755.1	actinobacteria
WP_065513488.1	GAP1:N2+GAP1:M+GAP1:C	HRDC-like?+Fibronectin-like_repeats→ GAP1:N2+GAP1:M+GAP1:C*→??+DO-GTPase2.2→	819	Mycolicibacterium vulneris	GCA_001686675.1	actinobacteria
WP_065537050.1	GAP1:N2+GAP1:M+GAP1:C	GAP1:N2+GAP1:M+GAP1:C*→	804	Streptomyces mutomycini	GCF_001704005.1	actinobacteria
WP_065919640.1	GAP1:N2+GAP1:M+GAP1:C	GrpE→ HSP70→ TPR_containing_alpha_helical+Fibronectin-like_repeats→ TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1:N2+GAP1:M+GAP1:C*→?→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→ HSP70→?→?→?→|=|→PSE→|unknown+CASPASE	385	Leuteea guizhouensis	GCF_001701025.1	actinobacteria
WP_066053004.1	GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YrKA-like+TM+??→ Tubulin+coiled_coil+??→|=|→Tubulin+coiled_coil+HTH?+?? → TM+TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+?? → ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich* →	953	Bacillus soli	GCF_001501665.1	firmicutes
WP_066091928.1	GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YrKA-like+TM+??→ Tubulin+coiled_coil+?? → Tubulin+coiled_coil+HTH?+?? → TM+TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+?? → ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich*→	954	Bacillus aerophilus	GCF_001591875.1	firmicutes
WP_066199613.1	GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YrKA-like+TM+??→ Tubulin+coiled_coil+HTH?+?? → TM+TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+?? → ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich*→	726	Bacillus sp. FJAT-27225	GCF_001685025.1	firmicutes
WP_066513511.1	GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YrKA-like+TM+??→ Tubulin+coiled_coil+?? → Tubulin+coiled_coil+HTH?+?? → TM+TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+?? → ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich*→	942	Bacillus sp. FJAT-29814	GCF_001687115.1	firmicutes
WP_066362451.1	GAP1:N2+GAP1:M+GAP1:C	GrpE→ HSP70→ TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1:N2+GAP1:M+GAP1:C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM→	717	Herbidospora mongoliensis	GCF_001570545.1	actinobacteria
WP_066570919.1	GAP1:N2+GAP1:M+GAP1:C+TM+low_complexity+TM	vWA(canonical)→ DO-GTPase1→ GAP1:N2+GAP1:M+GAP1:C+TM+low_complexity+TM*→	776	Herbidospora mongoliensis	GCF_001570545.1	actinobacteria
WP_066377148.1	GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YrKA-like+TM+??→ Tubulin+coiled_coil+?? → Tubulin+coiled_coil+HTH?+?? → TM+TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+?? → ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich*→	1010	Bacillus sp. FJAT-27264	GCF_001682855.1	firmicutes
WP_066629665.1	GAP1:N2+GAP1:M+GAP1:C	HRDC-like?+Fibronectin-like_repeats→ GAP1:N2+GAP1:M+GAP1:C*→??+DO-GTPase2.2→	825	Mycobacterium sp. 852013-51886_SCH5428379	GCF_001665575.1	actinobacteria
WP_066869695.1	GAP1:N2+GAP1:M+GAP1:C	GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1:N2+GAP1:M+GAP1:C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→ TM+DUF4190+TM+PknH_C→ TM+DUF4190+TM+PknH_C→ TM+DUF4190+TM+PknH_C→ TM+DUF4190+TM+PknH_C→	829	Mycobacterium sp. 1482292.6	GCF_001672995.1	actinobacteria
WP_066876398.1	GAP1:N2+GAP1:M+GAP1:C	GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1:N2+GAP1:M+GAP1:C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→ TM+DUF4190+TM+PknH_C→ TM+DUF4190+TM→	829	Mycobacterium sp. 1241601.1	GCA_001673055.1	actinobacteria
WP_066944787.1	GAP1:N2+GAP1:M+GAP1:C	GAP1:N2+GAP1:M+GAP1:C*→	841	Streptomyces lydicamycinus	GCF_001705515.1	actinobacteria
WP_066957622.1	GAP1:N2+GAP1:M+GAP1:C	TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1:N2+GAP1:M+GAP1:C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM→ vWA(canonical)→ PPZC→ Pkinase+ZnR+beta-rich→	892	Streptomyces cellostaticus	GCA_001513965.1	actinobacteria
WP_067021906.1	GAP1:N2+GAP1:M+GAP1:C	GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1:N2+GAP1:M+GAP1:C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→ TM+DUF4190+TM+PknH_C→ TM+DUF4190+TM+PknH_C→ PSE→?→ TM+DUF4190+TM+PknH_C→	829	Mycobacterium	GCA_001673415.1	actinobacteria
WP_070436909.1	GAP1:N2+GAP1:M+GAP1:C	GrpE→ HSP70→|=|→PSE|ZnR+ZnR+DO-GTPase2.2→ GAP1:N2+GAP1:M+GAP1:C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+Jelly_roll+beta-sandwich+|=|→STAND_NTPase+TM+TM+TM+TM+TM+TM+TM+TM	478	Corynebacterium sp. FXJ1.172	GCA_001677005.1	actinobacteria
WP_070565811.1	GAP1:N2+GAP1:M+GAP1:C	TM+DUF4190+TM→ TM+DUF4190+TM→ polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+?? → GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1:N2+GAP1:M+GAP1:C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→ TM+DUF4190+TM+PknH_C→ TM+DUF4190+TM+PknH_C→ TM+DUF4190+TM+PknH_C→ TM+DUF4190+TM+PknH_C→	829	Mycobacterium sp. 852002-40037_SCH5390672	GCA_001665875.1	actinobacteria

acc	architecture	operon	len	species	gca	taxend
WP_067124860.1.	GAP1:N2+GAP1-M+GAP1-C	TM+DUF4190+TM→ TM+DUF4190+TM→ polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1:N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2:2→ TM+DUF4190+TM+PknH_C→ TM+DUF4190+TM+PknH_C→ TM+DUF4190+TM+PknH_C→ TM+DUF4190+TM+PknH_C→	829	Mycobacterium sp. M20002-51971_SCH5477799-s	GCA_001667145.1 actinobacteria
WP_067142841.1	GAP1:N2+GAP1-M+GAP1-C	GAP1:N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2:2→ TM+DUF4190+TM+PknH_C→	829	Mycobacterium sp. 1245652.3	GCA_001669335.1 actinobacteria
WP_073487813.1	GAP1:N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1:N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2:2→ TM+DUF4190+TM+PknH_C→ TM+DUF4190+TM+PknH_C→ TM+DUF4190+TM+PknH_C→ TM+DUF4190+TM+PknH_C→	829	Mycobacterium sp. 1165178.9	GCA_001673555.1 actinobacteria
WP_067445675.1	GAP1:N2+GAP1-M+GAP1-C	GAP1:N2+GAP1-M+GAP1-C*→	780	Streptomyces sampsonii	GCA_001676576.1 actinobacteria
WP_067457622.1	GAP1:N2+GAP1-M+GAP1-C	GrpE→ HSP70→ TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2:2→ GAP1:N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2:2→TM→	675	Actinomadura macra	GCA_001552215.1 actinobacteria
WP_067491283.1	GAP1:N2+GAP1-M+GAP1-C	GrpE→ HSP70→ TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2:2→ GAP1:N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2:2→TM→	795	Actinomadura hibisca	GCA_001552835.1 actinobacteria
WP_067535570.1	GAP1:N2+GAP1-M+GAP1-C	Pkinase+TM→ ZnR+DO-GTPase2:1→ GAP1:N2+GAP1-M+GAP1-C*→	738	Nocardia crassotreae	GCA_001613405.1 actinobacteria
WP_067574139.1	GAP1:N2+GAP1-M+GAP1-C	Pkinase+TM→ ZnR+DO-GTPase2:1→ GAP1:N2+GAP1-M+GAP1-C*→	735	Nocardia acidiphoras	GCA_001625985.1 actinobacteria
WP_067657329.1	GAP1:N2+GAP1-M+GAP1-C	TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2:2→ GAP1:N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2:2→	653	Nocardiopsis lateri	GCA_001570765.1 actinobacteria
WP_067635518.1	GAP1:N2+GAP1-M+GAP1-C	GrpE→ HSP70→ TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2:2→ GAP1:N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2:2→TM→	665	Actinomadura latina	GCA_001552195.1 actinobacteria
WP_067651285.1	GAP1:N2+GAP1-M+GAP1-C	GrpE→ HSP70→ TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2:2→ FAD1:N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2:2→C→ HSP70→ vWA(canonical)→	809	Gordonia barense	GCA_001612885.1 actinobacteria
WP_067687461.1	GAP1:N2+GAP1-M+GAP1-C	Pkinase+TM→ ZnR+DO-GTPase2:1→ GAP1:N2+GAP1-M+GAP1-C*→	739	Nocardia jejuensis	GCA_001613145.1 actinobacteria
WP_067726867.1	GAP1:N2+GAP1-M+GAP1-C	GrpE→ HSP70→ TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2:2→ GAP1:N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2:2→ HSP70→ vWA(canonical)→	802	Mycobacterium sp. E802	GCA_001666875.1 actinobacteria
WP_067774504.1	GAP1:N2+GAP1-M+GAP1-C	HRDC-like?+Fibronectin-like_repeats→ GAP1:N2+GAP1-M+GAP1-C*→??+DO-GTPase2:2→	816	Mycobacterium sp. E802	GCA_001666875.1 actinobacteria
WP_067856376.1	GAP1:N2+GAP1-M+GAP1-C	FHA-like?+ZnR+ZnR+DO-GTPase2:2→ GAP1:N2+GAP1-M+GAP1-C*→	807	Aldumavania glycinaphila	GCA_001687553.1 veiromonirebha	
WP_067800015.1	GAP1:N2+GAP1-M+GAP1-C	GrpE→ HSP70→ TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2:2→ GAP1:N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2:2→TM→	666	Actinomadura formosensis	GCA_001552155.1 actinobacteria
WP_067806277.1	GAP1:N2+GAP1-M+GAP1-C	TM+DUF4190+TM→ TM+DUF4190+TM→ polar_leader+TM+TM→ PSE→ Tubulin+alpha_helical+??+??→ CAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1:N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2:2→?→ TM+DUF4190+TM+PknH_C→	807	Mycobacterium sp. ACS1612	GCA_001687565.1 actinobacteria
WP_067811217.1	GAP1:N2+GAP1-M+GAP1-C	GrpE→ HSP70→ TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2:2→ GAP1:N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2:2→TM→	818	Actinomadura kijanata	GCA_001552171.1 actinobacteria
WP_067834668.1	GAP1:N2+GAP1-M+GAP1-C	TM+DUF4190+TM→ TM+DUF4190+TM→ polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1:N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2:2→ TM+DUF4190+TM+PknH_C→ TM+DUF4190+TM+PknH_C→ TM+DUF4190+TM+PknH_C→ TM+DUF4190+TM+PknH_C→	829	Mycobacterium sp. E3078	GCA_001667835.1 actinobacteria
WP_067848906.1	GAP1:N2+GAP1-M+GAP1-C	HRDC-like?+Fibronectin-like_repeats→ GAP1:N2+GAP1-M+GAP1-C*→??+DO-GTPase2:2→	820	Mycolicibacterium wolinskyi	GCA_001545135.1 actinobacteria
WP_067890223.1	GAP1:N2+GAP1-M+GAP1-C	GrpE→ HSP70→ TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2:2→ GAP1:N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2:2→TM→	738	Actinomadura chibensis	GCA_001552135.1 actinobacteria
WP_067901346.1	GAP1:N2+GAP1-M+GAP1-C+TM	vWA(canonical)→ DO-GTPase1→ GAP1:N2+GAP1-M+GAP1-C+TM→	683	Actinomadura chibensis	GCA_001552135.1 actinobacteria
WP_067916876.1	GAP1:N2+GAP1-M+GAP1-C	TM+DUF4190+TM→ TM+DUF4190+TM→ polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1:N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2:2→ TM+DUF4190+TM+PknH_C→ TM+DUF4190+TM+PknH_C→ TM+DUF4190+TM+PknH_C→ TM+DUF4190+TM+PknH_C→	829	Mycobacterium sp. E3078	GCA_001667835.1 actinobacteria
WP_067919448.1	GAP1:N2+GAP1-M+GAP1-C	GrpE→ HSP70→ TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2:2→ GAP1:N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2:2→?→ unknown+CASPASE→ HSP70→	796	Actinomadura	GCA_003001795.1 actinobacteria
WP_067914006.1	GAP1:N2+GAP1-M+GAP1-C	HSP70→ TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2:2→ GAP1:N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2:2→TM→	745	Actinomadura	GCA_003001795.1 actinobacteria
WP_068075338.1	GAP1:N2+GAP1-M+GAP1-C	Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1:N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→	833	Mycobacterium	GCA_001667553.1 actinobacteria
WP_068134295.1	GAP1:N2+GAP1-M	FGS-fold_domain→ ZnR+DO-GTPase2:1→ GAP1:N2+GAP1-M*→	759	Streptomyces ulvae	GCA_001642955.1 planctomycetes
WP_068245530.1	GAP1:N2+GAP1-M+GAP1-C	Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1:N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2:2→ TM+DUF4190+TM+PknH_C→	841	Mycobacterium sp. ACS4331	GCA_001667265.1 actinobacteria
WP_068294235.1	GAP1:N2+GAP1-M+GAP1-C	TM+DUF4190+TM→ TM+DUF4190+TM→ polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1:N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2:2→ TM+DUF4190+TM+PknH_C→ TM+DUF4190+TM+PknH_C→ TM+DUF4190+TM+PknH_C→ TM+DUF4190+TM+PknH_C→	829	Mycobacterium sp. E2660	GCA_001667995.1 actinobacteria
WP_068287942.1	GAP1:N2+GAP1-M	Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1:N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2:2→ TM+DUF4190+TM+PknH_C→ TM+DUF4190+TM+PknH_C→ TM+DUF4190+TM+PknH_C→ TM+DUF4190+TM+PknH_C→	831	Mycobacterium sp. E2462	GCA_001672685.1 actinobacteria
WP_068420276.1	GAP1:N2+GAP1-M	GAP1:N2+GAP1-M*→	229	Planctomyces sp. SH-PL62	GCA_001610895.1 planctomycetes
WP_068496314.1	GAP1:N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)→TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2:2+ZnR+ZnR→ GAP1:N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*	1001	Paenibacillus kribbensis	GCA_001705305.1 firmicutes
WP_068528491.1	GAP1:N2+GAP1-M+GAP1-C+polar_tail	Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→?→ ZnR+ZnR+DO-GTPase2:2→ GAP1:N2+GAP1-M+GAP1-C+polar_tail*	1002	Paenibacillus glacialis	GCA_001652705.1 firmicutes
WP_068592502.1	GAP1:N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)→TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2:2+ZnR+ZnR→ GAP1:N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*	1046	Paenibacillus macquinensis	GCA_001637165.1 firmicutes
WP_068592715.1	GAP1:N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)→TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2:2+ZnR+ZnR→ GAP1:N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*	1053	Paenibacillus macquinensis	GCA_001637165.1 firmicutes
WP_068613626.1	GAP1:N2+GAP1-M+GAP1-C+polar_tail	Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2:2→ GAP1:N2+GAP1-M+GAP1-C+polar_tail*	1085	Paenibacillus tuaregi	GCA_900086655.1 firmicutes
WP_068593973.1	GAP1:N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)→TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2:2+ZnR+ZnR→ GAP1:N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*	1053	Paenibacillus antarcticus	GCA_001705305.1 firmicutes
WP_068660114.1	GAP1:N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)→TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2:2+ZnR+ZnR→ GAP1:N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*	1045	Paenibacillus crassotreae	GCA_001657945.1 firmicutes
WP_068675538.1	GAP1:N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)→TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2:2+ZnR+ZnR→ GAP1:N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*	915	Paenibacillus oryzae	GCA_001675445.1 firmicutes
WP_068723609.1	GAP1:N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+TM+TM+vWA(canonical)→TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2:2+ZnR+ZnR→ GAP1:N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*	892	Paenibacillus sp. DMB5	GCA_001517085.1 firmicutes
WP_068792552.1	GAP1:N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)→TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2:2+ZnR+ZnR→ GAP1:N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*	1143	Paenibacillus sp. GM2	GCA_000690905.1 firmicutes
WP_068792605.1	GAP1:N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)→TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2:2+ZnR+ZnR→ GAP1:N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*	833	Brevibacillus laterosporus	GCA_001692605.1 firmicutes
WP_068940787.1	GAP1:N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)→TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2:2+ZnR+ZnR→ GAP1:N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*	1002	Paenibacillus	GCA_001707685.1 firmicutes
WP_069076658.1	GAP1:N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)→TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2:2+ZnR+ZnR→ GAP1:N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*	1002	Paenibacillus polymyxa	GCA_001706135.1 firmicutes
WP_069169430.1	GAP1:N2+GAP1-M+GAP1-C	GAP1:N2+GAP1-M+GAP1-C*→	803	Streptomyces griseus	GCA_001715295.1 actinobacteria
WP_069219908.1	GAP1:N2+GAP1-M+GAP1-C+polar_tail	Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2:2→ GAP1:N2+GAP1-M+GAP1-C+polar_tail*	1009	Paenibacillus polymyxa	GCA_001705305.1 firmicutes
WP_069329620.1	GAP1:N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)→TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2:2+ZnR+ZnR→ GAP1:N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*	1077	Paenibacillus sp. T145-13ar	GCA_001721045.1 firmicutes
WP_069369143.1	GAP1:N2+GAP1-M+GAP1-C	GrpE→ HSP70→ TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2:2→ GAP1:N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2:2→?→ HSP70_domain_1→ HSP70→ vWA(canonical)→	806	Dietzia alimentaria	GCA_001722515.1 actinobacteria

acc	architecture	operon	len	species	gca	taxend
WP_069601145.1	GAP1-N2+GAP1-M+GAP1-C	TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+?? → GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2-2->	978	Brevibacterium linens	GCA_001729525.1	actinobacteria
WP_069630652.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→ vWA(canonical)→ PP2C→ Pkinase+ZnR+beta-rich→||+ TPR_containing_alpha_helical+Fibronectin-like_repeats	865	Streptomyces niveus	GCF_001723055.1	actinobacteria
WP_069756381.3	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*	827	Streptomyces sp. EN16	GCF_001746285.1	actinobacteria
WP_069849891.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2-2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	832	Brevibacillus brevis	GCF_001748185.1	firmicutes
WP_069887135.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→ vWA(canonical)→ PP2C→ Pkinase+ZnR+beta-rich→||+ TPR_containing_alpha_helical+Fibronectin-like_repeats	803	Streptomyces fuscoceleor	GCF_001745805.1	actinobacteria
WP_069922599.1	GAP1-N2+GAP1-M+GAP1-C	PP2C→ Pkinase→?→?→?→ HSP70_domain_2+low_complexity+domain_betaX→ ZnR+ZnR+DO-GTPase2-2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2-2→	862	Streptomyces	GCA_001751375.1	actinobacteria
WP_070026745.1	GAP1-N2+GAP1-M+GAP1-C	PP2C→ Pkinase→?→?→?→ HSP70_domain_2+low_complexity+domain_betaX→ ZnR+ZnR+DO-GTPase2-2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2-2→	814	Streptomyces sp. F-1	GCA_900670405.3	actinobacteria
WP_070185344.1	GAP1-N2+GAP1-M+GAP1-C	HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→??+DO-GTPase2-2->	819	Mycolicibacterium sp. (ex Dasypsis americana)	GCF_001756795.1	actinobacteria
WP_070192257.1	GAP1-N2+GAP1-M+GAP1-C	TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+?? → GAP_unknown1+TM+TM+GAP_unknown2→?→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→?→??+DO-GTPase2-2->	638	Humibacillus sp. DSM 29435	GCF_001758225.1	actinobacteria
WP_070204886.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*	820	Streptomyces nanshensis	GCA_001751305.1	actinobacteria
WP_070236295.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+?? → GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2-2→ polar_leader+TM+TM+TM→	535	Corynebacterium sp. HMSC06C06	GCA_001685235.1	actinobacteria
WP_070433390.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+?? → GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2-2→ polar_leader+TM+TM+TM→	515	Corynebacterium sp. HMSC06D04	GCA_001687315.1	actinobacteria
WP_070444258.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+?? → GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2-2→ polar_leader+TM+TM+TM→	565	Corynebacterium sp. HMSC06D03	GCA_001687258.1	actinobacteria
WP_070455659.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+?? → PSE→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2-2→ polar_leader+TM+TM+TM→	515	Corynebacterium	GCA_001810285.1	actinobacteria
WP_070494624.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+?? → GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→?→??+DO-GTPase2-2→?→(|=?→?→ HSP70	326	Corynebacterium sp. HMSC30G07	GCA_001804213.1	actinobacteria
WP_070497539.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+?? → GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2-2→ polar_leader+TM+TM+TM→	515	Corynebacterium sp. HMSC06G04	GCA_001807365.1	actinobacteria
WP_070508619.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+?? → GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2-2→ polar_leader+TM+TM+TM→	535	Corynebacterium sp. HMSC05D08	GCA_001807215.1	actinobacteria
WP_070596573.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+?? → GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2-2→ polar_leader+TM+TM+TM→	560	Corynebacteriaceae	GCA_001811515.1	actinobacteria
WP_070616323.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+?? → GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2-2→ polar_leader+TM+TM+TM→	560	Turicella sp. HMSC07G08	GCA_001811515.1	actinobacteria
WP_070623203.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+?? → GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2-2→ polar_leader+TM+TM+TM→	850	Corynebacterium sp. HMSC11E11	GCA_001807025.1	actinobacteria
WP_070245152.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+?? → GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2-2→ polar_leader+TM+TM+TM→	565	Corynebacteriaceae	GCA_001811845.1	actinobacteria
WP_070525188.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+?? → GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2-2→ polar_leader+TM+TM+TM→	567	Corynebacterium sp. HMSC07E01	GCA_001808885.1	actinobacteria
WP_070533827.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+?? → GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2-2→ polar_leader+TM+TM+TM→	577	Corynebacteriaceae	GCA_001811255.1	actinobacteria
WP_070546917.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+?? → GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2-2→ polar_leader+TM+TM+TM→	560	Corynebacterium sp. HMSC07B08	GCA_001808895.1	actinobacteria
WP_070562458.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+?? → GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2-2→ polar_leader+TM+TM+TM→	577	Corynebacterium sp. HMSC07A02	GCA_001810085.1	actinobacteria
WP_070564251.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+?? → GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2-2→ polar_leader+TM+TM+TM→	577	Corynebacterium	GCA_001811565.1	actinobacteria
WP_070602349.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+?? → GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→?→??+DO-GTPase2-2→	933	Actinomyces	GCA_001812965.1	actinobacteria
WP_070712905.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+?? → GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2-2→ polar_leader+TM+TM+TM→	559	Corynebacterium sp. HMSC07H07	GCA_001812805.1	actinobacteria
WP_070679262.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+?? → GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2-2→ polar_leader+TM+TM+TM→	560	Turicella sp. HMSC04H07	GCA_001815175.1	actinobacteria
WP_070683138.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+?? → GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2-2→ polar_leader+TM+TM+TM→	577	Corynebacterium sp. HMSC05G09	GCA_001813425.1	actinobacteria
WP_070685436.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+?? → GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2-2→ polar_leader+TM+TM+TM→	577	Turicella sp. HMSC05E07	GCA_001814395.1	actinobacteria
WP_070701282.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+?? → GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2-2→ polar_leader+TM+TM+TM→	564	Corynebacterium sp. HMSC06G04	GCA_001814885.1	actinobacteria
WP_070731489.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+?? → GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2-2→ polar_leader+TM+TM+TM→	565	Corynebacterium sp. HMSC06C02	GCA_001814945.1	actinobacteria
WP_070731802.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ PSE→ PSE→ Tubulin+alpha_helical+??+?? → GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2-2→ polar_leader+TM+TM+TM→	515	Corynebacterium sp. HMSC07G02	GCA_001813815.1	actinobacteria
WP_070818055.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+?? → GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2-2→ polar_leader+TM+TM+TM→	567	Corynebacterium sp. HMSC03B02	GCA_001836165.1	actinobacteria
WP_070823728.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+?? → GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2-2→ polar_leader+TM+TM+TM→	515	Corynebacterium sp. HMSC03D03	GCA_001836185.1	actinobacteria
WP_070946900.1	GAP1-N2+GAP1-M+GAP1-C	HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→??+DO-GTPase2-2->	819	Mycobacterium sp. 24999	GCA_001835325.1	actinobacteria
WP_071065126.1	GAP1-N2+GAP1-M+GAP1-C	HSP70→ TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2-2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2-2→	887	Frankia sp. NRRL B-16219	GCA_001854695.1	actinobacteria
WP_071239805.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2-2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	961	Paenibacillus sp. LC231	GCA_001860225.1	firmicutes
WP_071289221.1	GAP1-N2+GAP1-M+GAP1-C	GrpE→ HSP70→ TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2-2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2-2→?→ HSP70→ vWA(canonical)→	802	Mycolicibacterium llatzerense	GCF_001865165.1	actinobacteria
WP_071339378.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	789	Streptomyces albidoflavus	GCF_001862795.1	actinobacteria

acc	architecture	operon	len	species	gca	taxend
WP_071386702.1	GAP1-N2+GAP1-M+GAP1-C	ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→	832	Streptomyces sp. MUSC 1	GCA_001866665.1	actinobacteria
WP_071409829.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→ polar_leader+TM+TM+TM→	564	Corynebacterium sp.	GCA_001813735.1	actinobacteria
WP_071621470.1	GAP1-N2+GAP1-M+GAP1-C	TPR_containing_alpha_helical+Fibronectin-like_repeats+extended_insert+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→	903	Nocardiopsis dassonville1	GCA_001837055.1	actinobacteria
WP_071682263.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	863	Streptomyces cinnamoceus	GCF_001882765.1	actinobacteria
WP_072333659.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+Cadherin-like	TM+vWA(canonical)+YrKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+Cadherin-like*→	919	Paenibacillus	GCA_900101595.1	firmicutes
WP_072417066.1	GAP1-N2+GAP1-M+GAP1-C	GrpE→ HSP70→ ZnR+ZnR+DO-GTPase2.2→?→?→ GAP1-N2+GAP1-M+GAP1-C*→	1016	Ruminococcus	GCA_900103235.1	firmicutes
WP_072485992.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	820	Streptomyces atratus	GCA_900119365.1	actinobacteria
WP_072537017.1	GAP1-N2+GAP1-M+GAP1-C	TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→ GrpE→ HSP70→ HSP70+vWA(canonical)→ Dna2+Dna2+ZnR+ZnR+coiled_coil→Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→	866	Anaerococcus mediterraneensis	GCF_900128415.1	firmicutes
WP_072634855.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→	921	Rhodococcus sp. M8	actinobacteria	
WP_072728943.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YrKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	935	Paenibacillus sp. NAIST15-1	GCF_001894745.1	firmicutes
WP_072736015.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YrKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	1058	Paenibacillus sp. oc031	GCA_900099615.1	firmicutes
WP_072804085.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→	906	Rhodococcus yunnanensis	GCF_001895005.1	actinobacteria
WP_072845703.1	GAP1-N2+GAP1-M+GAP1-C	Tubulin+alpha_helical+??+??→ GAP_unknown2→ HRDC-like?→ Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→	922	Rhodococcus tukisamuensis	GCF_900107015.1	actinobacteria
WP_072944212.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→	914	Rhodococcus koreensis	GCA_900105905.1	actinobacteria
WP_072969113.1	GAP1-N2+GAP1-M+GAP1-C	HSP70→ HSP70+vWA(canonical)→?→?→ Dna2+Dna2+ZnR+ZnR+coiled_coil→Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→	879	Rhodococcus fascibiens	GCF_900113025.1	actinobacteria
WP_073186675.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→?→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→?→?→DO-GTPase2.2→	452	Tessaracoccus bendigoensis	GCA_900141915.1	actinobacteria
WP_073193137.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	831	Streptomyces sp. NBRC 110465	GCF_001985105.1	actinobacteria
WP_073563615.1	GAP1-N2+GAP1-M+GAP1-C	TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→	924	Rhodococcus	GCA_002340155.1	actinobacteria
WP_073754663.1	GAP1-N2+GAP1-M+GAP1-C	GrpE→ HSP70→ TPR_containing_alpha_helical+Fibronectin-like_repeats+extended_insert+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→	805	Nocardiopsis flavescens	GCA_900141985.1	actinobacteria
WP_073535728.1	GAP1-N2+GAP1-M+GAP1-C	Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→ TM+vWA(canonical)+YrKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→	887	Clostridium khuyani	GCA_001902255.1	firmicutes
WP_073702812.1	GAP1-N2+GAP1-M+GAP1-C	TPR_containing_alpha_helical+Fibronectin-like_repeats+extended_insert+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→	926	Nocardiopsis sp. TSRI0078	GCA_001965145.1	actinobacteria
WP_073719141.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	807	Streptomyces sp. TSRI0281	GCA_001965165.1	actinobacteria
WP_073748900.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	825	Streptomyces sp. CB02488	GCA_001965365.1	actinobacteria
WP_073743189.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	822	Streptomyces sp. CB02115	GCA_001965545.1	actinobacteria
WP_073748419.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	804	Streptomyces sp. CB02058	GCA_001965505.1	actinobacteria
WP_073764134.1	GAP1-N2+GAP1-M+GAP1-C	TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM→ vWA(canonical)→ PP2C→ Pkinase+ZnR+beta-rich→	820	Streptomyces sp. CB02923	GCA_001965005.1	actinobacteria
WP_073778800.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	836	Streptomyces sp. TSRI0445	GCA_001965495.1	actinobacteria
WP_073783338.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	836	Streptomyces sp. CB01580	GCA_001965795.1	actinobacteria
WP_073829567.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	830	Streptomyces sp. CB02130	GCA_001965785.1	actinobacteria
WP_073846654.1	GAP1-N2+GAP1-M+GAP1-C+TM	vWA(canonical)+beta-rich+low_complexity→ Tubulin+alpha_helical+??+??→?+??→ TM+vWA(canonical)+TM+TM+TM+TM+??→ Pkinase+TM→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C+TM*	476	Amycolatopsis sp. CB00013	GCA_001965755.1	actinobacteria
WP_073861388.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	815	Streptomyces sp. CB01249	GCA_001965735.1	actinobacteria
WP_073869343.1	GAP1-N2+GAP1-M+GAP1-C	TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM→ vWA(canonical)→ PP2C→ Pkinase+ZnR+beta-rich→[=e-7e-7]{GAP1-N2+GAP1-M+GAP1-C→	823	Streptomyces sp. CB00072	GCA_001965575.1	actinobacteria
WP_073869557.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→ TM→ vWA(canonical)→ PP2C→ Pkinase+ZnR+beta-rich→[=e-7e-7]{GAP1-N2+GAP1-M+GAP1-C*→	823	Streptomyces sp. CB00072	GCA_001965615.1	actinobacteria
WP_073881706.1	GAP1-N2+GAP1-M+GAP1-C	TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM→ vWA(canonical)→ PP2C→ Pkinase+ZnR+beta-rich→	855	Streptomyces sp. CB00316	GCA_001965095.1	actinobacteria
WP_073884323.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→	577	Corynebacterium variabile	GCA_900015285.1	actinobacteria
WP_073906875.1	GAP1-N2+GAP1-M+GAP1-C	TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM→ vWA(canonical)→ PSE→ Pkinase+ZnR+beta-rich→	824	Streptomyces sp. CB02009	GCA_001965635.1	actinobacteria
WP_073907729.1	GAP1-N2+GAP1-M+GAP1-C	GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→ TM+DUF4190+TM+PhzH_C→ TM+DUF4190+TM+PhzH_C→	826	Mycobacterium sp. SWH-M1	GCA_001907615.1	actinobacteria
WP_073966105.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	815	Streptomyces sp. CB02460	GCA_001965705.1	actinobacteria
WP_074082948.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YrKA-like+TM+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	1030	Paenibacillus sp. P32E	GCA_001990085.1	firmicutes
WP_074102861.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail	Tubulin+coiled_coil+HTH?→ TM+TM+TM+vWA+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C+polar_tail*→	1069	Paenibacillus xylanexedens	GCF_001886765.1	firmicutes
WP_074102231.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YrKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	1030	Paenibacillus sp. P3E	GCA_001990045.1	firmicutes
WP_074090944.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YrKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	1030	Paenibacillus sp. P2E	GCA_001990055.1	firmicutes
WP_074110925.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YrKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	1025	Paenibacillus sp. P4E	GCA_001990095.1	firmicutes
WP_074311874.1	GAP1-N2+GAP1-M+GAP1-C	DO-GTPase2.1→TM→ GAP1-N2+GAP1-M+GAP1-C*→	468	Singulisphaera sp. GP187	GCF_900129635.1	planctomycetes
WP_074315831.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	1117	Singulisphaera sp. GP187	GCF_900129635.1	planctomycetes
WP_074609604.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→	631	Corynebacterium	GCF_000610225.1	actinobacteria
WP_074919173.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→	631	Corynebacterium glutamicum	GCF_001912725.1	actinobacteria
WP_074505991.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→	631	Corynebacterium glutamicum	GCF_001912755.2	actinobacteria
WP_074508801.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→	631	Corynebacterium glutamicum	GCF_000828015.1	actinobacteria
WP_074648409.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YrKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	1037	Paenibacillus jilunlii	GCA_900102965.1	firmicutes
WP_074991131.1	GAP1-N2+GAP1-M+GAP1-C	PP2C→ Pkinase→?→?→?→ HSP70_domain_2+low_complexity+domain_betaX→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→	814	Streptomyces misionensis	GCA_900104815.1	actinobacteria

acc	architecture	operon	len	species	gca	taxend
WP_075998663.1	GAP1-N2+GAP1-M+GAP1-C	PP2C→ Pkinase–+?→+?→ HSP70_domain_2+low_complexity+domain_betaX→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→	862	Streptomyces ginglanensis	GCA_900111245.1	actinobacteria
WP_075092843.1	GAP1-N2+GAP1-M+TM+GAP1-C	DO-GTPase2.2→ GAP1-N2+GAP1-M+TM+GAP1-C*–+?+TM+?+beta-rich?→ GYF+GYF+Trypsin→	874	Planctomyces sp. SH-PL14	GCF_001610835.1	planctomycetes
WP_075093035.1	GAP1-N2+GAP1-M+TM+GAP1-C	ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+TM+GAP1-C*–+?+TM+?+beta-rich?→ GYF+GYF+Trypsin→ Pkinase+low_complexity+TM→	907	Planctomyces sp. SH-PL14	GCF_001610835.1	planctomycetes
WP_075154132.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YrKA-like+TM+?→ Tubulin+coiled_coil+?→ Tubulin+coiled_coil+HTH?+?→ TM+TM+TM+vWA(canonical)+TM+TM+polar_tail→ Fibronectin-like_repeats+?→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C*→ +?+DO-GTPase2.2→	1002	Paenibacillus polymyxa	GCA_001922145.1	firmicutes
WP_075249970.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+?7+?→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ +?+DO-GTPase2.2→	934	Actinomyces oris	GCA_001929075.1	actinobacteria
WP_075348368.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+?7+?→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)+?7+DO-GTPase2.2→	631	Corynebacterium glutamicum	GCF_001936195.1	actinobacteria
WP_075373567.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+?7+?→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ +?+DO-GTPase2.2→	919	Actinomyces oris	GCA_001937455.1	actinobacteria
WP_075389620.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+?7+?→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ +?+DO-GTPase2.2→	920	Actinomyces oris	GCA_001937415.1	actinobacteria
WP_075392311.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+?7+?→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ +?+DO-GTPase2.2→	920	Actinomyces oris	GCA_001937725.1	actinobacteria
WP_075401773.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+?7+?→u[e-?]GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ +?→ +?+DO-GTPase2.2→	931	Actinomyces oris	GCA_001937425.1	actinobacteria
WP_075103382.1	GAP1-N2+GAP1-M+GAP1-C	TM+DUF4190+TM→ TM+DUF4190+TM→ polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+?7+?→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→?7+DO-GTPase2.2→	818	Mycobacterium kansasii	GCA_001638285.1	actinobacteria
WP_075343295.1	GAP1-N2+GAP1-M+GAP1-C	TM+DUF4190+TM→ TM+DUF4190+TM→ polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+?7+?→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→?7+DO-GTPase2.2→	818	Mycobacterium kansasii	GCA_001638275.1	actinobacteria
WP_075405858.1	GAP1-N2+GAP1-M+GAP1-C	TM+DUF4190+TM→ TM+DUF4190+TM→ polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+?7+?→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→?7+DO-GTPase2.2→	818	Mycobacterium kansasii	GCA_001638265.1	actinobacteria
WP_076939075.1	GAP1-N2+GAP1-M+GAP1-C	Tubulin+coiled_coil+?→ Tubulin+coiled_coil+HTH?+?→ SP+vWA+YrKA-like+TM+?→ Tubulin+coiled_coil→ Fibronectin-like_repeats+?→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ +?→	727	Bacillus sp. MBMB1	GCF_001931005.1	firmicutes
WP_076691160.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+?7+?→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→?7+DO-GTPase2.2→	792	Corynebacterium sphenisci	GCA_001941505.1	actinobacteria
WP_076792445.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+?7+?→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→?7+DO-GTPase2.2→	793	Corynebacterium aquilae	GCF_001941415.1	actinobacteria
WP_075298333.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+?7+?→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→?7+DO-GTPase2.2→ polar_leader+TM+TM+TM→	512	Corynebacterium flavescens	GCA_003394655.1	actinobacteria
WP_075861320.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+?7+?→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→?7+DO-GTPase2.2→	780	Corynebacterium	GCA_001683055.1	actinobacteria
WP_076910681.1	GAP1-N2+GAP1-M+GAP1-C	HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→?7+DO-GTPase2.2→	819	Mycobacterium sp. 27335	GCA_001936205.1	actinobacteria
WP_075924409.1	GAP1-N2+GAP1-M+GAP1-C	HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→?7+DO-GTPase2.2→	819	Mycobacterium porcinum	GCF_001942005.1	actinobacteria
WP_076682175.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	780	Streptomyces sp. FH-008	GCF_001631705.1	actinobacteria
WP_076078930.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YrKA-like+TM+?7→ Tubulin+coiled_coil+HTH?+?→ TM+TM+TM+vWA(canonical)+TM+TM+polar_tail→ Fibronectin-like_repeats+?7→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	1057	Paenibacillus sp. FSL R7-0333	GCA_001955915.1	firmicutes
WP_076958584.1	GAP1-N2+GAP1-M+GAP1-C	GrpE→ HSP70→ TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+Inlb_coil+beta-sandwich→i[e-?]STAND_NTPase+TM+TM+TM+TM+TM	877	Oceanisphaera sp. DITIB 2501	GCF_000935685.1	firmicutes
WP_076099552.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YrKA-like+TM+?7→ Tubulin+coiled_coil+HTH?+?→ TM+TM+TM+vWA(canonical)+TM+TM+polar_tail→ Fibronectin-like_repeats+?7→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	998	Paenibacillus odoriifer	GCF_001945285.1	firmicutes
WP_076102241.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YrKA-like+TM+?7→ Tubulin+coiled_coil+HTH?+?→ TM+TM+TM+vWA(canonical)+TM+TM+polar_tail→ Fibronectin-like_repeats+?7→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	998	Paenibacillus odoriifer	GCF_001945245.1	firmicutes
WP_076110325.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YrKA-like+TM+?7→ Tubulin+coiled_coil+HTH?+?→ TM+TM+TM+vWA(canonical)+TM+TM+polar_tail→ Fibronectin-like_repeats+?7→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	1050	Paenibacillus borealis	GCA_001944415.1	firmicutes
WP_076119840.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YrKA-like+TM+?7→ Tubulin+coiled_coil+HTH?+?→ TM+TM+TM+vWA(canonical)+TM+TM+polar_tail→ Fibronectin-like_repeats+?7→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	994	Paenibacillus odoriifer	GCF_001944425.1	firmicutes
WP_076295865.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YrKA-like+TM+?7→ Tubulin+coiled_coil+HTH?+?→ TM+TM+TM+vWA(canonical)+TM+TM+polar_tail→ Fibronectin-like_repeats+?7→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	998	Paenibacillus odoriifer	GCF_001945565.1	firmicutes
WP_076137120.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YrKA-like+TM+?7→ Tubulin+coiled_coil+HTH?+?→ TM+TM+TM+vWA(canonical)+TM+TM+polar_tail→ Fibronectin-like_repeats+?7→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	998	Paenibacillus odoriifer	GCF_003258535.1	firmicutes
WP_076155755.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YrKA-like+TM+?7→ Tubulin+coiled_coil+HTH?+?→ TM+TM+TM+vWA(canonical)+TM+TM+polar_tail→ Fibronectin-like_repeats+?7→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	998	Paenibacillus odoriifer	GCF_003255755.1	firmicutes
WP_076147313.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YrKA-like+TM+?7→ Tubulin+coiled_coil+HTH?+?→ TM+TM+TM+vWA(canonical)+TM+TM+polar_tail→ Fibronectin-like_repeats+?7→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	998	Paenibacillus odoriifer	GCF_001957565.1	firmicutes
WP_076157515.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YrKA-like+TM+?7→ Tubulin+coiled_coil+HTH?+?→ TM+TM+TM+vWA(canonical)+TM+TM+polar_tail→ Fibronectin-like_repeats+?7→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	1002	Paenibacillus glucanolyticus	GCF_001957585.1	firmicutes
WP_076150913.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail	TM+TM+TM+vWA+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+?7→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C+polar_tail*→	1055	Paenibacillus sp. FSL R7-0337	GCA_001959295.1	firmicutes
WP_076172963.1	GAP1-N2+GAP1-M+GAP1-C	GrpE→ HSP70→ TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ PSE–+?→ HSP70→ vWA(canonical)–i[e-?]s–?→ SelB2Tb→ unknown+CASPASE	818	Amycolatopsis coloradensis	GCF_001729654.1	actinobacteria
WP_076160261.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YrKA-like+TM+?7→ Tubulin+coiled_coil+HTH?+?→ TM+TM+TM+vWA(canonical)+TM+TM+polar_tail→ Fibronectin-like_repeats+?7→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	1002	Paenibacillus peoriae	GCF_001956115.1	firmicutes
WP_076172896.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YrKA-like+TM+?7→ Tubulin+coiled_coil+HTH?+?→ TM+TM+TM+vWA(canonical)+TM+TM+polar_tail→ Fibronectin-like_repeats+?7→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	1087	Paenibacillus rhinophaenae	GCF_001956185.1	firmicutes
WP_076190370.1	GAP1-N2+GAP1-M+GAP1-C	Tubulin+alpha_helical+?7+?→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→?7+DO-GTPase2.2→	828	Mycobacterium fortuitum	GCF_001956035.1	actinobacteria
WP_076182336.1	GAP1-N2+GAP1-M+GAP1-C	HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→?7+DO-GTPase2.2→	820	Mycolicibacterium fortuitum	GCF_001954035.1	actinobacteria
WP_076194144.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YrKA-like+TM+?7→ Tubulin+coiled_coil+HTH?+?→ TM+TM+TM+vWA(canonical)+TM+TM+polar_tail→ Fibronectin-like_repeats+?7→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	998	Paenibacillus odoriifer	GCF_001954155.1	firmicutes
WP_076194147.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YrKA-like+TM+?7→ Tubulin+coiled_coil+HTH?+?→ TM+TM+TM+vWA(canonical)+TM+TM+polar_tail→ Fibronectin-like_repeats+?7→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	998	Paenibacillus odoriifer	GCF_001954145.1	firmicutes
WP_076195135.1	GAP1-N2+GAP1-M+GAP1-C	HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→?7+DO-GTPase2.2→	816	Mycobacterium sp. GA-1841	GCF_001954135.1	actinobacteria
WP_076207257.1	GAP1-N2+GAP1-M+GAP1-C	HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→?7+DO-GTPase2.2→	820	Mycolicibacterium fortuitum	GCF_001954145.1	actinobacteria
WP_076207455.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YrKA-like+TM+?7→ Tubulin+coiled_coil+HTH?+?→ TM+TM+TM+vWA(canonical)+TM+TM+polar_tail→ Fibronectin-like_repeats+?7→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	998	Paenibacillus odoriifer	GCF_001954595.1	firmicutes
WP_076209732.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YrKA-like+TM+?7→ Tubulin+coiled_coil+HTH?+?→ TM+TM+TM+vWA(canonical)+TM+TM+polar_tail→ Fibronectin-like_repeats+?7→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	1072	Paenibacillus sp. FSL R5-0765	GCA_001958855.1	firmicutes
WP_076105721.1	GAP1-N2+GAP1-M+GAP1-C	HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→?7+DO-GTPase2.2→	819	Mycolicibacterium conceptionense	GCF_001954265.1	actinobacteria
WP_076214936.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YrKA-like+TM+?7→ Tubulin+coiled_coil+HTH?+?→ TM+TM+TM+vWA(canonical)+TM+TM+polar_tail→ Fibronectin-like_repeats+?7→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	998	Paenibacillus odoriifer	GCF_001954655.1	firmicutes
WP_076219742.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	Tubulin+coiled_coil+?→ Tubulin+coiled_coil+HTH?+?→ TM+TM+TM+vWA(canonical)+TM+TM+polar_tail→ Fibronectin-like_repeats+?7→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	853	Paenibacillus odoriifer	GCF_001955595.1	firmicutes
WP_076219571.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YrKA-like+TM+?7→ Tubulin+coiled_coil+HTH?+?→ TM+TM+TM+vWA(canonical)+TM+TM+polar_tail→ Fibronectin-like_repeats+?7→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	998	Paenibacillus odoriifer	GCF_001955775.1	firmicutes
WP_076228825.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+Cadherin-like	TM+vWA(canonical)+YrKA-like+TM+?7→ Tubulin+coiled_coil+?→ Tubulin+coiled_coil+HTH?+?→ TM+TM+TM+vWA(canonical)+TM+TM+polar_tail→ Fibronectin-like_repeats+?7→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+Cadherin-like*→	962	Paenibacillus sp. FSL R7-0331	GCF_001956045.1	firmicutes
WP_076305572.1	GAP1-N2+GAP1-M+GAP1-C	HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→?7+DO-GTPase2.2→	816	Mycobacterium sp. NS-7484	GCF_001956275.1	actinobacteria
WP_076247349.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YrKA-like+TM+?7→ Tubulin+coiled_coil+HTH?+?→ TM+TM+TM+vWA(canonical)+TM+TM+polar_tail→ Fibronectin-like_repeats+?7→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	1070	Paenibacillus sp. FSL R8-0259	GCA_001956105.1	firmicutes
WP_076253673.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YrKA-like+TM+?7→ Tubulin+coiled_coil+HTH?+?→ TM+TM+TM+vWA(canonical)+TM+TM+polar_tail→ Fibronectin-like_repeats+?7→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	1067	Paenibacillus	GCA_001956175.1	firmicutes

acc	architecture	operon	len	species	gca	taxend
WP_076265333.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+T1M+beta-rich	TM+vWA(canonical)+YiKA-like+TM+??-→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	1002	Paenibacillus peoriae	GCA_001956235.1	firmicutes
WP_076269554.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+T1M+beta-rich	TM+vWA(canonical)+YiKA-like+TM+??-→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	982	Paenibacillus sp. FSL A5-0031	GCA_001956295.1	firmicutes
WP_076274908.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+T1M+beta-rich	TM+vWA(canonical)+YiKA-like+TM+??-→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	998	Paenibacillus odoriifer	GCA_001954335.1	firmicutes
WP_076278424.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+T1M+beta-rich	TM+vWA(canonical)+YiKA-like+TM+??-→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	998	Paenibacillus odoriifer	GCA_001954535.1	firmicutes
WP_076279866.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+T1M+beta-rich	TM+vWA(canonical)+YiKA-like+TM+??-→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	998	Paenibacillus odoriifer	GCA_001954675.1	firmicutes
WP_076282101.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+T1M+beta-rich	TM+vWA(canonical)+YiKA-like+TM+??-→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	998	Paenibacillus odoriifer	GCA_001955555.1	firmicutes
WP_076283866.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+T1M+beta-rich	TM+vWA(canonical)+YiKA-like+TM+??-→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	996	Paenibacillus odoriifer	GCA_001955545.1	firmicutes
WP_076287520.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail	TM+TM+TM+vWA+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C+polar_tail*→	1045	Paenibacillus pabuli	GCF_001955985.1	firmicutes
WP_076294127.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+T1M+beta-rich	TM+vWA(canonical)+YiKA-like+TM+??-→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	1002	Paenibacillus peoriae	GCA_001956155.1	firmicutes
WP_076294815.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+T1M+beta-rich	TM+vWA(canonical)+YiKA-like+TM+??-→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	1002	Paenibacillus peoriae	GCA_001956235.1	firmicutes
WP_076296144.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+T1M+beta-rich	TM+vWA(canonical)+YiKA-like+TM+??-→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	998	Paenibacillus odoriifer	GCA_001954375.1	firmicutes
WP_076299415.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+T1M+beta-rich	TM+vWA(canonical)+YiKA-like+TM+??-→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	996	Paenibacillus odoriifer	GCA_001954115.1	firmicutes
WP_076302827.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+T1M+beta-rich	TM+vWA(canonical)+YiKA-like+TM+??-→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	998	Paenibacillus odoriifer	GCA_001954495.1	firmicutes
WP_076305163.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+T1M+beta-rich	TM+vWA(canonical)+YiKA-like+TM+??-→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	998	Paenibacillus odoriifer	GCA_001954615.1	firmicutes
WP_076307182.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+T1M+beta-rich	TM+vWA(canonical)+YiKA-like+TM+??-→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	998	Paenibacillus odoriifer	GCA_001954585.1	firmicutes
WP_076309565.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+T1M+beta-rich	TM+vWA(canonical)+YiKA-like+TM+??-→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	998	Paenibacillus odoriifer	GCA_001954655.1	firmicutes
WP_076309542.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+T1M+beta-rich	TM+vWA(canonical)+YiKA-like+TM+??-→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	998	Paenibacillus odoriifer	GCA_001955495.1	firmicutes
WP_076316988.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+T1M+beta-rich	TM+vWA(canonical)+YiKA-like+TM+??-→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	998	Paenibacillus odoriifer	GCA_001955835.1	firmicutes
WP_076319295.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail	Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C+polar_tail*→	1067	Paenibacillus amylolyticus	GCA_001925095.1	firmicutes
WP_076325290.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+T1M+beta-rich	TM+vWA(canonical)+YiKA-like+TM+??-→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	991	Paenibacillus lautus	GCA_001952975.1	firmicutes
WP_076332455.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+T1M+beta-rich	TM+vWA(canonical)+YiKA-like+TM+??-→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	1061	Paenibacillus amylolyticus	GCA_003324555.1	firmicutes
WP_076335950.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+T1M+beta-rich	TM+vWA(canonical)+YiKA-like+TM+??-→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	1004	Paenibacillus sp. FSL H8-0548	GCA_001956095.1	firmicutes
WP_076345505.1	GAP1-N2+GAP1-M+GAP1-C	ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→??+TM+??+beta-rich?→	788	Paludibacter propionicigenes	GCA_001925085.1	planctomycetes
WP_076347977.1	GAP1-N2+GAP1-M	GAP1-N2+GAP1-M*→	231	Paludisphaera borealis	GCA_001956985.1	planctomycetes
WP_076349998.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→ vWA(canonical)→ PP2C→ Pkinase+ZnR+beta-rich→	790	Streptomyces albaflav	GCA_001957995.1	actinobacteria
WP_076376054.1	GAP1-N2+GAP1-M+TM+TM	PP2C→?→ DO-GTPase2.1→ GAP1-N2+GAP1-M+TM+TM*→	389	Lachnoclostridium phocaeense	GCF_900120345.1	firmicutes
WP_076393656.1	GAP1-N2+GAP1-M+GAP1-C	GrpE→ HSP70→ TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→	879	Frankia asymbiotica	GCA_001963105.1	actinobacteria
GAP1-N2+GAP1-M+GAP1-C+ZnR+DO-GTPase2	GAP1-N2+GAP1-M+GAP1-C*→	GAP1-N2+GAP1-M+GAP1-C+ZnR+DO-GTPase2*→	954	Frankia sp. CcI49	GCA_002592015.1	actinobacteria
WP_076966755.1	GAP1-N2+GAP1-M+GAP1-C	TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM→ vWA(canonical)→ PP2C→ Pkinase+ZnR+beta-rich→	1246	Streptomyces sp. HB2014 011-1	GCA_001983395.1	actinobacteria
WP_076993471.1	GAP1-N2+GAP1-M+GAP1-C+TM+beta-rich	vWA(canonical)+beta-rich+low_complexity+??→ TM+TM+TM+TM+??→ Pkinase+??→ GAP1-N2+GAP1-M+GAP1-C+TM+beta-rich*→	610	Saccharothrix sp. ALI-22-I	GCA_001984175.1	actinobacteria
WP_076269422.1	GAP1-N2+GAP1-M+TM	ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+TM*→	370	Faresia marisgermanicae	GCF_001983935.1	planctomycetes
WP_076013475.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→ vWA(canonical)→ PP2C→ Pkinase+ZnR+beta-rich→	1127	Streptomyces sp. MP131-18	GCA_001984575.1	actinobacteria
WP_076763430.1	GAP1-N2+GAP1-M+GAP1-C	TM+TM+TM+TM+TM+TM+DO-GTPase2.1→ GAP1-N2+GAP1-M+GAP1-C*→??→ TM_region+DO-GTPase1→	55	Cuniculiplasma divulgatum	GCA_900090055.1	euryarchaeota
WP_076992367.1	GAP1-N2+GAP1-M+GAP1-C	TM+DUF4190+TM→ TM+DUF4190+TM→ polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ PSE→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ PSE→ GAP1-M-GAP1-C*→ PSE→?→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→ TM+DUF4190+TM+PknH_C→ TM+DUF4190+TM+PknH_C→ TM+DUF4190+TM+PknH_C→ TM+DUF4190+TM+PknH_C→	1000	Mycobacterium colombiense	GCF_000277835.1	actinobacteria
WP_076313322.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→	631	Corynebacterium glutamicum	GCA_000732735.1	actinobacteria
WP_076343605.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→?→??+DO-GTPase2.2→	864	Streptomyces flavus	GCA_001997295.1	actinobacteria
WP_073499637.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→?→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→?→??+DO-GTPase2.2→	456	Tessaracoccus flavescens	GCA_001998865.1	actinobacteria
WP_076997249.1	GAP1-N2+GAP1-M+GAP1-C	??+TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→?→?→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→?→??+DO-GTPase2.2→	455	Tessaracoccus aquimaris	GCF_001998275.1	actinobacteria
WP_076933371.1	GAP1-N2+GAP1-M+GAP1-C	TPR_containing_alpha_helical+Fibronectin-like_repeats+extended_insert+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→	932	Nocardiopsis sinuspersici	GCA_001998325.1	actinobacteria
WP_077385220.1	GAP1-N2+GAP1-M+GAP1-C	HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→??+DO-GTPase2.2→	819	Mycobacterium hoenisei	GCA_002000005.1	actinobacteria
WP_079369054.1	GAP1-N2+GAP1-M+GAP1-C	GrpE→ HSP70→ TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→	814	Micromonospora sp. Rc5	GCA_002006875.1	actinobacteria
WP_076749715.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→ vWA(canonical)→ PP2C→ Pkinase+ZnR+beta-rich→	866	Streptomyces silvens	GCA_002009175.1	actinobacteria
WP_078501498.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+T1M+beta-rich	TM+vWA(canonical)+YiKA-like+TM+??-→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	968	Paenibacillus selenitireducens	GCA_002021565.1	firmicutes
WP_078332238.1	GAP1-N2+GAP1-M+GAP1-C	TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM→ vWA(canonical)→ PP2C→ Pkinase+ZnR+beta-rich→?→?→?(GAP1-N2+GAP1-M+GAP1-C*→	813	Streptomyces sp. SceaMP-e10	GCF_002073405.1	actinobacteria
WP_078543661.1	GAP1-N2+GAP1-M+GAP1-C	GrpE→ HSP70→ HSP70→vWA→ DnaJ→DnaJ+ZnR+ZnR+coiled_coil+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→	859	Bacillus alkalidiluria	GCF_002019645.1	firmicutes
WP_078570212.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	835	Streptomyces sp. CNS654	GCF_000702365.1	actinobacteria
WP_078593212.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	848	Streptomyces	GCF_000717015.1	actinobacteria
WP_078585189.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	822	Streptomyces auratus	GCF_000717105.1	actinobacteria
WP_076609864.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	840	Streptomyces albus	GCF_000717065.1	actinobacteria
WP_076611209.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	840	Streptomyces baarnensis	GCF_000716025.1	actinobacteria
WP_076612249.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	848	Streptomyces vinaceus	GCF_000717215.1	actinobacteria

acc	architecture	operon	len	species	gca	taxend
WP_078613167.1	GAP1-N2+GAP1-M		834	Streptomyces kaznie	-	actinobacteria
WP_078615787.1	GAP1-N2+GAP1-M+GAP1-C	TM+TM+TM+TM+ZnR+D0-GTPase2:2+TM→ vWA(canonical)→ PP2C→ Pkinase+ZnR+beta-rich→[=-?+-?=-?]GAP1-N2+GAP1-M+GAP1-C*→	813	Streptomyces cyaneofuscatus	GCF_000718135.1	actinobacteria
WP_078621939.1	GAP1-N2+GAP1-M		865	Streptomyces sp. NRRL S-244	-	actinobacteria
WP_078625710.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	837	Streptomyces sp. CNB091	GCF_000377965.1	actinobacteria
WP_078639163.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	845	Streptomyces	GCF_000718915.1	actinobacteria
WP_078652198.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	836	Streptomyces globisporus	GCF_000718455.1	actinobacteria
WP_078654160.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	835	Streptomyces albus	GCF_000716945.1	actinobacteria
WP_078657336.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	812	Streptomyces	GCF_002633395.1	actinobacteria
WP_078696301.1	GAP1-N2+GAP1-M+GAP1-C	PNPase→?→ GAP1-N2+GAP1-M+GAP1-C*→	826	Caloramator quinhayensis	GCA_900165905.1	firmicutes
WP_078845919.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	841	Streptomyces albus	GCF_000720915.1	actinobacteria
WP_078859204.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	845	Streptomyces sp. NRRL F-2202	GCF_000719925.1	actinobacteria
WP_078860453.1	GAP1-N2+GAP1-M		841	Streptomyces sp. NRRL F-2747	-	actinobacteria
WP_078866750.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	845	Streptomyces griseus group	GCF_000718695.1	actinobacteria
WP_078874115.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	848	Streptomyces sp. NRRL F-5702	GCF_000721415.1	actinobacteria
WP_078879411.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	848	Streptomyces sp. NRRL F-5681	GCF_000719585.1	actinobacteria
WP_078883214.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	848	Streptomyces	GCF_000720065.1	actinobacteria
WP_078890683.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	848	Streptomyces sp. NRRL B-1381	GCF_000719655.1	actinobacteria
WP_078906652.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	812	Streptomyces sp. NRRL S-623	GCF_000723705.1	actinobacteria
WP_078935843.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	845	Streptomyces sp. NRRL F-2295	GCF_001275813.1	actinobacteria
WP_078951059.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	848	Streptomyces griseus	GCF_000718235.1	actinobacteria
WP_078955675.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	826	Streptomyces griseus group	GCA_003147545.1	actinobacteria
WP_078968860.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	845	Streptomyces sp. MMG1522	GCF_001279735.1	actinobacteria
WP_078987566.1	GAP1-N2+GAP1-M		886	Streptomyces sp. XY332	-	actinobacteria
WP_079036103.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	811	Streptomyces luridiscabiei	GCF_001418625.1	actinobacteria
WP_079139809.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	838	Streptomyces sp. EN23	GCF_001736365.1	actinobacteria
WP_079137652.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	826	Streptomyces sp. PTY087E2	GCA_001687325.1	actinobacteria
WP_079149733.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	846	Streptomyces sp. EN27	GCF_001736315.1	actinobacteria
WP_079181260.1	GAP1-N2+GAP1-M+GAP1-C	TM+TM+TM+TM+ZnR+D0-GTPase2:2+TM→ vWA(canonical)→ PP2C→ Pkinase+ZnR+beta-rich→[=-?+-?=-?]GAP1-N2+GAP1-M+GAP1-C*→	812	Streptomyces sp. CB00316	GCF_001905505.1	actinobacteria
WP_079181421.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	826	Streptomyces sp. Tue 6075	GCF_001931635.1	actinobacteria
WP_079182575.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	822	Streptomyces sp. TSRB0605	GCF_001905525.1	actinobacteria
WP_079190473.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	835	Streptomyces sp. CB02366	GCF_001905905.1	actinobacteria
WP_079253362.1	GAP1-N2+GAP1-M+GAP1-C	TM+TM+TM+TM+ZnR+D0-GTPase2:2+TM→ vWA(canonical)→ PP2C→ Pkinase+ZnR+beta-rich→[=-?+-?=-?]GAP1-N2+GAP1-M+GAP1-C*→	812	Streptomyces sp. HB2011 011-1	GCA_003635045.1	actinobacteria
WP_079272259.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	838	Streptomyces sp. TSRB0261	GCA_001965485.1	actinobacteria
WP_079347725.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YrKA-like+TM+?? → Tubulin+coiled_coil+?? → PSE→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+?? → ZnR+ZnR+D0-GTPase2:2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	1070	Paenibacillus sp. VT-16-81	GCA_003027255.1	firmicutes
WP_079433033.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	618	Streptomyces katrae	GCA_003814735.1	actinobacteria
WP_079005523.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YrKA-like+TM+?? → Tubulin+coiled_coil+?? → Tubulin+coiled_coil+HTH?+?? → TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+?? → ZnR+ZnR+D0-GTPase2:2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	1057	Paenibacillus	GCA_900168365.1	firmicutes
WP_079013482.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+Cadherin-like	TM+vWA(canonical)+YrKA-like+TM+?? → Tubulin+coiled_coil+?? → Tubulin+coiled_coil+HTH?+?? → TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+?? → ZnR+ZnR+D0-GTPase2:2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+Cadherin-like*→	974	Paenibacillus sp. 32352	GCA_002046965.1	firmicutes
WP_080793004.1	GAP1-N2+GAP1-M+GAP1-C	TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+?? → GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→ polar_leader+TM+TM+TM→	529	Corynebacterium sp.	GCF_900169525.1	actinobacteria
WP_080807098.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→?→	984	Marseille-P2417	-	
WP_080109969.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+?? → GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→	1070	Paenibacillus gallinarum	GCA_900318955.1	firmicutes
WP_081558132.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+?? → GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→	631	Corynebacterium glutamicum	GCF_001549955.2	actinobacteria
WP_082936370.1	GAP1-N2+GAP1-M+GAP1-C	GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ GAP1-N2+GAP1-M+GAP1-C→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→	992	Rhodococcus sp. BH4	GCA_002079265.1	actinobacteria
WP_082868338.1	GAP1-N2+GAP1-M+GAP1-C	TM+TM+TM+ PSE→ Tubulin+alpha_helical+??+?? → GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→	150	Mycobacterium kansasii	GCA_002630025.1	actinobacteria
WP_083038677.1	GAP1-N2+GAP1-M+GAP1-C	TM+DUF4190+TM→ TM+DUF4190+TM→ polar_leader+TM+TM+TM→ PSE→ Tubulin+alpha_helical+??-??→[=PSE][PSE→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→	652	Corynebacterium cruzillactis	GCF_001643305.1	actinobacteria
WP_083099237.1	GAP1-N2+GAP1-M+GAP1-C	TM+DUF4190+TM→ TM+DUF4190+TM→ polar_leader+TM+TM+TM→ PSE→ Tubulin+alpha_helical+??-??→[=PSE][PSE→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→	827	Mycobacterium insubricum	GCA_002986255.1	actinobacteria
WP_083156298.1	GAP1-N2+GAP1-M+GAP1-C	TM+DUF4190+TM→ polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→ TM+DUF4190+TM+PknH_C→ TM+DUF4190+TM+PknH_C→ TM+DUF4190+TM+PknH_C→ TM+DUF4190+TM+PknH_C→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→	827	Mycobacterium massiliae	GCA_002986335.1	actinobacteria
WP_083164133.1	GAP1-N2+GAP1-M+GAP1-C	TM+DUF4190+TM→ polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+?? → GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→ TM+DUF4190+TM+PknH_C→ TM+DUF4190+TM+PknH_C→ TM+DUF4190+TM+PknH_C→ TM+DUF4190+TM+PknH_C→ GAP1-N2+GAP1-M+GAP1-C*→	828	Mycobacterium aquaticum	GCA_002986485.1	actinobacteria
WP_083326197.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	845	Streptomyces violaceoruber	GCA_002982175.1	actinobacteria
WP_081313735.1	GAP1-N2+GAP1-M+GAP1-C+ZnR+D0-GTPase2	GAP1-N2+GAP1-M+GAP1-C+ZnR+D0-GTPase2*→	885	Frankia sp. Cc1.17	GCF_001854655.1	actinobacteria
WP_084424213.1	GAP1-N2+GAP1-M+GAP1-C	GrpE→ HSP70→ TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+D0-GTPase2:2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+D0-GTPase2:2→?→ HSP70→ vWA(canonical)→ unknown+CASPASE→ HSP70→	819	Kibdelosporangium aridum	GCA_900176515.1	actinobacteria

acc	architecture	operon	len	species	gca	taxend
WP_084751128.1	GAP1:N2+GAP1:M+GAP1:C	GAP1:N2+GAP1:M+GAP1:C*→	813	Kitasatospora albolonga	GCA_003282585.1	actinobacteria
WP_084884445.1	GAP1:N2+GAP1:M+GAP1:C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?→Fibronectin-like_repeats→ GAP1:N2+GAP1:M+GAP1:C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→	842	Rhodococcus hoagii	GCA_003013675.1	actinobacteria
WP_084991422.1	GAP1:N2+GAP1:M	??→ PP2C→ Pkinase+helical_region+TM_region→ ZnR+ZnR+DO-GTPase2.2→ GAP1:N2+GAP1:M+low_complexity+TM+TM*→	877	Streptomyces sp. S8	GCA_000172175.1	actinobacteria
WP_085926611.1	GAP1:N2+GAP1:M+low_complexity+TM+TM	HSP70→ HSP70→vWA(canonical)→?→ DO-GTPase2.2(frag)→ GAP1:N2+GAP1:M+GAP1:C*→?→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→	536	Cumbaetor physomitrellae	GCA_002996055.1	actinobacteria
WP_085806797.1	GAP1:N2+GAP1:M+GAP1:C	HSP70→ HSP70→vWA(canonical)→?→ DO-GTPase2.2(frag)→ GAP1:N2+GAP1:M+GAP1:C*→?→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→	865	Amycolatopsis oryzae	GCA_001775151.1	alphaproteobacteria
WP_085906040.1	GAP1:N2+GAP1:M+GAP1:C	TM+DUF4190+TM→ TM+DUF4190+TM→ polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?→Fibronectin-like_repeats→ GAP1:N2+GAP1:M+GAP1:C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→	807	Mycolicibacterium fallax	GCA_002101995.1	actinobacteria
WP_085140691.1	GAP1:N2+GAP1:M+GAP1:C	HRDC-like?→Fibronectin-like_repeats→ GAP1:N2+GAP1:M+GAP1:C*→	819	Mycolicibacterium conceptionense	GCA_001052995.1	actinobacteria
WP_085143633.1	GAP1:N2+GAP1:M+GAP1:C	HRDC-like?→Fibronectin-like_repeats→ GAP1:N2+GAP1:M+GAP1:C*→?→ DO-GTPase2.2→	820	Mycolicibacterium wolinskyi	GCA_002101965.1	actinobacteria
WP_085153380.1	GAP1:N2+GAP1:M+GAP1:C	Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?→Fibronectin-like_repeats→ GAP1:N2+GAP1:M+GAP1:C*→ beta-rich+vWA(canonical)→ ZnR+ZnR+DO-GTPase2.2→	840	Mycolicibacterium confluentia	GCA_002102105.1	actinobacteria
WP_085160821.1	GAP1:N2+GAP1:M+GAP1:C	HRDC-like?→Fibronectin-like_repeats→ GAP1:N2+GAP1:M+GAP1:C*→?→ DO-GTPase2.2→	833	Mycolicibacterium doricum	GCA_002102211.1	actinobacteria
WP_085470330.1	GAP1:N2+GAP1:M+GAP1:C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?→Fibronectin-like_repeats→ GAP1:N2+GAP1:M+GAP1:C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→	909	Rhodococcus rhodochrous	GCA_900177095.1	actinobacteria
WP_085475630.1	GAP1:N2+GAP1:M+GAP1:C	GAP1:N2+GAP1:M+GAP1:C*→	780	Streptomyces albidoflavus	GCA_001580125.1	actinobacteria
WP_085494889.1	GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich*→	974	Paenibacillus agaitagani	GCA_900177815.1	firmicutes
WP_085503724.1	GAP1:N2+GAP1:M+GAP1:C	TM+vWA(canonical)+TM+beta-rich+lc_tail→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1:N2+GAP1:M+GAP1:C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→	653	Corynebacterium pilosum	GCA_900177241.1	actinobacteria
WP_085160702.1	GAP1:N2+GAP1:M+GAP1:C	GAP1:N2+GAP1:M+GAP1:C*→ PSE→ PP2C→ Pkinase+ZnR+beta-rich→?→?→|→TPR_containing_alpha_helical+Fibronectin-like_repeats→	520	Streptomyces sp. SCSIO 03032	GCA_002128305.1	actinobacteria
WP_086651033.1	GAP1:N2+GAP1:M+SLATT+SLATT	vWA(canonical)+beta-rich+low_complexity→ Tubulin+alpha_helical+??+??→??+TM+TM+TM+TM+??→ Pkinase+TM→ ZnR+ZnR+DO-GTPase2.2→ GAP1:N2+GAP1:M+SLATT+SLATT*→ TIR+??→?→?→ STAND_NTPase+TPR_region→	634	Lentzea kentuckyensis	GCA_002102765.1	actinobacteria
WP_086671185.1	GAP1:N2+GAP1:M+GAP1:C	GAP1:N2+GAP1:M+GAP1:C*→	826	Streptomyces albovinaceus	GCA_002154385.1	actinobacteria
WP_086778841.1	GAP1:N2+GAP1:M+GAP1:C	GAP1:N2+GAP1:M+GAP1:C*→	828	Streptomyces fimicarius	GCA_002154345.1	actinobacteria
WP_086876917.1	GAP1:N2+GAP1:M+GAP1:C	GAP1:N2+GAP1:M+GAP1:C*→ PSE→?→|→TPR_containing_alpha_helical+Fibronectin-like_repeats	792	Streptomyces cacaoi	GCA_006539715.1	actinobacteria
WP_086843588.1	GAP1:N2+GAP1:M+GAP1:C+TM+beta-rich	vWA(canonical)+beta-rich+low_complexity→?→?→ Tubulin+alpha_helical+??+??→??+TM+TM+TM+TM+??→ Pkinase+TM→ ZnR+ZnR+DO-GTPase2.2→ GAP1:N2+GAP1:M+GAP1:C+TM+beta-rich*→	578	Amycolatopsis kentuckyensis	GCA_002155975.1	actinobacteria
WP_086693405.1	GAP1:N2+GAP1:C	GAP1:M+GAP1:C*→	690	Streptomyces sulbenzyniticus	GCA_002154605.1	actinobacteria
WP_086892272.1	GAP1:N2+GAP1:M+GAP1:C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?→Fibronectin-like_repeats→ GAP1:N2+GAP1:M+GAP1:C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→ polar_leader+TM+TM+TM→	527	Corynebacterium striatum	GCA_002156805.1	actinobacteria
WP_087063585.1	GAP1:N2+GAP1:M+GAP1:C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?→Fibronectin-like_repeats→ GAP1:N2+GAP1:M+GAP1:C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→	631	Corynebacterium glutamicum	GCA_000166345.1	actinobacteria
WP_087081230.1	GAP1:N2+GAP1:M+GAP1:C	TM+DUF4190+TM→ polar_leader+TM+TM+TM→ PSE→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?→Fibronectin-like_repeats→ GAP1:N2+GAP1:M+GAP1:C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→ TM+DUF4190+TM+PknH_C→ TM+DUF4190+TM+PknH_C→ TM+DUF4190+TM+PknH_C→	828	Mycobacterium diouxanotrophicus	GCA_002157835.1	actinobacteria
WP_087016156.1	GAP1:N2+GAP1:M+GAP1:C	TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1:N2+GAP1:M+GAP1:C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→	659	Nocardiopsis sp. JB363	GCA_900143625.1	actinobacteria
WP_087117134.1	GAP1:N2+GAP1:M+GAP1:C	Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?→Fibronectin-like_repeats→ GAP1:N2+GAP1:M+GAP1:C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→	604	Corynebacterium	GCA_900155535.1	actinobacteria
WP_087166954.1	GAP1:N2+GAP1:M+GAP1:C	TM+vWA(canonical)+YtKA-like+IG-like+TM+??→ Tubulin+coiled_coil+??→?→?→ ZnR+insert+ZnR+DO-GTPase2.2+ZnR→ GAP1:N2+GAP1:M+GAP1:C*→ Pkinase→	816	Dranocottella sp. Au12	GCA_002160935.1	firmicutes
WP_087218558.1	GAP1:N2+GAP1:M+TM+GAP1:C+TM+TM+TM	Tubulin+coiled_coil+??→ Tubulin+coiled_coil+??→?→?→ ZnR+ZnR+DO-GTPase2.2→ GAP1:N2+GAP1:M+TM+GAP1:C+TM+TM+TM→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→	808	Lachnoclostridium sp. Au14	GCA_002160755.1	firmicutes
WP_087225596.1	GAP1:N2+GAP1:M+GAP1:C	Tubulin+coiled_coil+??→ Tubulin+coiled_coil+??→?→?→ ZnR+insert+ZnR+DO-GTPase2.2+??→ GAP1:N2+GAP1:M+GAP1:C*→?→?→ Pkinase→	953	Blautia sp. Au249	GCA_002159635.1	firmicutes
WP_087230700.1	GAP1:N2+GAP1:M+GAP1:C	GAP1:N2+GAP1:M+GAP1:C*→	923	Pseudoflavonifractor sp. Au176	GCA_002160435.1	firmicutes
WP_087348406.1	GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich*→	832	Brevibacillus brevis	GCA_002161835.1	firmicutes
WP_087435655.1	GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich*→	971	Paenibacillus apiarius	GCA_002161865.1	firmicutes
WP_087537243.1	GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich*→	1019	Paenibacillus thiaminolyticus	GCA_004001005.1	firmicutes
WP_087557944.1	GAP1:N2+GAP1:M+GAP1:C	GAP1:N2+GAP1:M+GAP1:C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→	914	Rhodococcus sp. NCIMB 12038	GCA_002165735.1	actinobacteria
WP_087765566.1	GAP1:N2+GAP1:M+GAP1:C	GAP1:N2+GAP1:M+GAP1:C*→	833	Streptomyces sp. CS057	GCA_002168345.1	actinobacteria
WP_087772534.1	GAP1:N2+GAP1:M+GAP1:C	GAP1:N2+GAP1:M+GAP1:C*→	780	Streptomyces sp. CS227	GCA_002168555.1	actinobacteria
WP_087799167.1	GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→?→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→?→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich*→	1140	Saccharibacillus sp. O16	GCA_002189105.1	firmicutes
WP_087682961.1	GAP1:N2+GAP1:M+GAP1:C	GAP1:N2+GAP1:M+GAP1:C*→ vWA(canonical)→ Pkinase+ZnR+beta-rich→|→TPR_containing_alpha_helical+Fibronectin-like_repeats	950	Streptomyces albolavus	GCA_002329675.1	actinobacteria
WP_087919925.1	GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich*→	1019	Paenibacillus donghaensis	GCA_002192415.1	firmicutes
WP_088069667.1	GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich*→	939	Bacillus sp. OV166	GCA_000172635.1	firmicutes
WP_088252361.1	GAP1:N2+GAP1:M+TM+low_complexity+TM	GAP1:N2+GAP1:M+TM+low_complexity+TM*→	828	Fimbriiglobus ruber	GCA_002197845.1	planctomycetes
WP_088294054.1	GAP1:N2+GAP1:M+TM+GAP1:C	GAP1:N2+GAP1:M+TM+GAP1:C*→	738	Fimbriiglobus ruber	GCA_002197845.1	planctomycetes
WP_088304970.1	GAP1:N2+GAP1:M+GAP1:C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?→Fibronectin-like_repeats→ GAP1:N2+GAP1:M+GAP1:C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→ TM+DUF4190+TM+PknH_C→ TM+DUF4190+TM+PknH_C→	828	Mycobacterium peregrinum	GCA_002198105.1	actinobacteria
WP_088488102.1	GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→?→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich*→	1136	Saccharibacillus sp. O23	GCA_002205995.1	firmicutes
WP_088548123.1	GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich*→	974	Paenibacillus sp. S-o	GCA_900188525.1	firmicutes
WP_088574934.1	GAP1:N2+GAP1:M+GAP1:C	GAP1:N2+GAP1:M+GAP1:C*→	835	Streptomyces sp. FgraA7	GCA_900187925.1	actinobacteria
WP_088631747.1	GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+Cadherin-like	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+Cadherin-like*→	936	Paenibacillus sigii	GCA_900188505.1	firmicutes
WP_088867775.1	GAP1:N2+GAP1:M+GAP1:C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?→Fibronectin-like_repeats→ GAP1:N2+GAP1:M+GAP1:C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→	909	Rhodococcus sp. BUPNP1	GCA_002215235.1	actinobacteria
WP_088920915.1	GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich*→	832	Bacillus sp. FJ2-1	GCA_002219505.1	firmicutes
WP_088943649.1	GAP1:N2+GAP1:M+GAP1:C	Gygl→ HSP70→ TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1:N2+GAP1:M+GAP1:C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→??→ HSP70→	802	Rhodococcus sp. I168	GCA_002891955.1	actinobacteria
WP_089000279.1	GAP1:N2+GAP1:M+GAP1:C	TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1:N2+GAP1:M+GAP1:C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→	797	Micromonospora echinofusca	GCA_900091445.1	actinobacteria

acc	architecture	operon	len	species	gca	taxend
WP_089146955.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	826	Streptomyces sp. SS07	GCF_002217715.1	actinobacteria
WP_089295102.1	GAP1-N2+GAP1-M+GAP1-C	HSP70→ TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C* → TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→ TPR_region+CASPASE→7-+[+-CASPASE+low_complexity	787	Actinoplanes regularis	GCA_900188005.1	actinobacteria
WP_089306581.1	GAP1-N2+GAP1-M+GAP1-C	Pkinase→TM→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ Pkinase+low_complexity→	556	Geodermatophilus polyvoris	GCF_900188275.1	actinobacteria
WP_089315832.1	GAP1-N2+GAP1-M+GAP1-C	GrpE→ HSP70→ TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C* → TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM→	740	Actinomadura mexicana	GCA_900188105.1	actinobacteria
WP_089326846.1	GAP1-N2+GAP1-M+GAP1-C	GrpE→ HSP70→ TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C* → TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM→	670	Actinomadura meyerae	GCA_900188415.1	actinobacteria
WP_089507784.1	GAP1-N2+GAP1-M+GAP1-C	PP2C→ Pkinase-+7-+7-+7-+ HSP70_domain_2+low_complexity+domain_betaX→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C* → TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→	817	Streptomyces sp. NBS 14/10	GCA_002224125.1	actinobacteria
WP_089509017.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	808	Streptomyces sp. NBS 14/10	GCA_002224125.1	actinobacteria
WP_089549257.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	1087	Pasnibacillus sp. SSG-1	GCA_002224835.1	firmicutes
WP_090263386.1	GAP1-N2+GAP1-M+GAP1-C	TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→7-→ HSP70→ HSP70+vWA(canonical)→ DnaJ+DnaJ+ZnR+ZnR+coiled_coil+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→	916	Eubacteriaceae bacterium	GCA_900067665.1	firmicutes
WP_090429383.1	GAP1-N2+GAP1-M+GAP1-C	HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→?7+DO-GTPase2→	819	Mycobacterium	CHBCR005	firmicutes
WP_090510225.1	GAP1-N2+GAP1-M+GAP1-C	HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→?7+DO-GTPase2→	819	Mycobacterium neworleansense	GCA_001215615.1	firmicutes
WP_090690001.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+Cadherin-like	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→?→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+Cadherin-like*→	933	Pasnibacillus tianmuensis	GCA_900100345.1	firmicutes
WP_090699615.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	935	Pasnibacillus typhae	GCA_900100955.1	firmicutes
WP_090761118.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	935	Bacillus sp. OK048	GCA_900103525.1	firmicutes
WP_090809575.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail	TM+TM+TM+vWA+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+GAP1-M+GAP1-C+polar_tail*→	1058	Pasnibacillus sp. 276b	GCA_900100575.1	firmicutes
WP_090834503.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	1028	Pasnibacillus sophorae	GCA_900110315.1	firmicutes
WP_090896958.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail	Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C+polar_tail*→	1009	Pasnibacillus sp. 181mfosf5.1	GCA_900109125.1	firmicutes
WP_090931630.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail	TM+TM+TM+vWA+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C+polar_tail*→	1057	Pasnibacillus sp. OK076	GCF_900110055.1	firmicutes
WP_090913398.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	991	Pasnibacillus sp. cl11a	GCA_900109305.1	firmicutes
WP_090921019.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	1071	Pasnibacillus polysaccharolyticus	GCA_900109325.1	firmicutes
WP_090952035.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	1057	Pasnibacillus sp. OK060	GCA_900101205.1	firmicutes
WP_090995055.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail	TM+TM+TM+vWA+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C+polar_tail*→	1060	Pasnibacillus sp. OK003	GCF_900100755.1	firmicutes
WP_091012817.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail	Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C+polar_tail*→	1072	Pasnibacillus amylolyticus	GCF_900095775.1	firmicutes
WP_091036116.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail	Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C+polar_tail*→	1063	Pasnibacillus sp. CF005	GCA_900101225.1	firmicutes
WP_091069568.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	1006	Pasnibacillus sp. NFR01	-	firmicutes
WP_091151701.1	GAP1-N2+GAP1-M+GAP1-C	Pkinase+TM→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→[+-?+-?]7+→ Pkinase+low_complexity→	559	Geodermatophilus africanus	-	actinobacteria
WP_091174406.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+Cadherin-like	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+Cadherin-like*→	965	Geodermatophilus sp. 1_12	GCA_900114475.1	firmicutes
WP_091216627.1	GAP1-N2+GAP1-M+GAP1-C	Pkinase+TM→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→[+-?+-?]7+→ Pkinase+low_complexity→	557	Geodermatophilus siccatus	-	actinobacteria
WP_091235374.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	1024	Fontibacillus panacagrotis	GCA_900102215.1	firmicutes
WP_091280726.1	GAP1-N2+GAP1-M+GAP1-C+ZnR+DO-GTPase2	GAP1-N2+GAP1-M+GAP1-C+ZnR+DO-GTPase2*→	1000	Frankia sp. G2	GCA_001536285.1	actinobacteria
WP_091284184.1	GAP1-N2+GAP1-M+GAP1-C	GrpE→ HSP70→ TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C* → TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→	814	Micromonospora halkosensis	GCA_900091595.1	actinobacteria
WP_091326582.1	GAP1-N2+GAP1-M+GAP1-C	Pkinase+TM→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→	567	Geodermatophilus ruber	GCF_900143385.1	actinobacteria
WP_091361672.1	GAP1-N2+GAP1-M+GAP1-C	Pkinase+TM→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→[+-?+-?]7+→ Pkinase+low_complexity→	556	Geodermatophilus sp. DSM 45219	GCF_900149251.1	actinobacteria
WP_091442415.1	GAP1-N2+GAP1-M+GAP1-C	Pkinase+TM→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→[+-?+-?]7+→ Pkinase+low_complexity→	555	Geodermatophilus poikilotrophus	-	actinobacteria
WP_091459228.1	GAP1-N2+GAP1-M+GAP1-C	GrpE→ HSP70→ TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C* → TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→+[+-?+-?+-?HSP70	801	Alloactinosynnema iranicum	GCA_900101685.1	actinobacteria
WP_091525929.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown2→ TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→ HSP70_domain_1→	980	Nocardioides sediminis	GCA_900105385.1	actinobacteria
WP_091603699.1	GAP1-N2+GAP1-M+TM+GAP1-C	ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+TM+GAP1-C*→??+TM+??+beta-rich?→+?→ GYF+GYF+ZnR+TM+TM+TM→	842	Planctomicrobium piriforme	GCA_900113665.1	planctomycetes
WP_092274467.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	834	Brevibacillus sp. OK042	GCA_900110475.1	firmicutes
WP_092611337.1	GAP1-N2+GAP1-M+low_complexity	ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+low_complexity*→	541	Raiseyella antarctica	GCA_900092135.1	actinobacteria
WP_092783411.1	GAP1-N2+GAP1-M	CASPASE→TPR_region→7-→ GAP1-N2+GAP1-M*→	183	Actinokineospora terra	GCF_900111175.1	actinobacteria
WP_092943636.1	GAP1-N2+GAP1-M+GAP1-C	HSP70→ HSP70+??→ DnaJ+DnaJ+ZnR+ZnR+coiled_coil+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C* → TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→	843	Ruminococcaceae bacterium	GCA_900099715.1	firmicutes
WP_093149955.1	GAP1-N2+GAP1-M+GAP1-C	GrpE→ HSP70→ TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C* → PSE-+7-+?-+[+-?+-?]+-HSP70→ unknown+CASPASE	798	Saccharopolyspora antimicrobica	GCA_003635025.1	actinobacteria
WP_093275372.1	GAP1-N2+GAP1-M+GAP1-C	GrpE→ HSP70→ TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C* → TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→ HSP70→ +vWA(canonical)→	800	Saccharopolyspora shandongensis	GCA_900106995.1	actinobacteria
WP_093551331.1	GAP1-N2+GAP1-M+GAP1-C	GrpE→ HSP70→ TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C* → PSE-+7-+?-+[+-?+-?]+-HSP70→ unknown+CASPASE	798	Saccharopolyspora	GCA_003553965.1	actinobacteria
WP_093442214.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	828	Streptomyces sp. Cmuel-A718b	GCA_900092005.1	actinobacteria
WP_093679049.1	GAP1-N2+GAP1-M+GAP1-C	TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C* → PSE-→ vWA(canonical)→ PP2C→ Pkinase+Kelch+beta-rich→	822	Streptomyces	GCA_002787635.1	actinobacteria
WP_093527836.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	803	Streptomyces	GCA_900091765.1	actinobacteria
WP_093542221.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	843	Streptomyces sp. DvalAA-43	GCA_900092175.1	actinobacteria
WP_093562468.1	GAP1-N2+GAP1-M+GAP1-C	HSP70_domain_2+low_complexity+domain_betaX→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C* →	843	Streptomyces sp. OpMP-M43	GCA_900091905.1	actinobacteria
WP_093590040.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	860	Streptomyces sp. MaarMP-M17	GCA_900091995.1	actinobacteria

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WP_093675522.1	GAP1:N2+GAP1:M+GAP1:C	GAP1:N2+GAP1:M+GAP1:C*→	803	Streptomyces sp. 0spMP-M45	GCA_900090065.1	actinobacteria
WP_093684023.1	GAP1:N2+GAP1:M+GAP1:C	GAP1:N2+GAP1:M+GAP1:C*→	813	Streptomyces sp. 0luat3MP-M77	GCA_900090075.1	actinobacteria
WP_093686110.1	GAP1:N2+GAP1:M+GAP1:C	GAP1:N2+GAP1:M+GAP1:C*→	811	Streptomyces sp. ScaMP-e83	GCA_900091775.1	actinobacteria
WP_093705090.1	GAP1:N2+GAP1:M+GAP1:C	GAP1:N2+GAP1:M+GAP1:C*→	816	Streptomyces sp. 2131.1	GCA_900105515.1	actinobacteria
WP_093705645.1	GAP1:N2+GAP1:M+GAP1:C	GAP1:N2+GAP1:M+GAP1:C*→	894	Streptomyces sp. DvalAA-19	GCA_900091865.1	actinobacteria
WP_093735661.1	GAP1:N2+GAP1:M+GAP1:C	TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2:2→ GAP1:N2+GAP1:M+GAP1:C*→|=:PSE:||=WA(canonical)→ PP2C→ Pkinase+ZnR+beta-rich→ PSE:=|[=:?=:?=:?]|GAP1:N2+GAP1:M+GAP1:C→	873	Streptomyces sp. DvalAA-19	GCA_900091865.1	actinobacteria
WP_093776162.1	GAP1:N2+GAP1:M+GAP1:C	GAP1:N2+GAP1:M+GAP1:C*→	802	Streptomyces sp. 13bMPCu5.1	GCA_900110575.1	actinobacteria
WP_093813336.1	GAP1:N2+GAP1:M+GAP1:C	GAP1:N2+GAP1:M+GAP1:C*→	835	Streptomyces sp. Ncost-T6T-1	GCA_900090085.1	actinobacteria
WP_093831399.1	GAP1:N2+GAP1:M+GAP1:C	GAP1:N2+GAP1:M+GAP1:C*→ vWA(canonical)→ PP2C→ Pkinase+ZnR+beta-rich→	775	Streptomyces sp. SolWorkMP-5a-2	GCA_900091845.1	actinobacteria
WP_093845333.1	GAP1:N2+GAP1:M+GAP1:C	GAP1:N2+GAP1:M+GAP1:C*→	789	Streptomyces sp. ScaMP-6W	GCA_900090345.1	actinobacteria
WP_093899303.1	GAP1:N2+GAP1:M+GAP1:C	GAP1:N2+GAP1:M+GAP1:C*→	814	Streptomyces sp. Ncost-T10-10d	GCA_900091955.1	actinobacteria
WP_093902715.1	GAP1:N2+GAP1:M+GAP1:C	GAP1:N2+GAP1:M+GAP1:C*→	845	Streptomyces sp. LaPyMR-19p	GCA_900090355.1	actinobacteria
WP_093910651.1	GAP1:N2+GAP1:M+GAP1:C	TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2:2→ GAP1:N2+GAP1:M+GAP1:C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2:2+TM+ vWA(canonical)→ PP2C→ Pkinase+ZnR+beta-rich→	981	Streptomyces sp. cE86	GCA_900110535.1	actinobacteria
WP_093930212.1	GAP1:N2+GAP1:M+GAP1:C	GAP1:N2+GAP1:M+GAP1:C*→	802	Streptomyces sp. cK210	GCA_900110125.1	actinobacteria
WP_094017499.1	GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+Cadherin-like	TM+vWA(canonical)+YrKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2:2+ZnR+ZnR→ GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+Cadherin-like*→	975	Paenibacillus rigui	GCA_002234615.1	firmicutes
WP_094219215.1	GAP1:N2+GAP1:M+GAP1:C	TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2:2→?→ HSP70→ HSP70→vWA(canonical)→ Dnaj+DnaJ+ZnR+ZnR+coiled_coil+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2:2→ GAP1:N2+GAP1:M+GAP1:C*→	898	Leptorichella sp. oral taxon 498	GCA_002244255.1	fusobacteria
WP_094155297.1	GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YrKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2:2+ZnR+ZnR→ GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich*→	1000	Paenibacillus kribbensis	GCA_002240415.1	firmicutes
WP_094224859.1	GAP1:N2+GAP1:M+GAP1:C	GAP1:N2+GAP1:M+GAP1:C*→	812	Streptomyces sp. 2B	GCA_002242735.1	actinobacteria
WP_094274170.1	GAP1:N2+GAP1:M+GAP1:C	polar_leader+TM+TM+TM→ TM+vWA(canonical)→ Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1:N2+GAP1:M+GAP1:C*→ beta-rich+vWA(canonical)→??+DO-GTPase2:2→	981	Rhodococcus sp. OK302	GCA_002245085.1	actinobacteria
WP_094360273.1	GAP1:N2+GAP1:M+GAP1:C	GrpE→ HSP70→ TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2:2→ GAP1:N2+GAP1:M+GAP1:C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2:2→??→?→?→?→?→ HSP70→	800	Propionibacteriaceae bacterium NML 150272	GCA_002250525.1	actinobacteria
WP_094365183.1	GAP1:N2+GAP1:M+GAP1:C	TM+vWA(canonical)→Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1:N2+GAP1:M+GAP1:C*→ beta-rich+vWA(canonical)→??+DO-GTPase2:2→	881	Propionibacteriaceae bacterium NML 130396	GCA_002250625.1	actinobacteria
WP_094372855.1	GAP1:N2+GAP1:M+GAP1:C	TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2:2→ GAP1:N2+GAP1:M+GAP1:C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2:2+TM→ vWA(canonical)→ PSE:=|[=:PSE:||Pkinase+ZnR+beta-rich→	941	Streptomyces sp. FHKL.4005	GCA_002251155.1	actinobacteria
WP_094413564.1	GAP1:N2+GAP1:M+GAP1:C	ZnR+ZnR+DO-GTPase2:2→ GAP1:N2+GAP1:M+TM+GAP1:C*→??+TM+??+beta-rich??→ GYF+GYF+TM+TM+TM→	698	Rhodopirellula sp. SM50	GCA_002251265.1	planctomycetes
WP_094418663.1	GAP1:N2+GAP1:M	FGS-fold_domain→ ZnR+DO-GTPase2.1→ GAP1:N2+GAP1:M*→	257	Rhodopirellula sp. SM50	GCA_002251265.1	planctomycetes
WP_094439561.1	GAP1:N2+GAP1:M+GAP1:C	polar_leader+TM+TM+TM→ TM+vWA(canonical)→Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1:N2+GAP1:M+GAP1:C*→ beta-rich+vWA(canonical)→??+DO-GTPase2:2→	904	Propionibacteriaceae bacterium NML 160184	GCA_002250475.1	actinobacteria
WP_094452326.1	GAP1:N2+GAP1:M+GAP1:C	polar_leader+TM+TM+TM→ TM+vWA(canonical)→Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1:N2+GAP1:M+GAP1:C*→ beta-rich+vWA(canonical)→??+DO-GTPase2:2→	1040	Propionibacteriaceae bacterium NML 150081	GCA_002250565.1	actinobacteria
WP_094598655.1	GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YrKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→?→ ZnR+ZnR+DO-GTPase2:2+ZnR+ZnR→ GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich*→	1078	Paenibacillus sp. XY044	GCA_002257645.1	firmicutes
WP_094639927.1	GAP1:N2+GAP1:M+GAP1:C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1:N2+GAP1:M+GAP1:C*→ beta-rich+vWA(canonical)→??+DO-GTPase2:2→	904	Rhodococcus	GCA_002259035.1	actinobacteria
WP_094661437.1	GAP1:N2+GAP1:M+GAP1:C	TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2:2→ GrpE→ HSP70→ DnaJ+DnaJ+ZnR+ZnR+coiled_coil+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2:2→ GAP1:N2+GAP1:M+GAP1:C*→	933	Pseudoscardovia radai	GCA_002259605.1	actinobacteria
WP_094723575.1	GAP1:N2+GAP1:M+GAP1:C	TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2:2→ GrpE→ HSP70→ HSP70→vWA(canonical)→ Dnaj+DnaJ+ZnR+ZnR+coiled_coil+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2:2→ GAP1:N2+GAP1:M+GAP1:C*→	946	Bifidobacterium tissieri	GCA_002259645.1	actinobacteria
WP_094700136.1	GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YrKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2:2+ZnR+ZnR→ GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich*→	833	Brevibacillus laterosporus	GCF_002259955.1	firmicutes
WP_094861232.1	GAP1:N2+GAP1:M+GAP1:C	TPR_containing_alpha_helical+Fibronectin-like_repeats+extended_insert+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2:2→ GAP1:N2+GAP1:M+GAP1:C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2:2→	903	Nocardiopsis dassonvillei	GCA_002260685.1	actinobacteria
WP_094875310.1	GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YrKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2:2+ZnR+ZnR→ GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich*→	986	Paenibacillus sp. VTT E-133280	GCA_002264385.1	firmicutes
WP_094875450.1	GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YrKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2:2+ZnR+ZnR→ GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich*→	986	Paenibacillus sp. VTT E-133291	GCA_002264395.1	firmicutes
WP_094904341.1	GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YrKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2:2+ZnR+ZnR→ GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich*→	978	Paenibacillus odorifer	GCA_002264435.1	firmicutes
WP_09529398.1	GAP1:N2+GAP1:M+GAP1:C	PIN+WG_repeats+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2:2→ GAP1:N2+GAP1:M+GAP1:C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2:2→	878	Bacillus sp. SA5d-f	GCA_002282935.1	firmicutes
WP_094938305.1	GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich	ZnR+ZnR+DO-GTPase2:2→ZnR+ZnR→ GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich*→	1078	Paenibacillus macerans	GCF_002364305.1	firmicutes
WP_095258437.1	GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich	GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich*→	746	Bacillus circulans	GCF_002271635.1	firmicutes
WP_095291711.1	GAP1:N2+GAP1:M+GAP1:C+polar_tail	Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2:2→ GAP1:N2+GAP1:M+GAP1:C+polar_tail*→	1063	Paenibacillus sp. 7516	GCA_002272715.1	firmicutes
WP_095329927.1	GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich	GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich*→	746	Bacillus circulans	GCA_002271985.1	firmicutes
WP_095360032.1	GAP1:N2+GAP1:M+GAP1:C+polar_tail	Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2:2→ GAP1:N2+GAP1:M+GAP1:C+polar_tail*→	1062	Paenibacillus sp. T523-1	GCA_002276415.1	firmicutes
WP_095414977.1	GAP1:N2+GAP1:M+GAP1:C	ZnR+ZnR+DO-GTPase2:2→ GAP1:N2+GAP1:M+GAP1:C*→??+TM+??+beta-rich??→ GYF+GYF+TM+TM+TM→	731	Thermogutta terrifontis	GCA_002277955.1	planctomycetes
WP_095614595.1	GAP1:N2+GAP1:M+GAP1:C	TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2:2→ GrpE→ HSP70→ HSP70→vWA(canonical)→ Dnaj+DnaJ+ZnR+ZnR+coiled_coil+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2:2→ GAP1:N2+GAP1:M+GAP1:C*→	850	Bifidobacterium criceti	GCF_002286395.1	actinobacteria
WP_095658866.1	GAP1:N2+GAP1:M+GAP1:C	GAP1:N2+GAP1:M+GAP1:C*→	772	Streptomyces sp. CLI2509	GCA_002288075.1	actinobacteria
WP_095705542.1	GAP1:N2+GAP1:M+GAP1:C	GAP1:N2+GAP1:M+GAP1:C*→	698	Streptomyces albidoflavus	GCA_002289305.1	actinobacteria
WP_095728605.1	GAP1:N2+GAP1:M+TM+GAP1:C	ZnR+ZnR+DO-GTPase2:2→ GAP1:N2+GAP1:M+TM+GAP1:C*→??+TM+??+beta-rich??→ GYF+GYF+TM+TM+TM→	642	Rhodopirellula sp. SM50	GCA_002289565.1	planctomycetes
WP_095747143.1	GAP1:N2+GAP1:M	FGS-fold_domain→ ZnR+DO-GTPase2.1→ GAP1:N2+GAP1:M*→	257	Rhodopirellula sp. SM50	GCA_002289565.1	planctomycetes
WP_095795750.1	GAP1:N2+GAP1:M+GAP1:C	TM+DUF4190+TM→ TM+DUF4190+TM→ polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1:N2+GAP1:M+GAP1:C(frag)*→ beta-rich+vWA(canonical)→??+DO-GTPase2:2→	363	Mycobacterium chimaera	GCA_002292625.1	actinobacteria

acc	architecture	operon	len	species	gca	taxend
WP_095865817.1	GAP1:N2+GAP1:M+GAP1:C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1:N2+GAP1:M+GAP1:C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→	914	Rhodococcus sp. ACS1	GCA_002360715.1	actinobacteria
WP_095969334.1	GAP1:N2+GAP1:M+GAP1:C	GrpE→ HSP70→ TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1:N2+GAP1:M+GAP1:C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→??→ HSP70→ +WA(canonical)→	798	Rhodococcus erythropolis	GCA_002403875.1	actinobacteria
WP_096095145.3	GAP1:N2+GAP1:M+GAP1:C	GAP1:N2+GAP1:M+GAP1:C*→	751	Streptomyces albidoflavus	GCA_002317035.1	actinobacteria
WP_096096486.1	GAP1:N2+GAP1:M+GAP1:C	GAP1:N2+GAP1:M+GAP1:C*→	789	Streptomyces albidoflavus	GCA_002317005.1	actinobacteria
WP_096168504.1	GAP1:N2+GAP1:M+GAP1:C	TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1:N2+GAP1:M+GAP1:C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→	978	Brevibacterium linens	GCA_002332445.1	actinobacteria
WP_096179630.1	GAP1:N2+GAP1:M+GAP1:C	GrpE→ HSP70→ TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1:N2+GAP1:M+GAP1:C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→	693	Brevibacterium	GCA_002332325.1	actinobacteria
WP_096212307.1	GAP1:N2+GAP1:M+GAP1:C	TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1:N2+GAP1:M+GAP1:C*→ PSE→ +WA(canonical)→ PP2C→ Pkinase+ZnR+beta-rich→	822	Streptomyces sp. 2323.1	GCA_900221035.1	actinobacteria
WP_096337284.1	GAP1:N2+GAP1:M+GAP1:C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1:N2+GAP1:M+GAP1:C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→ polar_leader+TM+TM+TM→	519	Corynebacterium accolens	GCA_002354405.1	actinobacteria
WP_096458547.1	GAP1:N2+GAP1:M+GAP1:C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1:N2+GAP1:M+GAP1:C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→	631	Corynebacterium glutamicum	GCA_002353155.1	actinobacteria
WP_096624144.3	GAP1:N2+GAP1:M+GAP1:C	GAP1:N2+GAP1:M+GAP1:C*→	611	Streptomyces sp. WZ.A164	GCA_002382885.1	actinobacteria
WP_096778660.1	GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich*→	992	Paenibacillus lautus	GCA_002467025.1	firmicutes
WP_096965121.1	GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich*→	833	Bacillus hisashiae	GCA_002930325.1	firmicutes
WP_097059724.1	GAP1:N2+GAP1:M+GAP1:C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1:N2+GAP1:M+GAP1:C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→	891	Salinibacterium xinjiangense	GCA_900230175.1	actinobacteria
WP_097156225.1	GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich*→	1056	Paenibacillus sp. RC96A	GCF_900322275.1	firmicutes
WP_097207620.1	GAP1:N2+GAP1:M+GAP1:C	Pkinase+TM→ ZnR+ZnR+DO-GTPase2.2→ GAP1:N2+GAP1:M+GAP1:C*→?→|=|=?→?||?→ Pkinase+low_complexity→	554	Geodermatophilus salsuli	GCA_900215145.1	actinobacteria
WP_097432990.1	GAP1:N2+GAP1:M+GAP1:C	GAP1:N2+GAP1:M+GAP1:C*→	804	Streptomyces microflavus	GCA_003289965.1	actinobacteria
WP_097632881.1	GAP1:N2+GAP1:M+GAP1:C	TPR_containing_alpha_helical+Fibronectin-like_repeats+extended_insert+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1:N2+GAP1:M+GAP1:C*→ TM+TM+ZnR+ZnR+DO-GTPase2.2→	947	Glycomyces fuscus	GCA_002529455.1	actinobacteria
WP_097871877.1	GAP1:N2+GAP1:M+GAP1:C	GAP1:N2+GAP1:M+GAP1:C*→	817	Streptomyces sp. rk34	GCF_002511245.1	actinobacteria
WP_097874643.1	GAP1:N2+GAP1:M+GAP1:C	GAP1:N2+GAP1:M+GAP1:C*→	864	Streptomyces sp. mr184	GCF_002514335.1	actinobacteria
WP_097885163.1	GAP1:N2+GAP1:M+GAP1:C	GAP1:N2+GAP1:M+GAP1:C*→	826	Streptomyces sp. st140	GCF_002551135.1	actinobacteria
WP_097892195.1	GAP1:N2+GAP1:M+GAP1:C	GAP1:N2+GAP1:M+GAP1:C*→	598	Streptomyces sp. st170	GCF_002521105.1	actinobacteria
WP_097912485.1	GAP1:N2+GAP1:M+GAP1:C	GAP1:N2+GAP1:M+GAP1:C→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM→ +vWA(canonical)→ PP2C→ Pkinase+ZnR+beta-rich→|=?+-?|GAP1:N2+GAP1:M+GAP1:C*→	838	Streptomyces sp. b84	GCF_002514665.1	actinobacteria
WP_097924903.1	GAP1:N2+GAP1:M+GAP1:C	TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1:N2+GAP1:M+GAP1:C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM→ +vWA(canonical)→ PP2C→ Pkinase+ZnR+beta-rich→|=?+-?|GAP1:N2+GAP1:M+GAP1:C→	821	Streptomyces sp. b84	GCF_002514465.1	actinobacteria
WP_097924466.1	GAP1:N2+GAP1:M+GAP1:C	TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1:N2+GAP1:M+GAP1:C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM→ +vWA(canonical)→ PP2C→ Pkinase+ZnR+beta-rich→	821	Streptomyces sp. wa1063	GCF_002551045.1	actinobacteria
WP_097935513.1	GAP1:N2+GAP1:C	GAP1:N2+GAP1:C*→	708	Streptomyces sp. rk207	GCF_002551215.1	actinobacteria
WP_097946984.1	GAP1:N2+GAP1:M+GAP1:C	GAP1:N2+GAP1:M+GAP1:C*→	830	Streptomyces sp. mr115	GCF_002551345.1	actinobacteria
WP_097957347.1	GAP1:N2+GAP1:M+GAP1:C	ZnR+ZnR+DO-GTPase2.2→ GAP1:N2+GAP1:M+GAP1:C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2+TM→ +vWA(canonical)→ PP2C→ Pkinase+ZnR+beta-rich→	821	Streptomyces	GCF_002551015.1	actinobacteria
WP_097965558.1	GAP1:N2+GAP1:M+GAP1:C	GAP1:N2+GAP1:M+GAP1:C*→	828	Streptomyces sp. or20	GCF_002551305.1	actinobacteria
WP_097974788.1	GAP1:N2+GAP1:M+GAP1:C	GAP1:N2+GAP1:M+GAP1:C*→	829	Streptomyces sp. gh14	GCF_002551375.1	actinobacteria
WP_097985947.1	GAP1:N2+GAP1:M+GAP1:C	GAP1:N2+GAP1:M+GAP1:C*→	826	Streptomyces sp. fl50	GCF_002551435.1	actinobacteria
WP_097991446.1	GAP1:N2+GAP1:M+GAP1:C	GAP1:N2+GAP1:M+GAP1:C*→	829	Streptomyces sp. f51	GCF_002551415.1	actinobacteria
WP_098009811.1	GAP1:N2+GAP1:M+GAP1:C	GAP1:N2+GAP1:M+GAP1:C*→	848	Streptomyces sp. sk226	GCF_002551185.1	actinobacteria
WP_098014371.1	GAP1:N2+GAP1:M+GAP1:C	GAP1:N2+GAP1:M+GAP1:C*→	828	Streptomyces sp. rk195	GCF_002551235.1	actinobacteria
WP_098024903.1	GAP1:N2+GAP1:M+GAP1:C	GAP1:N2+GAP1:M+GAP1:C*→	826	Streptomyces sp. b62	GCF_002551475.1	actinobacteria
WP_098025836.1	GAP1:N2+GAP1:M+GAP1:C	GAP1:N2+GAP1:M+GAP1:C*→	842	Streptomyces sp. st115	GCF_002551145.1	actinobacteria
WP_098035459.1	GAP1:N2+GAP1:M+GAP1:C	GAP1:N2+GAP1:M+GAP1:C*→ +WA(canonical)→ PP2C→ Pkinase+ZnR+beta-rich→|=|=TPR_containing_alpha_helical+Fibronectin-like_repeats	813	Streptomyces farmicus	GCF_002556545.1	actinobacteria
WP_098530676.1	GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1:N2+GAP1:M+GAP1:C*→	641	Streptomyces sp. AFS076308	GCA_002356135.1	firmicutes
WP_098749063.1	GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→?+ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich*→	991	Paenibacillus sp. EZ-K15	GCF_002573715.1	firmicutes
WP_098831195.1	GAP1:N2+GAP1:M+GAP1:C	GAP1:N2+GAP1:M+GAP1:C*→	827	Streptomyces sp. or3	GCF_002511295.1	actinobacteria
WP_098895192.1	GAP1:N2+GAP1:M+GAP1:C	GAP1:N2+GAP1:M+GAP1:C*→	787	Streptomyces sp. r99	GCF_002551065.1	actinobacteria
WP_098898071.1	GAP1:N2+GAP1:M+GAP1:C	GAP1:N2+GAP1:M+GAP1:C*→	835	Streptomyces sp. st77	GCF_002511175.1	actinobacteria
WP_098933598.1	GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich*→	939	Bacillus sp. AFS031507	GCA_002548635.1	firmicutes
WP_099064535.1	GAP1:N2+GAP1:M+GAP1:C	GAP1:N2+GAP1:M+GAP1:C*→	641	Bacillus sp. AFS037270	GCA_002565305.1	firmicutes
WP_099174916.1	GAP1:N2+GAP1:M+GAP1:C	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1:N2+GAP1:M+GAP1:C*→	804	Streptomyces sp. LamerLS-316	GCA_900090175.1	actinobacteria
WP_099092720.1	GAP1:N2+GAP1:M+GAP1:C	GAP1:N2+GAP1:M+GAP1:C*→	811	Streptomyces cinnamomeus	GCA_002727115.1	actinobacteria
WP_099219868.1	GAP1:N2+GAP1:M+GAP1:C	GAP1:N2+GAP1:M+GAP1:C*→	865	Streptomyces sp. AmelKG-D3	GCA_900090815.1	actinobacteria
WP_099318715.1	GAP1:N2+GAP1:M+GAP1:C	TM+DUF4190+TM→ polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1:N2+GAP1:M+GAP1:C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→	818	Mycobacterium kansasii	GCF_002702925.1	actinobacteria
WP_099329183.1	GAP1:N2+GAP1:M+GAP1:C	TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→?→ HSP70→ HSP70→vWA(canonical)→ DnaJ+DnaJ+ZnR+coiled_coil+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1:N2+GAP1:M+GAP1:C*→	916	Amycolatopsis Marseille-P4968	GCF_002822885.1	firmicutes
WP_099431986.1	GAP1:N2+GAP1:M+GAP1:C	TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→ GrpE→ HSP70→ HSP70→vWA(canonical)→ DnaJ+DnaJ+ZnR+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1:N2+GAP1:M+GAP1:C*→	880	Collinsella aerofaciens	GCA_002736145.1	actinobacteria
WP_099517532.1	GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich*→	1053	Paenibacillus sp. BIHB4019	GCA_002741035.1	firmicutes
WP_099657417.1	GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1:N2+GAP1:M+GAP1:C+polar_tail+TM+beta-rich*→	1057	Paenibacillus polymyxa	GCF_002754415.1	firmicutes

acc	architecture	operon	len	species	gca	taxend
WP_100869938.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→ polar_leader+TM+TM+TM→	535	Corynebacterium striatum	GCA_002275065.1	actinobacteria
WP_100301097.1	GAP1-N2+GAP1-M+GAP1-C	PP2C→ Pkinase-+?-+?-+?→ HSP70_domain_2+low_complexity+domain_betaX→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→	816	Streptomyces sp. CNZ306	GCA_002707655.1	actinobacteria
WP_100435397.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	780	Streptomyces sp. TSRB3084-2	GCA_002802945.1	actinobacteria
WP_100516541.1	GAP1-N2+GAP1-M+GAP1-C	HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→??+DO-GTPase2.2→	818	Mycolicibacterium goodii	GCA_002798385.1	actinobacteria
WP_100528329.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail	Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C+polar_tail*→	1068	Paenibacillus sp. GM1FR	GCA_002803315.1	firmicutes
WP_100541388.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	989	Paenibacillus sp. GM2FR	GCA_002803325.1	firmicutes
WP_100562496.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	833	Streptomyces sp. CNO613	GCA_002803175.1	actinobacteria
WP_100619210.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→ polar_leader+TM+TM+TM→	535	Corynebacterium striatum	GCA_002804085.1	actinobacteria
WP_100682531.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	612	Streptomyces sp. Ag109_G2-4	GCF_002813255.1	actinobacteria
WP_101261520.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C*→	789	Streptomyces sp. EAG2	GCA_002842015.1	actinobacteria
WP_101432330.1	GAP1-N2+GAP1-M+GAP1-C	TM+TM+TM+TM+ZnR+DO-GTPase2.2→?→ HSP70→ HSP70+vWA(canonical)→ Dna3+Dna3+ZnR+ZnR+coiled_coil+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→	916	Bifidobacterium asteroides	GCA_002846895.1	actinobacteria
WP_101557432.1	GAP1-N2+GAP1-M+GAP1-C	TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→	978	Brevibacterium aurantiacum	GCA_003332365.1	actinobacteria
WP_101600910.1	GAP1-N2+GAP1-M+GAP1-C	GrpE→ HSP70→ TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→	677	Brevibacterium sp. Mu109	GCA_900169375.1	actinobacteria
WP_101623189.1	GAP1-N2+GAP1-M+GAP1-C	TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→ GrpE→ HSP70→ HSP70+vWA(canonical)→ Dna4+Dna4+ZnR+ZnR+coiled_coil+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→	969	Bifidobacterium parmae	GCF_002860365.1	actinobacteria
WP_101680894.1	GAP1-N2+GAP1-M+GAP1-C	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C*→	562	Bacillus cucumis	GCA_002860255.1	firmicutes
WP_101692660.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	TM+vWA(canonical)+YtKA-like+TM+??→ Tubulin+coiled_coil+??→ Tubulin+coiled_coil+HTH?+??→ TM+TM+TM+vWA(canonical)+TM+TM+TM+polar_tail→ Fibronectin-like_repeats+??→ ZnR+ZnR+DO-GTPase2.2+ZnR+ZnR→ GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	833	Brevibacillus laterosporus	GCA_002865325.1	firmicutes
WP_101729374.1	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich	GAP1-N2+GAP1-M+GAP1-C+polar_tail+TM+beta-rich*→	750	Clostridiales bacterium mt7	GCF_900199605.1	firmicutes
WP_101736776.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→?→??+DO-GTPase2.2→?→[=|=?=?=-?=HSP70	326	Corynebacterium ringelii	GCA_002861325.1	actinobacteria
WP_101736469.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→ polar_leader+TM+TM+TM→	577	Corynebacterium surinamcosum	GCA_002861385.1	actinobacteria
WP_102234493.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→ beta-rich+vWA(canonical)→??+DO-GTPase2.2→ polar_leader+TM+TM+TM→	565	Corynebacterium surinamcosum	GCA_002871735.1	actinobacteria
WP_102239724.1	GAP1-N2+GAP1-M+GAP1-C	polar_leader+TM+TM+TM→ TM+vWA(canonical)+Fibronectin-like_repeats+TM+beta-rich+lc_tail→ Tubulin+alpha_helical+??+??→ GAP_unknown1+TM+TM+GAP_unknown2→ HRDC-like?+Fibronectin-like_repeats→ GAP1-N2+GAP1-M+GAP1-C*→?→??+DO-GTPase2.2→?→[=|=-?=-?=-?=TM+TM+vWA(canonical)+TM+TM+TM+vWA(canonical)+TM	962	Brevibacterium paraiorams	GCA_002871875.1	actinobacteria
WP_102240421.1	GAP1-N2+GAP1-M+GAP1-C	GrpE→ HSP70→ TPR_containing_alpha_helical+Fibronectin-like_repeats→ ZnR+ZnR+DO-GTPase2.2→ GAP1-N2+GAP1-M+GAP1-C*→ TM+TM+TM+TM+ZnR+ZnR+DO-GTPase2.2→	808	Actinomyces graevenitzii	GCA_002871975.1	actinobacteria
XP_021305019.1	GAP1-N2+GAP1-M+GAP1-C	GAP1-N2+GAP1-M+GAP1-C[frag]*→	514	Herrania umbratica	GCF_002168275.1	viridiplantae

NucA endonuclease-containing systems

acc	architecture	operon	len	species	gca	taxend
WP_053082004.1	EAD1+Trypsin+EAD1+STAND	EAD1+Trypsin+EAD1+STAND*→ low_complexity+TM+NucA(inactive)+iSvmX2→||←?←CASPASE+??||Trypsin→	841	Methylobacterium aquaticum	GCF_001043915.1	alphaproteobacteria
WP_084627253.1	EAD1+Trypsin+TM+TM+disordered	EAD1+Trypsin+TM+TM+disordered*→	465..487&TM	Mesorhizobium sp. LSHC422A00	GCF_000503075.1	-
WP_084629776.1	EAD1+Trypsin+TM+NPLC_P60	EAD1+Trypsin+TM+NPLC_P60*→	768	Mesorhizobium sp. LSHC412B00	GCF_000503035.1	alphaproteobacteria
WP_023715941.1	EAD1+Trypsin+TM+NPLC_P60	EAD1+Trypsin+TM+NPLC_P60*→	757	Mesorhizobium sp. LSHC422A00	GCF_000503075.1	alphaproteobacteria
ESX81659.1	EAD1+Trypsin+TM+NPLC_P60	EAD1+Trypsin+TM+NPLC_P60*→	746	Mesorhizobium sp. LSHC412B00	GCA_000503035.1	alphaproteobacteria
WP_092161432.1	EAD1+Trypsin	Trypsin_2+NucA+Calcineurin←?←?||EAD1+Trypsin*→?→??+TM+??+??+iSvmX2→	409	Bosea sp. DSM 18164	GCF_900112185.1	alphaproteobacteria
WP_083786386.1	EAD1+Trypsin	lysozyme+peptidase_MD→||←Trypsin+NucA||EAD1+Trypsin*→?→??+TM+SH3+iSvmX2→	401	Methylobacterium nodulans	GCF_000022085.1	alphaproteobacteria
WP_012044960.1	EAD1+Trypsin	EAD1+Trypsin*→?→ Ploop_NTPase+TM+??→	382	Bradyrhizobium sp. BTAi1	GCF_000015165.1	alphaproteobacteria
WP_082364706.1	EAD1+Trypsin	EAD1+Trypsin*→?→ AAA_ATPase(inactive)+TM+SH3+iSvmX2→||←PSE||?→ Trypsin+NucA→	381	Novosphingobium sp. AAP93	GCF_001296055.1	alphaproteobacteria
WP_083554684.1	EAD1+Trypsin	EAD1+Trypsin*→?→ AAA_ATPase(inactive)+TM+SH3+iSvmX2→||←PSE||?→ Trypsin+NucA→	381	Novosphingobium sp. NDB2Meth1	GCF_900117425.1	alphaproteobacteria
WP_046612924.1	EAD1+Trypsin	Trypsin+NucA||lysozyme+PGBD→ EAD1+Trypsin*→ EADunk+helical_domain→ low_complexity+TM+NucA(inactive)+iSvmX2→ GDSL→	373	Neorhizobium galegae	GCF_000985995.1	alphaproteobacteria
WP_056528335.1	EAD1+Trypsin	Trypsin+NucA→ EAD1+Trypsin*→?→ STAND+TM+iSvmX2→	373	Sphingomonas sp. Leaf339	GCF_001426195.1	alphaproteobacteria
WP_068292622.1	EAD1+Trypsin	EAD1+Trypsin*→ EADunk+helical_domain→??+TM+??→	372	Labrys sp. WJW	GCF_001676615.1	alphaproteobacteria
WP_015667733.1	EAD7+helical_domain	EAD1+Trypsin→ *EAD7+helical_domain*→ STAND+TM+TPRs→	370	Bradyrhizobium oligotrophicum	GCF_000344805.1	alphaproteobacteria
PLR28184.1	EAD1+Trypsin	EAD1+Trypsin*→?→||←?←?||Trypsin→	369	Caulobacter zeae	GCA_002858925.1	alphaproteobacteria
WP_068414758.1	EAD1+Trypsin	Trypsin_2+NucA+Subtilisin→ Trypsin→ bDLD2+Trypsin+STAND→ STAND+wHTH+TPRs→ EAD1+Trypsin*→?→ low_complexity+Pentapeptide_repeats+TPRs→	368	Labrenzia sp. OB1	GCF_001624695.1	alphaproteobacteria
WP_003613698.1	EAD1+Trypsin	subtilase→ EAD1+Trypsin*→ STAND+TM+TPRs→||←PLD+PLD	368	Methylosinus	GCF_000178815.2	alphaproteobacteria
WP_096786388.1	EAD1+Trypsin	GDSL←lysozyme+PGBD||??+Trypsin→ EAD1+Trypsin*→ EADunk+helical_domain→ low_complexity+TM+NucA(inactive)+iSvmX2→	368	Rhodobacter sp. CZR27	GCF_002407205.1	alphaproteobacteria
WP_101341742.1	EAD1+Trypsin	GDSL←lysozyme+PGBD||??+Trypsin→ EAD1+Trypsin*→ EADunk+helical_domain→ low_complexity+TM+NucA(inactive)+iSvmX2→	363	Rhodobacter azotoformans	GCF_002844445.1	alphaproteobacteria
WP_011909377.1	EAD1+Trypsin	GDSL←lysozyme+PGBD||??+Trypsin→ EAD1+Trypsin*→ EADunk+helical_domain→ low_complexity+TM+NucA(inactive)+iSvmX2→	363	Rhodobacter sphaeroides	GCF_000016405.1	alphaproteobacteria
WP_091925409.1	EAD1+Trypsin	EAD1+Trypsin*→||←?←?←Ploop_NTPase+TM+??	362	Phyllobacterium sp. CL33Tsu	GCF_900113985.1	alphaproteobacteria
WP_027229487.1	EAD1+Trypsin	EAD1+Trypsin*→||←?←?←Ploop_NTPase+TM+??	362	Phyllobacterium sp. UNC302MFCol5.2	GCF_000686005.1	alphaproteobacteria
WP_091943939.1	EAD1+Trypsin	EAD1+Trypsin*→||←?←?←Ploop_NTPase+TM+??	362	Phyllobacterium sp. YR620	GCF_900104165.1	alphaproteobacteria
WP_018082322.1	EAD1+Trypsin	Trypsin+NucA→?→ EAD1+Trypsin→ *EAD1+Trypsin*→?→ AAA_ATPase(inactive)+TM+SH3+iSvmX2→	361	Asticcacaulis benevestitus	GCF_000376105.1	alphaproteobacteria
WP_069910982.1	EAD1+Trypsin	EAD1+Trypsin*→	359	Devosia insulae	GCF_000970465.2	alphaproteobacteria
SDW97151.1	EAD1+Trypsin	Trypsin+NucA||EAD1+Trypsin*→?→??+TM+SH3+iSvmX2→ GDSL→	359	Paracoccus sanguinis	GCA_900106665.1	alphaproteobacteria
WP_023690135.1	EAD1+Trypsin	EAD1+Trypsin*→?→ STAND+wHTH+TPRs→	357	Mesorhizobium sp. LSJC269B00	GCF_000502815.1	alphaproteobacteria
WP_066997244.1	EAD1+Trypsin	Trypsin←subtilase←?←?←??+GDSL←PSE||EAD1+Trypsin*→?→ STAND+wHTH+TPRs→	355	Mesorhizobium sp. WSM3873	GCF_001672445.1	alphaproteobacteria
WP_069907699.1	EAD1+Trypsin	Trypsin→ EAD1+lysozyme→ EAD1+Trypsin→ *EAD1+helical_domain*→ low_complexity+TM+NucA(inactive)+iSvmX2→ Trypsin+NucA→	347	Devosia insulae	GCF_000970465.2	alphaproteobacteria
WP_052172061.1	EAD1+Trypsin	Trypsin+NucA||EAD1+Trypsin*→	347	Paracoccus sanguinis	GCF_000763825.1	alphaproteobacteria
WP_084582114.1	EAD1+Trypsin	Trypsin+NucA→?→?→ AAA_ATPase(inactive)+TM+SH3+iSvmX2→?→ EAD1+Trypsin*→	346	Sphingomonas azotifigens	GCF_002091475.1	alphaproteobacteria
CCD95925.1	EAD1+Trypsin	EAD1+Trypsin→ *EAD1+??+Ploop_NTPase+??*→	345	Bradyrhizobium sp. ORS 375	GCA_000239775.2	alphaproteobacteria
WP_050995937.1	EAD1+Trypsin	EAD1+Trypsin*→||←EAD5+Trypsin←STAND+wHTH+TPRs←?←PLD+PLD←Trypsin	344	Bradyrhizobium yuanmingense	GCF_000261805.1	alphaproteobacteria
WP_006205238.1	EAD1+Trypsin	Trypsin+NucA→ EAD1+Trypsin*→ EADunk+helical_domain→	327	Mesorhizobium amorphae	GCF_000233995.1	alphaproteobacteria
WP_023829837.1	EAD1+Trypsin	Trypsin+NucA→ EAD1+Trypsin*→ EADunk+helical_domain→ low_complexity+TM+NucA(inactive)+iSvmX2→	327	Mesorhizobium sp. L103C120A0	GCF_000502255.1	alphaproteobacteria
WP_023824922.1	EAD1+Trypsin	Trypsin+NucA→ EAD1+Trypsin*→ PSE→ EADunk+helical_domain→ low_complexity+TM+NucA(inactive)+iSvmX2→	327	Mesorhizobium sp. L103C565B0	GCF_000502295.1	alphaproteobacteria
WP_023730574.1	EAD1+Trypsin	Trypsin+NucA→ EAD1+Trypsin*→ EADunk+helical_domain→ low_complexity+TM+NucA(inactive)+iSvmX2→	327	Mesorhizobium sp. LNJC405B00	GCF_000502615.1	alphaproteobacteria
WP_023702264.1	EAD1+Trypsin	Trypsin+NucA→ EAD1+Trypsin*→ EADunk+helical_domain→ low_complexity+TM+NucA(inactive)+iSvmX2→	327	Mesorhizobium sp. LSJC264A00	GCF_000502755.1	alphaproteobacteria
WP_023696135.1	EAD1+Trypsin	Trypsin+NucA→ EAD1+Trypsin*→ EADunk+helical_domain→ low_complexity+TM+NucA(inactive)+iSvmX2→	327	Mesorhizobium sp. LSJC265A00	GCF_000502775.1	alphaproteobacteria
WP_017270711.1	EAD1+Trypsin	GDSL+CASPASE→ subtilase→?→ EAD1+Trypsin*→	327	Sinorhizobium meliloti	GCF_000427585.1	alphaproteobacteria
WP_023755269.1	EAD1+Trypsin	Trypsin+NucA→ EAD1+Trypsin*→ EADunk+helical_domain→ low_complexity+TM+NucA(inactive)+iSvmX2→	327	unclassified Mesorhizobium	GCF_000502475.1	alphaproteobacteria
WP_023745069.1	EAD1+Trypsin	Trypsin+NucA→ EAD1+Trypsin*→ EADunk+helical_domain→ low_complexity+TM+NucA(inactive)+iSvmX2→	327	unclassified Mesorhizobium	GCF_000502555.1	alphaproteobacteria
WP_023710499.1	EAD1+Trypsin	Trypsin+NucA→ EAD1+Trypsin*→ EADunk+helical_domain→ low_complexity+TM+NucA(inactive)+iSvmX2→	327	unclassified Mesorhizobium	GCF_000502695.1	alphaproteobacteria

acc	architecture	operon	len	species	gca	taxend
WP_023691332.1	EAD1+Trypsin	NucA→ EAD1+Trypsin*→ EADunk+helical_domain→ low_complexity+TM+NucA(inactive)+iSvmX2→	327	unclassified Mesorhizobium	GCF_000502795.1	alphaproteobacteria
WP_023688493.1	EAD1+Trypsin	Trypsin+NucA→ EAD1+Trypsin*→ EADunk+helical_domain→ low_complexity+TM+NucA(inactive)+iSvmX2→	327	unclassified Mesorhizobium	GCF_000502815.1	alphaproteobacteria
WP_023738836.1	EAD1+Trypsin	Trypsin+NucA→ EAD1+Trypsin*→ EADunk+helical_domain→ low_complexity+TM+NucA(inactive)+iSvmX2→	327	unclassified Mesorhizobium	GCF_000502995.1	alphaproteobacteria
WP_023726582.1	EAD1+Trypsin	Trypsin+NucA→ EAD1+Trypsin*→ EADunk+helical_domain→ low_complexity+TM+NucA(inactive)+iSvmX2→	327	unclassified Mesorhizobium	GCF_000503035.1	alphaproteobacteria
WP_023668985.1	EAD1+Trypsin	Trypsin+NucA→ EAD1+Trypsin*→ EADunk+helical_domain→ low_complexity+TM+NucA(inactive)+iSvmX2→	327	unclassified Mesorhizobium	GCF_000503155.1	alphaproteobacteria
WP_023832170.1	EAD1+Trypsin	Trypsin+NucA→ EAD1+Trypsin*→ EADunk+helical_domain→ low_complexity+TM+NucA(inactive)+iSvmX2→	325	Mesorhizobium sp. L103C119B0	GCF_000502235.1	alphaproteobacteria
WP_014497152.1	Trypsin+EAD1+coiled_coil	calcineurin(low_complexity_insert)→ Trypsin+EAD1+coiled_coil*→ wHTH+TM+PPRs+TPRs→	643	Bradyrhizobium japonicum	GCF_000284375.1	alphaproteobacteria
WP_049824938.1	Trypsin+EAD1+coiled_coil	calcineurin(low_complexity_insert)→ Trypsin+EAD1+coiled_coil*→ wHTH+TM+PPRs+TPRs→	611	Bradyrhizobium japonicum	GCF_000472985.1	alphaproteobacteria
WP_041955985.1	Trypsin+EAD1+coiled_coil	calcineurin(low_complexity_insert)→ Trypsin+EAD1+coiled_coil*→ wHTH+TM+PPRs+TPRs→	643	Bradyrhizobium japonicum	GCF_000773865.1	alphaproteobacteria
WP_015666606.1	Trypsin+EAD1+coiled_coil	calcineurin(low_complexity_insert)→ Trypsin+EAD1+coiled_coil*→ wHTH+TM+PPRs+TPRs→	674	Bradyrhizobium oligotrophicum	GCF_000344805.1	alphaproteobacteria
WP_065745691.1	Trypsin+EAD1+coiled_coil	calcineurin(low_complexity_insert)→ Trypsin+EAD1+coiled_coil*→ wHTH+TM+PPRs+TPRs→	661	Bradyrhizobium sp. LMTR 3	GCF_001693485.1	alphaproteobacteria
WP_063691614.1	Trypsin+EAD1+coiled_coil	calcineurin(low_complexity_insert)→ Trypsin+EAD1+coiled_coil*→ wHTH+TM+PPRs+TPRs→	643	Bradyrhizobium stylosanthis	GCF_001641335.1	alphaproteobacteria
BAM90641.1	EAD7+Lysozyme	EAD1+Trypsin→ EAD7+Lysozyme*→ STAND+TM+TPRs→	440	Bradyrhizobium oligotrophicum S58	GCA_000344805.1	alphaproteobacteria
WP_091921759.1	IG-like+EAD1	IG-like+EAD1*→	233..255&TM	Phyllobacterium sp. CL33Tsu	GCF_900113985.1	-
WP_027231496.1	IG-like+EAD1	IG-like+EAD1*→	233..255&TM	Phyllobacterium sp. UNC302MFCol5.2	GCF_000686005.1	-
WP_011082909.1	HNH+PNPase+EAD7	HNH+PNPase+EAD7*→	474	Bradyrhizobium	GCF_000011365.1	alphaproteobacteria
WP_069907698.1	EAD1+TM+coiled_coil	Trypsin→ EAD1+TM+coiled_coil*→ EAD1+Trypsin→ EAD1+helical_domain→ low_complexity+TM+NucA(inactive)+iSvmX2→ Trypsin+NucA→	359	Devosia insulae	-	alphaproteobacteria
OWK18362.1	EAD1	Trypsin→ Trypsin→ NucA→ EAD1*→ Trypsin→ EAD1→ EADunk+helical_domain→??+TM+??→ NucA→	108	Mesorhizobium amorphae CCBAU 01583	GCA_002200945.1	alphaproteobacteria
WP_089387726.1	EAD1+Trypsin	Trypsin→||←?||EAD1+Trypsin→ *EAD1+STAND*→ STAND+wHTH+TPRs→	349	Paracoccus sediminis	GCF_900188295.1	alphaproteobacteria

Effector Associated Constant Component 1 (EACC1)-containing two gene conflict system

acc	architecture	operon	len	species	gca	taxend
AAZ23093.1	EACC1	EACC1*→ CASPASE+Pkinase+??→	139	Streptomyces fradiae	-	actinobacteria
AEM80885.1	EACC1	TetR_N+TetR_C_6→ EACC1*→ CASPASE+low-complexity+TM+PBPB→	129	Streptomyces violaceusniger Tu 4113	GCA_000147815.3	actinobacteria
AEM84200.1	EACC1	EACC1*→ CASPASE+TM+TM→	127	Streptomyces violaceusniger Tu 4113	GCA_000147815.3	actinobacteria
AEV85592.1	EACC1	EACC1*→ CASPASE+JAB→	115	Actinoplanes sp. SE50/110	GCA_000237145.1	actinobacteria
AGP55504.1	EACC1	EACC1*→ CASPASE+low-complexity+TM+PBPB→	132	Streptomyces rapamycinicus NRRL 5491	GCA_000418455.1	actinobacteria
AGP55984.1	EACC1	EACC1*→	147	Streptomyces rapamycinicus NRRL 5491	GCA_000418455.1	actinobacteria
AGZ40359.1	EACC1	EACC1*→	116	Actinoplanes friuliensis DSM 7358	GCA_000494755.1	actinobacteria
AGZ45935.1	EACC1	EACC1*→ CASPASE+DUF179→ SIR2+??→??→	117	Actinoplanes friuliensis DSM 7358	GCA_000494755.1	actinobacteria
AHH15007.1	EACC1	EACC1*→ TM+TM→	86	Nocardia nova SH22a	GCA_000523235.1	actinobacteria
AHH97879.1	EACC1	polar_lead?+TM+TM+TM+polar_tail?+low-complexity→??→ EACC1*→ CASPASE+TPRs→?→ CASPASE+??+TPRs?→	119	Kutzneria albida DSM 43870	GCA_000525635.1	actinobacteria
AIA00737.1	EACC1	EACC1*→ CASPASE+TM+TM+bPH_domain?→	134	Streptomyces albulus	GCA_000695235.1	actinobacteria
AJE85450.1	EACC1	EACC1*→ CASPASE+HisKA+HATPase_c→	139	Streptomyces albus	GCA_000827005.1	actinobacteria
AJP05873.1	EACC1	EACC1*→	107	Streptomyces cyaneogriseus subsp. noncyanogenus	GCA_000931445.1	actinobacteria
AJT62559.1	EACC1	EACC1*→ CASPASE+low-complexity+TM+PBPB→	155	Streptomyces lydicus	GCA_000952035.2	actinobacteria
AKG44342.1	EACC1	TM+TM+TM+PP2C→ EACC1*→ CASPASE+PBPB+vWA→	152	Streptomyces xiamenensis	GCA_000993785.2	actinobacteria
AKJ15647.1	EACC1	EACC1*→ CASPASE+TPRs→	138	Streptomyces incarnatus	GCA_001027185.1	actinobacteria
AKN69758.1	EACC1	??→??→ EACC1*→ CASPASE+??→	129	Streptomyces sp. PBH53	GCA_001040905.1	actinobacteria
AKN75595.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	128	Streptomyces sp. PBH53	GCA_001040905.1	actinobacteria
ANO41895.1	EACC1	TPRs→ EACC1*→ CASPASE+TPRs→	114	Streptomyces sp. SAT1	-	actinobacteria
AOP46710.1	EACC1	EACC1*→ CASPASE+FGS_fold-domain→??→??→ TM+TM+BaxI_1→?→ NUDIX→	191	Streptomyces lydicus	GCA_001729485.1	actinobacteria
AOR36787.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	121	Streptomyces puniciscabiei	GCA_001735805.1	actinobacteria
AOS63691.1	EACC1	EACC1*→ CASPASE+??+SF1-helicase+Vsr(PDDEXK)?→	126	Actinoalloteichus hymeniacidonis	GCA_001747425.1	actinobacteria
APA99415.1	EACC1	EACC1*→ CASPASE+STAND+TPRs→	123	Nocardia seriolae	GCA_001865855.1	actinobacteria
APE36223.1	EACC1	EACC1*→ CASPASE+TPRs→	121	Nocardia sp. Y48	GCA_001886715.1	actinobacteria
APE38064.1	EACC1	EACC1*→	109	Nocardia sp. Y48	GCA_001886715.1	actinobacteria
APU44471.1	EACC1	EACC1*→ CASPASE+RE_Eco29kI+??→	117	Streptomyces sp. TN58	GCA_001941845.1	actinobacteria
AQU70505.1	EACC1	EACC1*→ CASPASE+??→	130	Streptomyces niveus	GCA_002009175.1	actinobacteria
AQW52911.1	EACC1	TetR_N+TetR_C_6→ EACC1*→ CASPASE+low-complexity+TM+PBPB→	129	Streptomyces hygroscopicus	GCA_002021875.1	actinobacteria
AQY20485.1	EACC1	EACC1*→	87	Streptomyces lydicus	GCA_000952035.2	actinobacteria
ASQ93024.1	EACC1	Pkinase+TPRs→ EACC1*→ CASPASE+TPRs→	141	Streptomyces sp. 11-1-2	GCA_003595545.1	actinobacteria
ASQ93155.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	147	Streptomyces sp. 11-1-2	GCA_003595545.1	actinobacteria
ATL84945.1	EACC1	TetR_N+TetR_C_6→ EACC1*→ CASPASE+low-complexity+TM+PBPB→	131	Streptomyces malaysiensis	GCA_002591335.1	actinobacteria
ATL88100.1	EACC1	EACC1*→ CASPASE+HisKA+HATPase_c→	164	Streptomyces malaysiensis	GCA_002591335.1	actinobacteria
AUA11757.1	EACC1	TetR_N+TetR_C_6→ EACC1*→ CASPASE+low-complexity+TM+PBPB→	141	Streptomyces sp. M56	GCA_002812405.1	actinobacteria
AUG75451.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	125	Kitasatospora sp. MMS16-BH015	GCA_002943525.1	actinobacteria
AUG81298.1	EACC1	EACC1*→	115	Kitasatospora sp. MMS16-BH015	GCA_002943525.1	actinobacteria
AUI64191.1	EACC1	EACC1*→ TM+ZU5+??→	67	Amycolatopsis sp. BJA-103	GCA_002849735.1	actinobacteria
BAL90824.1	EACC1	EACC1*→ CASPASE+TPRs→	118	Actinoplanes missouriensis 431	GCA_000284295.1	actinobacteria
CAJ62793.1	EACC1+EAD1	FHA+??+low-complexity+FHA+ABC-ATPase+TM→||←?||EACC1+EAD1*→||←CASPASE+STAND+polar_region+TM+BetaPropeller	233	Frankia alni ACN14a	GCA_000058485.1	actinobacteria
CCF64831.1	EACC1	RNR_N+Ribonuc_red_lgN+Ribonuc_red_lgC→ EACC1*→ CASPASE+FTSK+FTSK+FTSK+FTSK→	118	Nocardia cyriacigeorgica GUH-2	GCA_000284035.1	actinobacteria

acc	architecture	operon	len	species	gca	taxend
CDR06555.1	EACC1	EACC1*→	113	Streptomyces iranensis	GCA_000938975.1	actinobacteria
CEL16981.1	EACC1	PALP→ Trp_syntA→ TM+LGT→ EACC1*→	132	Kibdelosporangium sp. MJ126-NF4	GCA_000826545.1	actinobacteria
CUW28376.1	EACC1	??→??→ EACC1*→ CASPASE+??→	135	Streptomyces reticuli	GCA_001511815.1	actinobacteria
CUW29406.1	EACC1	EACC1*→ CASPASE+TM?+DUF3558+DUF3558→	145	Streptomyces reticuli	GCA_001511815.1	actinobacteria
CUW32072.1	EACC1	AMP-binding+AMP-binding_C→ AMP-binding+AMP-binding_C→ EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	156	Streptomyces reticuli	GCA_001511815.1	actinobacteria
EDN65281.1	EACC1	EACC1*→	131	Beggiatoa sp. PS	GCA_000170715.1	gammaproteobacteria
EDY66027.1	EACC1	low-complexity+HD+Tox-RelA+TGS+ACT→ Pkinase+TPRs→ EACC1*→ CASPASE+TPRs→	125	Streptomyces pristinaespiralis ATCC 25486	GCA_000154945.1	actinobacteria
EEP70832.1	EACC1	TM+TM+TM+Peptidase_M48+TM+DUF4864+??→ EACC1*→	191	Micromonospora sp. ATCC 39149	GCA_000158815.1	actinobacteria
EFE74311.1	EACC1	EACC1*→ CASPASE+Beta_rich_repeat→	138	Streptomyces roseosporus NRRL 15998	GCA_000156455.1	actinobacteria
EFF88992.1	EACC1	TPRs→ EACC1*→ CASPASE+TPRs→	121	Streptomyces sp. e14	GCA_000162775.1	actinobacteria
EFL23145.1	EACC1	EACC1*→ CASPASE+TPRs→ Clp_N+Clp_N+Clp_N+Clp_N+ClpABN-AAA→	138	Streptomyces himastatinicus ATCC 53653	GCA_000158915.1	actinobacteria
EFL27052.1	EACC1	HATPase_c_2→ EACC1*→	131	Streptomyces himastatinicus ATCC 53653	GCA_000158915.1	actinobacteria
EFL39449.1	EACC1	MglB→?→ sGTP-MglA→?→ Beta_rich?→ EACC1*→ CASPASE+TPRs→??→??→	133	Streptomyces griseoflavus Tu4000	GCA_000158975.1	actinobacteria
EHM26604.1	EACC1	EACC1*→ CASPASE+PBPB→	116	Streptomyces sp. W007	GCA_000239075.2	actinobacteria
EHR51770.1	EACC1	EACC1*→ CASPASE+TM+TM+TM+TM→	121	Saccharomonospora marina XMU15	GCA_000244955.1	actinobacteria
EMF56432.1	EACC1	EACC1*→ CASPASE+TPRs→	109	Streptomyces bottropensis ATCC 25435	GCA_000340335.2	actinobacteria
EOD64476.1	EACC1	PBPB→?→?→ Aminotran_5+PAS_6+HTH_22→ EACC1*→ CASPASE+??+TM+TM→||←Glyco_trans_4_4+UDPGT	135	Amycolatopsis vancoresmycina DSM 44592	GCA_000388135.1	actinobacteria
EPH45012.1	EACC1	EACC1*→	141	Streptomyces aurantiacus JA 4570	GCA_000414115.1	actinobacteria
EST24898.1	EACC1	EACC1*→ CASPASE+Beta_rich_repeat→	128	Streptomyces niveus NCIMB 11891	GCA_000497425.1	actinobacteria
EST29781.1	EACC1	EACC1*→ CASPASE+BetaPropeller→||←?←?||HATPase_c_2→	139	Streptomyces roseochromogenus subsp. oscitans DS 12.976	GCA_000497445.1	actinobacteria
ESU49840.1	EACC1	EACC1*→ CASPASE+Beta_rich_repeat→	131	Streptomyces sp. HCCB10043	GCA_000498935.1	actinobacteria
EWC63377.1	EACC1	EACC1*→ CASPASE+??+ART→	111	Actinokineospora spheciospongiae	GCA_000564855.1	actinobacteria
EYT80103.1	EACC1	EACC1*→	114	Streptomyces sp. Tu 6176	GCA_000611795.1	actinobacteria
EYT80250.1	EACC1	EACC1*→	134	Streptomyces sp. Tu 6176	GCA_000611795.1	actinobacteria
GAT70183.1	EACC1	EACC1*→ CASPASE+SAD+HNH→	116	Planomonospora sphaerica	GCA_001653075.1	actinobacteria
GAT71384.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	123	Planomonospora sphaerica	GCA_001653075.1	actinobacteria
GAT81834.1	EACC1	EACC1*→ CASPASE+??→	114	Streptomyces sp. F-3	GCA_001653115.1	actinobacteria
KDN73846.1	EACC1	EACC1*→ CASPASE+TM?+BetaPropeller→	153	Streptomyces olindensis	GCA_000696115.1	actinobacteria
KDN73958.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	171	Streptomyces olindensis	GCA_000696115.1	actinobacteria
KDQ68047.1	EACC1	EACC1*→ CASPASE+STAND+PBPB→	138	Streptomyces sp. NTK 937	GCA_000698495.1	actinobacteria
KEF14169.1	EACC1	EACC1*→ CASPASE+??+SF1-helicase+Vsr(PDDEXK)?→ REase+STAND→	138	Streptomyces rimosus R6-500	GCA_000707925.1	actinobacteria
KIA61331.1	EACC1	DUF2510(W3)+BicD+DUF4041+T5orf172→ EACC1*→	122	Nocardia vulneris	GCA_000811985.1	actinobacteria
KIF00454.1	EACC1	EACC1*→ CASPASE+STAND(fragment)→ AAA(fragment-helical-region)+wHTH+TM+BetaPropeller→	135	Streptomyces sp. RSD-27	GCA_000817655.1	actinobacteria
KIX79887.1	EACC1	EACC1*→ CASPASE+STAND+TM+polar_region+TM+BetaPropeller→	80	Streptomyces sp. MBRL 601	GCA_000932205.1	actinobacteria
KJY28680.1	EACC1	FAD_binding_4+FAD-oxidase_C→ DAGK_cat+DAGK_acc→ EACC1*→	132	Streptomyces sp. NRRL S-495	GCA_000966955.1	actinobacteria
KJY43406.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	133	Streptomyces sp. NRRL B-1568	GCA_000967025.1	actinobacteria
KMS82330.1	EACC1	EACC1*→	137	Streptomyces regensis	GCA_001047335.1	actinobacteria
KND30816.1	EACC1	EACC1*→ CASPASE+TM+TM+PBPB+vWA→	116	Streptomyces acidiscabies	GCA_001189015.1	actinobacteria
KND37468.1	EACC1	EACC1*→ CASPASE+Beta_rich_repeat→??+SUKH→	143	Streptomyces europaeiscabiei	GCA_001189025.1	actinobacteria
KOU85740.1	EACC1	EACC1*→ CASPASE+??+SF1-helicase+Vsr(PDDEXK)?→	120	Streptomyces sp. XY593	GCA_001279885.1	actinobacteria
KOV11283.1	EACC1	EACC1*→	110	Streptomyces sp. XY431	GCA_001279805.1	actinobacteria
KOV50628.1	EACC1	EACC1*→	104	Streptomyces sp. AS58	GCA_001279985.1	actinobacteria
KOV61478.1	EACC1	EACC1*→	121	Streptomyces sp. NRRL WC-3618	GCA_001280005.1	actinobacteria
KOV91281.1	EACC1	EACC1*→	145	Streptomyces sp. NRRL B-3648	GCA_001279545.1	actinobacteria
KPH99478.1	EACC1	EACC1*→ CASPASE+TPRs→	130	Actinobacteria bacterium OK006	GCA_001298565.1	actinobacteria

acc	architecture	operon	len	species	gca	taxend
KPI03761.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	186	Actinobacteria bacterium OK006	GCA_001298565.1	actinobacteria
KPI06058.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	147	Actinobacteria bacterium OK074	GCA_001298575.1	actinobacteria
KPI29333.1	EACC1	EACC1*→ CASPASE+low-complexity+BetaPropeller→	115	Actinobacteria bacterium OK074	GCA_001298575.1	actinobacteria
KQU66405.1	EACC1	EACC1*→ CASPASE+??+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM→	135	Phycicoccus sp. Root101	GCA_001426245.1	actinobacteria
KQX58974.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→||←MFS_1	174	Streptomyces sp. Root1304	GCA_001426405.1	actinobacteria
KSU68257.1	EACC1	EACC1*→ CASPASE+??→	128	Rhodococcus enclensis	GCA_001456965.1	actinobacteria
KUF13397.1	EACC1	EACC1*→ CASPASE+Type_III_YscG+VHL→	82	Streptomyces silvensis	GCA_001482415.1	actinobacteria
KUJ54561.1	EACC1	EACC1*→ CASPASE+TPRs→	121	Streptomyces albus subsp. albus	GCA_001507455.1	actinobacteria
KUJ66425.1	EACC1	EACC1*→ CASPASE+??→	137	Streptomyces albus subsp. albus	GCA_001507455.1	actinobacteria
KUJ70077.1	EACC1	EACC1*→ CASPASE+PBPB+vWA→	133	Streptomyces albus subsp. albus	GCA_001507455.1	actinobacteria
KUL21378.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	114	Streptomyces regalis	GCA_001509475.1	actinobacteria
KUL31772.1	EACC1	EACC1*→ CASPASE+??→	105	Actinoplanes awajinensis subsp. mycoplanecinus	GCA_001509495.1	actinobacteria
KUM90168.1	EACC1	EACC1*→ CASPASE+low-complexity+BetaPropeller→	141	Streptomyces cellostaticus	GCA_001513965.1	actinobacteria
KWT62307.1	EACC1	EACC1*→	210	Streptomyces albus subsp. albus	GCA_001541145.1	actinobacteria
KZB85498.1	EACC1	EACC1*→	67	Amycolatopsis regifaucium	GCA_001613935.1	actinobacteria
OBG60369.1	EACC1	EACC1*→ TM+TM→	96	Mycobacterium sp. E188	GCA_001666935.1	actinobacteria
OCC10925.1	EACC1	EACC1*→ CASPASE+TPRs→	87	Streptomyces sp. PTY087I2	GCA_001687325.1	actinobacteria
OEJ28906.1	EACC1	EACC1*→ CASPASE+BetaPropeller→	149	Streptomyces agglomeratus	GCA_001746415.1	actinobacteria
OEV32520.1	EACC1	EACC1*→	127	Kitasatospora aureofaciens	GCA_001188955.3	actinobacteria
OIJ66728.1	EACC1	Pkinase+TPRs→ EACC1*→ CASPASE+TPRs→	124	Streptomyces mangrovisoli	GCA_000974985.2	actinobacteria
OIJ93039.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	145	Streptomyces sp. MUSC 14	GCA_001866675.1	actinobacteria
OIK01659.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	131	Streptomyces sp. MUSC 1	GCA_001866665.1	actinobacteria
OIK08128.1	EACC1	EACC1*→	123	Streptomyces sp. MUSC 1	GCA_001866665.1	actinobacteria
OKJ53082.1	EACC1	EACC1*→ CASPASE+Beta_rich_repeat→??+SUKH→	143	Streptomyces sp. CB02115	GCA_001905645.1	actinobacteria
OKJ90725.1	EACC1	EACC1*→	134	Streptomyces sp. TSRI0107	GCA_001905845.1	actinobacteria
OKK02612.1	EACC1	EACC1*→	119	Streptomyces sp. CB03234	GCA_001905885.1	actinobacteria
OKK04987.1	EACC1	FAD_binding_4+??+BBE→ EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	123	Streptomyces sp. CB03234	GCA_001905885.1	actinobacteria
OKK25374.1	EACC1	MglB→ DUF742→ sGTP-MglA→?→?→ EACC1*→	114	Streptomyces sp. CB02488	GCA_001905365.1	actinobacteria
OLB75938.1	EACC1	EACC1*→	123	Actinobacteria bacterium 13_2_20CM_2_71_6	GCA_001917385.1	actinobacteria
OLB81125.1	EACC1	EACC1*→ CASPASE+FTSK+FTSK+FTSK+FTSK→	127	Actinobacteria bacterium 13_2_20CM_2_71_6	GCA_001917385.1	actinobacteria
OLE22616.1	EACC1+CASPASE+TPR_repeats+low_complexity+TM_region	EACC1+CASPASE+TPR_repeats+low_complexity+TM_region*→	748	Actinobacteria bacterium 13_1_20CM_3_71_11	GCA_001920275.1	actinobacteria
OLE22806.1	EACC1	EACC1*→ CASPASE+PBPB→	123	Catenulispora sp. 13_1_20CM_3_70_7	GCA_001920315.1	actinobacteria
OLE29346.1	EACC1	EACC1*→ CASPASE+DUF179→ SIR2+??→	112	Actinobacteria bacterium 13_1_20CM_3_71_11	GCA_001920275.1	actinobacteria
OLT26847.1	EACC1	EACC1*→	130	Nocardiopsis sp. CNR-923	GCA_001942255.1	actinobacteria
ONK14370.1	EACC1	EACC1*→ CASPASE+TPRs→	154	Streptomyces sp. MP131-18	GCA_001984575.1	actinobacteria
OON81606.1	EACC1	EACC1*→ CASPASE+??+SF1-helicase+Vsr(PDDEXK)?→	138	Streptomyces tsukubensis	GCA_002007125.1	actinobacteria
OPF83920.1	EACC1	EACC1*→ CASPASE+Peripla_BP_5→	122	Streptomyces antioxidans	GCA_000968685.2	actinobacteria
OPG04755.1	EACC1	EACC1*→	114	Streptomyces sp. GKU 895	GCA_002027195.1	actinobacteria
OSC72785.1	EACC1	low-complexity+HD+Tox-RelA+TGS+ACT→ Pkinase+TPRs→ EACC1*→ CASPASE+TPRs→	124	Streptomyces sp. 4F	GCA_002104855.1	actinobacteria
OSY45817.1	EACC1	EACC1*→ CASPASE+Beta_rich_repeat→	133	Streptomyces platensis	GCA_002119195.1	actinobacteria
OXL29487.1	EACC1	low-complexity+HD+Tox-RelA+TGS+ACT→ Pkinase+TPRs→ EACC1*→ CASPASE+TPRs→	131	Streptomyces sp. NBS 14/10	GCA_002224125.1	actinobacteria
OXY99187.1	EACC1	EACC1*→ CASPASE+low-complexity+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+BetaPropeller→	148	Streptomyces diastatochromogenes	GCA_002242805.1	actinobacteria
OXY99708.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→ TM+Acid_phosphat_B→	137	Streptomyces diastatochromogenes	GCA_002242805.1	actinobacteria
PAK26487.1	EACC1	low-complexity+HD+Tox-RelA+TGS+ACT→ Pkinase+TPRs→ EACC1*→ CASPASE+TPRs→	138	Streptomyces sp. alain-838	GCA_002276245.1	actinobacteria
PBC97306.1	EACC1	EACC1*→ CASPASE+BetaPropeller→	205	Streptomyces sp. Ag82_O1-15	GCA_002300485.1	actinobacteria
PFG48271.1	EACC1	GATase→ ABC-ATPase+DUF4162→ cNMP_cyclase+TM+TM+TM+TM+TM+TM→ EACC1*→	138	Amycolatopsis sulphurea	GCA_002564045.1	actinobacteria

acc	architecture	operon	len	species	gca	taxend
PIF83911.1	EACC1	EACC1*→	126	Micromonospora sp. CNZ299	GCA_002754415.1	actinobacteria
PIF88722.1	EACC1	Phage_int_SAM_3+Phage_integrase→ EACC1*→ CASPASE+TPRs→	121	Streptomyces sp. 2233.5	GCA_002754455.1	actinobacteria
PIG15861.1	EACC1	EACC1*→ CASPASE+TM+??→	125	Streptomyces sp. 94	GCA_002754555.1	actinobacteria
PIG17351.1	EACC1	EACC1*→ CASPASE+TPRs+LysM+PG-binding→	120	Streptomyces sp. 94	GCA_002754555.1	actinobacteria
PIG38694.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	147	Streptomyces sp. 93	GCA_002754595.1	actinobacteria
PIG46972.1	EACC1	low-complexity+HD+Tox-RelA+TGS+ACT→ Pkinase+TPRs→ EACC1*→ CASPASE+TPRs→	138	Streptomyces sp. 61	GCA_002754535.1	actinobacteria
PIY08225.1	EACC1	EACC1*→ CASPASE+??→	123	Flexibacter sp. CG_4_10_14_3_um_filter_32_15	GCA_002784125.1	bacteroidetes
PKB35290.1	EACC1	EACC1*→ CASPASE+STAND→ TM+BetaPropeller→ TM+Acid_phosphat_B→	148	Streptomyces sp. 69	GCA_002813405.1	actinobacteria
PKB39967.1	EACC1	EACC1*→ CASPASE+STAND+TPRs→	129	Streptomyces sp. 69	GCA_002813405.1	actinobacteria
PKK11963.1	EACC1	EACC1*→ CASPASE+??+NUDIX→	140	Thermomonospora sp. CIF 1	GCA_001896795.2	actinobacteria
PKT68436.1	EACC1	EACC1*→ CASPASE(fragment)→	120	Streptomyces populi	GCA_002911015.1	actinobacteria
PKV35908.1	EACC1	EACC1*→?→ CASPASE+STAND+polar_region+TM+BetaPropeller→ TM+Acid_phosphat_B→	137	Streptomyces sp. 59	GCA_002846295.1	actinobacteria
PKV38657.1	EACC1	EACC1*→ CASPASE+BetaPropeller→	140	Streptomyces sp. 59	GCA_002846295.1	actinobacteria
PKV55963.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	138	Streptomyces sp. 73	GCA_002846315.1	actinobacteria
PKV70128.1	EACC1	EACC1*→ CASPASE+??+STAND+??→	144	Streptomyces sp. GP55	GCA_002846355.1	actinobacteria
PKV72783.1	EACC1	polar_lead?+TM+TM+TM+polar_tail?+low-complexity→??→ EACC1*→ CASPASE+TPRs→	122	Streptomyces sp. GP55	GCA_002846355.1	actinobacteria
PKV83071.1	EACC1	EACC1*→ CASPASE+low-complexity+BetaPropeller→	157	Streptomyces sp. TLI_146	GCA_002846415.1	actinobacteria
PKV88670.1	EACC1	EACC1*→	157	Streptomyces sp. TLI_146	GCA_002846415.1	actinobacteria
PKW40573.1	EACC1	EACC1*→ CASPASE+TPRs→ Pkinase+??→	141	Streptomyces sp. OK885	GCA_002846625.1	actinobacteria
PLK97651.1	EACC1	EACC1*→	93	Klebsiella pneumoniae	GCA_002855875.1	gammaproteobacteria
POG43333.1	EACC1	Pkinase+TPRs→ EACC1*→ CASPASE+TPRs→	132	Streptomyces sp. ZL-24	GCA_002907485.1	actinobacteria
POX40554.1	EACC1	EACC1*→	90	Streptomyces sp. Ru73	GCA_002920575.1	actinobacteria
POX56155.1	EACC1	EACC1*→ CASPASE+TPRs→ Clp_N+Clp_N+ClpABN-AAA→	59	Streptomyces sp. Ru71	GCA_002920535.1	actinobacteria
PPK63807.1	EACC1	EACC1*→ CASPASE+TM+TM→ TM+PBPB→	117	Actinokineospora auranticolor	GCA_002934265.1	actinobacteria
PPQ61001.1	EACC1	low-complexity+HD+Tox-RelA+TGS+ACT→ Pkinase+TPRs→ EACC1*→ CASPASE+TPRs→	136	Streptomyces sp. QL37	GCA_002941025.1	actinobacteria
PRX04721.1	EACC1+CASPASE+TPR_repeats+low_complexity+TM_region	EACC1+CASPASE+TPR_repeats+low_complexity+TM_region*→ STAND+TPRs→	819	Actinoplanes italicus	GCA_003001815.1	actinobacteria
PRX21968.1	EACC1	Glyco_trans_4_4+UDPGT→ EACC1*→ CASPASE+PBPB+vWA→ TM+PBPB→	141	Actinoplanes italicus	GCA_003001815.1	actinobacteria
PRX63748.1	EACC1	EACC1*→ CASPASE+PBPB→	130	Nonomuraea fuscirosea	GCA_003001935.1	actinobacteria
PRY54979.1	EACC1	EACC1*→ CASPASE+TPRs→	112	Glycomyces artemisiae	GCA_003002955.1	actinobacteria
PTH84465.1	EACC1	EACC1*→ CASPASE+??→	123	Streptomyces sp. A244	GCA_003041235.1	actinobacteria
PWK45066.1	EACC1	EACC1*→ CASPASE+TM+PASTA+PASTA+PASTA→	128	Actinoplanes xinjiangensis	GCA_003148685.1	actinobacteria
PWV79680.1	EACC1	EACC1*→ CASPASE+TPRs→	125	Nocardia neocaledoniensis	GCA_003182135.1	actinobacteria
SAP16349.1	EACC1	EACC1*→ CASPASE→?+BetaPropeller→	119	Nonomuraea gerenzanensis	-	actinobacteria
SBO93207.1	EACC1	ARSR-HTH+RHOD-CDC25→??→??→ EACC1*→	132	Nonomuraea gerenzanensis	-	actinobacteria
SBW28797.1	EACC1	EACC1*→ CASPASE+SF1-helicase→	126	Candidatus Frankia californiensis	GCA_900067225.1	actinobacteria
SCD30855.1	EACC1	EACC1*→ CASPASE+??→	122	Streptomyces sp. DvalAA-14	GCA_900091855.1	actinobacteria
SCD65879.1	low_complexity+EACC1	low_complexity+EACC1*→ CASPASE+GAF+PAS→	245	Streptomyces sp. Termitarium-T10T-6	GCA_900091795.1	actinobacteria
SCD80496.1	EACC1	EACC1*→ CASPASE+STAND+PBPB→	88	Streptomyces sp. PpalLS-921	GCA_900091835.1	actinobacteria
SCF06083.1	EACC1	TM+TM+TM+Peptidase_M48+TM+DUF4864+??→ EACC1*→	153	Micromonospora carbonacea	GCA_900091535.1	actinobacteria
SCF09290.1	EACC1	EACC1*→	123	Micromonospora chokoriensis	GCA_900091505.1	actinobacteria
SCF63949.1	EACC1	EACC1*→	134	Streptomyces sp. Ncost-T6T-2b	GCA_900091965.1	actinobacteria
SCF67305.1	EACC1	TetR_N+TetR_C_6→ EACC1*→ CASPASE+TPRs→	139	Streptomyces sp. MnatMP-M27	GCA_900092015.1	actinobacteria
SCF81128.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	133	Streptomyces sp. Ncost-T10-10d	GCA_900091955.1	actinobacteria
SCK28094.1	EACC1	EACC1*→ CASPASE+Beta_rich_repeat→	163	Streptomyces sp. SceaMP-e96	GCA_900090095.1	actinobacteria
SCK31176.1	EACC1	EACC1*→ TM+TM→	73	Streptomyces sp. SceaMP-e96	GCA_900090095.1	actinobacteria
SCK35005.1	EACC1	EACC1*→ CASPASE+TPRs→	166	Streptomyces sp. AmelKG-E11A	GCA_900090165.1	actinobacteria
SDC39793.1	EACC1+CASPASE(frag)	CASPASE←?←?||HATPase_c_2→ EACC1+CASPASE(frag)*→	235	Streptomyces prasinopilosus	GCA_900101585.1	actinobacteria
SDE31791.1	EACC1	EACC1*→ CASPASE+TPRs→	112	Glycomyces harbinensis	GCA_900101745.1	actinobacteria
SDJ48636.1	EACC1	EACC1*→ CASPASE+low-complexity+DUF4190(has2TM)→	129	Frankineae bacterium MT45	GCA_900100325.1	actinobacteria

acc	architecture	operon	len	species	gca	taxend
SDN31180.1	EACC1	EACC1*→ CASPASE+TPRs→	118	Streptomyces sp. cf386	GCA_900103585.1	actinobacteria
SDQ56450.1	EACC1	EACC1*→ CASPASE+Astro_capsid_N→	119	Thermostaphylospora chromogena	GCA_900099985.1	actinobacteria
SDT41267.1	EACC1	FAD_binding_4+FAD-oxidase_C→ DAGK_cat+DAGK_acc→ EACC1*→ CASPASE+TPRs→ Clp_N+Clp_N+ClpABN-AAA→	141	Streptomyces sp. TLI_053	GCA_900105395.1	actinobacteria
SDW24590.1	EACC1	??+TM+TM+??+TM→ PBPB→ EACC1*→ CASPASE+TPRs→ PknG_rubred+Pkinase+PknG_TPR→ ZnR+PP2C→ vWA+alpha-helical→	113	Amycolatopsis xylanica	GCA_900107045.1	actinobacteria
SDW32577.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	166	Amycolatopsis xylanica	GCA_900107045.1	actinobacteria
SDY41344.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	127	Saccharopolyspora shandongensis	GCA_900106995.1	actinobacteria
SEC47799.1	EACC1	TetR_N+TetR_C_6→ EACC1*→ CASPASE+low-complexity+TM+PBPB→	130	Streptomyces melanosporofaciens	GCA_900105695.1	actinobacteria
SED09207.1	EACC1	PBPB→?→?→?→ EACC1*→ CASPASE+TM+TM→	130	Amycolatopsis tolypomycina	GCA_900105945.1	actinobacteria
SED41685.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	133	Streptomyces melanosporofaciens	GCA_900105695.1	actinobacteria
SEF56362.1	EACC1	ARSR-HTH+RHOD-CDC25→??→??→ EACC1*→	127	Nonomuraea solani	GCA_900108335.1	actinobacteria
SEG70419.1	EACC1	EACC1*→ CASPASE+BetaPropeller→ BetaPropeller(fragment)→	121	Saccharopolyspora hirsuta	GCA_900108315.1	actinobacteria
SEG73472.1	EACC1	low-complexity+HD+Tox-RelA+TGS+ACT→ Pkinase+TPRs→ EACC1*→ CASPASE+TPRs→	206	Streptomyces yangliensis	GCA_900107965.1	actinobacteria
SEH02685.1	EACC1	EACC1*→ CASPASE+BetaPropeller→	75	Nonomuraea solani	GCA_900108335.1	actinobacteria
SEJ62319.1	EACC1	EACC1*→ CASPASE+Pkinase→	112	Xiangella phaseoli	GCA_900109115.1	actinobacteria
SES39042.1	EACC1	EACC1*→ CASPASE+??+TM+TM+TM+TM+TM+TM+TM+TM→ CASPASE+??+TM+TM+TM+TM+TM+TM+TM→	123	Actinokineospora terrae	GCA_900111175.1	actinobacteria
SEU35263.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	103	Nonomuraea wenchangensis	GCA_900111685.1	actinobacteria
SEU43169.1	EACC1	TM+TM+vWA+TM→ TM+TM+vWA+TM→ EACC1*→ CASPASE+TPRs→	115	Nonomuraea wenchangensis	GCA_900111685.1	actinobacteria
SFF46366.1	EACC1	EACC1*→	155	Streptomyces alni	GCA_900112845.1	actinobacteria
SFQ15972.1	EACC1	EACC1*→ CASPASE+??+SF1-helicase+Vsr(PDDEXK)?→ vWA→	124	Amycolatopsis rubida	GCA_900115345.1	actinobacteria
SFQ20437.1	EACC1	EACC1*→ CASPASE+??+TM+TM+TM→	126	Actinomadura madurae	GCA_900115095.1	actinobacteria
SFW52991.1	EACC1	MFS_1→||←?||GATase→ ABC-ATPase+DUF4162→ cNMP_cyclase+TM+TM+TM+TM+TM+TM→ EACC1*→	118	Amycolatopsis australiensis	GCA_900119165.1	actinobacteria
SFY01652.1	EACC1	EACC1*→	139	Streptomyces atratus	GCA_900119365.1	actinobacteria
SHM52898.1	EACC1	EACC1*→ CASPASE+TM+MFS_1+TM+TM+TM+TM+TM+TM+TM→	125	Streptomyces yunnanensis	GCA_900142595.1	actinobacteria
SHM78180.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	152	Streptomyces paucisporeus	GCA_900142575.1	actinobacteria
SIM83978.1	EACC1	EACC1*→	131	Micromonospora cremea	GCA_900143515.1	actinobacteria
SNB88651.1	EACC1	EACC1*→	74	Streptomyces sp. PgraA7	GCA_900187925.1	actinobacteria
SNR23901.1	EACC1	EACC1*→ CASPASE+TM+TM→	85	Actinomadura mexicana	GCA_900188105.1	actinobacteria
SNR32426.1	EACC1	EACC1*→ CASPASE+TM+TM+TM+TM+TM+TM+TM+TM→ Aminotran_5→	124	Blastococcus sp. DSM 44272	GCA_900188025.1	actinobacteria
SNR65625.1	EACC1	EACC1*→ CASPASE+TPRs→	114	Actinoplanes regularis	GCA_900188005.1	actinobacteria
SNS54572.1	EACC1	EACC1*→ CASPASE+??+TM+TM→	132	Geodermatophilus saharensis	GCA_900188205.1	actinobacteria
SNS82844.1	EACC1	EACC1*→ CASPASE+??+TM+TM+TM→	130	Actinomadura mexicana	GCA_900188105.1	actinobacteria
SNT19761.1	EACC1	EACC1*→	75	Streptosporangium subroseum	GCA_900188345.1	actinobacteria
SOD66767.1	EACC1	EACC1*→ CASPASE+JAB→	163	Streptomyces zhaozhouensis	GCA_900230195.1	actinobacteria
SOD71875.1	EACC1	EACC1*→ CASPASE+low-complexity+DUF4190(has2TM)→?→ Glyoxalase→	129	Jatrophihabitans sp. GAS493	GCA_900230215.1	actinobacteria
SOD87477.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→ TM+Acid_phosphat_B→	137	Streptomyces sp. Ag109_G2-15	GCA_900215565.1	actinobacteria
SOE74808.1	EACC1	EACC1*→ CASPASE+TM+PBPI→	140	Streptomyces sp. OV198	GCA_900230275.1	actinobacteria
SOE81020.1	EACC1	EACC1*→ Tnp_DNA_bind+DDE_Tnp_1+Dimer_Tnp_Tn5→ CASPASE+TPRs→	131	Burkholderia sp. OK806	GCA_900230245.1	betaproteobacteria
SOR77037.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	175	Streptomyces chartreusis NRRL 3882	GCA_900236475.1	actinobacteria
WP_003079032.1	EACC1	GATase→ ABC-ATPase+DUF4162→ cNMP_cyclase+TM+TM+TM+TM+TM+TM→ EACC1*→	104	Amycolatopsis vancoresmycina	GCA_000388135.1	actinobacteria
WP_003962152.1	EACC1	EACC1*→ CASPASE+??+SF1-helicase+Vsr(PDDEXK)?→	141	Streptomyces clavuligerus	GCA_001693675.1	actinobacteria
WP_003966577.1	EACC1	Beta_rich?→ EACC1*→ CASPASE+TPRs→??→??→	133	Streptomyces sp. ACT-1	GCA_000177175.2	actinobacteria
WP_003971296.1	EACC1	EACC1*→ CASPASE+TPRs→	118	Streptomyces	GCA_000177175.2	actinobacteria
WP_003979897.1	EACC1	EACC1*→ CASPASE+TM?+BetaPropeller→	174	Streptomycetaceae	GCA_000331185.1	actinobacteria
WP_004559361.1	EACC1	EACC1*→ CASPASE+Cpn60_TCP1→	112	Amycolatopsis vancoresmycina	GCA_000388135.1	actinobacteria
WP_004945484.1	EACC1	EACC1*→	106	Streptomyces mobaraensis	GCA_000342125.1	actinobacteria
WP_005165699.1	EACC1	CASPASE+TPRs→?→ EACC1*→	131	Amycolatopsis azurea	GCA_000340415.1	actinobacteria
WP_005165783.1	EACC1	EACC1*→ CASPASE+TPRs→	110	Amycolatopsis azurea	GCA_000340415.1	actinobacteria
WP_006134566.1	EACC1	TM+TM+TM+PP2C→??→ EACC1*→ CASPASE+TM+TM+PBPB+vWA→	114	Streptomyces	GCA_000342345.1	actinobacteria
WP_006378561.1	EACC1	EACC1*→ CASPASE+TM+TM+bPH_domain+TM+TM+bPH_domain+TM+TM→	128	Streptomyces turgidiscabies	GCA_000331005.1	actinobacteria
WP_007024301.1	EACC1	CASPASE+??→ EACC1*→	129	Saccharomonospora paurometabolica	GCF_000231035.2	actinobacteria
WP_007032113.1	EACC1	MFS_1→?→||←?||EACC1*→	104	Amycolatopsis decaplanina	GCA_000342005.1	actinobacteria

acc	architecture	operon	len	species	gca	taxend
WP_007385288.1	EACC1	EACC1*→ CASPASE+??+SF1-helicase+Vsr(PDDEXK)?→	129	Streptomyces sviceus	GCA_000154965.1	actinobacteria
WP_007461575.1	EACC1	EACC1*→	137	Micromonospora lupini	GCA_000297395.2	actinobacteria
WP_007498037.1	EACC1	HATPase_c_2→ EACC1*→ CASPASE+??+SF1-helicase+Vsr(PDDEXK)?→	130	Streptomyces zinciresistens	GCA_000225525.2	actinobacteria
WP_007905045.1	EACC1	EACC1*→ CASPASE+STAND+??→	114	Ktedonobacter racemifer	GCA_000178855.1	chloroflexi
WP_008736615.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	154	Streptomyces sp. Mg1	GCA_000154885.1	actinobacteria
WP_009085569.1	EACC1	EACC1*→	108	Actinobacteria	GCA_002796545.1	actinobacteria
WP_009945795.1	EACC1	EACC1*→ CASPASE+??+SF1-helicase+Vsr(PDDEXK)?→	127	Saccharopolyspora erythraea	GCA_000448385.1	actinobacteria
WP_010033024.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	173	Streptomyces chartreusis	GCF_000226455.1	actinobacteria
WP_010311167.1	EACC1	EACC1*→ CASPASE+BetaPropeller→	121	Saccharopolyspora spinosa	GCA_002846475.1	actinobacteria
WP_010354247.1	EACC1	EACC1*→ CASPASE+TM+TM+PBPB+vWA→	115	Streptomyces acidiscabies	GCA_001485105.1	actinobacteria
WP_010692477.1	EACC1	EACC1*→ CASPASE+??+SF1-helicase+Vsr(PDDEXK)?→	131	Saccharopolyspora spinosa	GCA_002846475.1	actinobacteria
WP_011031247.1	EACC1	-	114	Streptomyces coelicolor	GCF_000203835.1	actinobacteria
WP_012379217.1	EACC1	Beta_rich?→ EACC1*→ CASPASE+TPRs→??→??→	133	Streptomyces griseus	GCA_000010605.1	actinobacteria
WP_012894232.1	EACC1+??	EACC1+??*→	456	Streptosporangium roseum	GCA_000024865.1	actinobacteria
WP_013015649.1	EACC1	Clp_N+ClpABN-AAA+CASPASE→ EACC1*→	139	Stackebrandtia nassauensis	GCA_000024545.1	actinobacteria
WP_013016199.1	EACC1	EACC1*→	115	Stackebrandtia nassauensis	GCA_000024545.1	actinobacteria
WP_013153739.1	EACC1	EACC1*→ CASPASE+TM?+BetaPropeller→	126	Nocardiopsis dassonvillei	GCA_000092985.1	actinobacteria
WP_013222002.1	EACC1	GATase→ ABC-ATPase+DUF4162→ cNMP_cyclase+TM+TM+TM+TM+TM+TM→ EACC1*→	105	Amycolatopsis mediterranei	GCA_000196835.1	actinobacteria
WP_013223403.1	EACC1	PBPB→?→?→ Aminotran_5+PAS_6+HTH_22→ EACC1*→||←Glyco_trans_4_4+UDPGT	125	Amycolatopsis mediterranei	GCA_000196835.1	actinobacteria
WP_013227198.1	EACC1	EACC1*→ CASPASE+??→	123	Amycolatopsis mediterranei	GCA_000196835.1	actinobacteria
WP_013423591.1	EACC1	EACC1*→ CASPASE+TIR→	110	Frankia inefficax	GCA_000166135.1	actinobacteria
WP_014142088.1	EACC1	EACC1→ *CASPASE+low-complexity+BetaPropeller___*_##*→	140	Streptomyces cattleya	GCA_000240165.1	actinobacteria
WP_014144110.1	EACC1	EACC1*→ CASPASE+PBPB+vWA→	151	Streptomyces cattleya	GCA_000240165.1	actinobacteria
WP_014145359.1	EACC1	EACC1*→ CASPASE+??+SF1-helicase+Vsr(PDDEXK)?→	144	Streptomyces cattleya	GCA_000240165.1	actinobacteria
WP_014182282.1	EACC1	EACC1*→ CASPASE+TM+TM+??+TM+TM+??+TM+TM+??→	120	Streptomyces	GCA_000092385.1	actinobacteria
WP_014445973.1	EACC1	EACC1*→ Clp_N+Clp_N+ClpABN-AAA+CASPASE→	118	Actinoplanes missouriensis	GCA_000284295.1	actinobacteria
WP_014670064.1	EACC1	EACC1*→ CASPASE+low-complexity+TM+PBPB→	140	Streptomyces hygroscopicus	GCA_000245355.1	actinobacteria
WP_014673606.1	EACC1	EACC1*→ CASPASE+TM?+BetaPropeller→ MDMPI_N+MDMPI_C→ META→	116	Streptomyces hygroscopicus	GCA_000245355.1	actinobacteria
WP_014796470.1	EACC1	EACC1*→ CASPASE+??→	123	Bernardetia litoralis	GCA_000265505.1	bacteroidetes
WP_015073716.1	EACC1	EACC1*→ CASPASE+GAPEAD1→	113	Gluconobacter oxydans	GCA_000311765.1	alphaproteobacteria
WP_015099360.1	EACC1	TM+TM+TM→ CASPASE+STAND+polar_region+TM+BetaPropeller→ EACC1*→	127	Saccharothrix espanaensis	GCA_000328705.1	actinobacteria
WP_015102978.1	EACC1	EACC1*→ CASPASE+TM+TM→ TM+PBPB→	118	Saccharothrix espanaensis	GCA_000328705.1	actinobacteria
WP_015655483.1	EACC1	EAD2+VMAP-M0+CASPASE→ EACC1*→	134	Streptomyces davaonensis	GCA_000349325.1	actinobacteria
WP_015655816.1	EACC1	EACC1*→	110	Streptomyces davaonensis	GCA_000349325.1	actinobacteria
WP_015656507.1	EACC1	EACC1*→ CASPASE+TM+TM+bPH_domain+TM+TM+bPH_domain+TM+TM→	123	Streptomyces davaonensis	GCA_000349325.1	actinobacteria
WP_015662965.1	EACC1	EACC1*→ CASPASE+TM?+DUF3558+DUF3558→	120	Streptomyces davaonensis	GCA_000349325.1	actinobacteria
WP_015792459.1	EACC1	EACC1*→ CASPASE+low-complexity+BetaPropeller→ CASPASE+low-complexity+BetaPropeller→	115	Catenulispora acidiphila	GCA_000024025.1	actinobacteria
WP_015801011.1	EACC1	EACC1*→	121	Actinosynnema mirum	GCA_000023245.1	actinobacteria
WP_016332521.1	EACC1	EACC1*→	104	Amycolatopsis orientalis	GCA_000400635.2	actinobacteria
WP_016335695.1	EACC1	EACC1*→ CASPASE+DnaJ_ZnR+DnaJ_ZnR+DnaJ_C→	122	Amycolatopsis orientalis	GCA_000400635.2	actinobacteria
WP_016432744.1	EACC1	EACC1*→ CASPASE+TPRs→	75	Streptomyces sp. HGB0020	GCA_000411315.1	actinobacteria
WP_016435707.1	EACC1	EACC1*→ CASPASE+??+TM+??→	118	Streptomyces sp. HGB0020	GCA_000411315.1	actinobacteria
WP_016572868.1	EACC1	EACC1*→	124	Streptomyces albulus	GCA_000963515.1	actinobacteria
WP_016640036.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	142	Streptomyces aurantiacus	GCA_000414115.1	actinobacteria
WP_017301504.1	EACC1	EACC1*→ CASPASE+DUF4062+??+HATPase_c_4+STAND→	125	Nodosilinea nodulosa	GCF_000309385.1	cyanobacteria
WP_017594165.1	EACC1	EACC1*→ CASPASE+TM?+BetaPropeller→	146	Nocardiopsis potens	GCF_000341105.1	actinobacteria
WP_017616278.1	EACC1	EACC1*→	122	Nocardiopsis salina	GCF_000341025.1	actinobacteria
WP_017982730.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	122	Amycolatopsis methanolica	GCA_000739085.1	actinobacteria
WP_018087816.1	EACC1	EACC1*→ CASPASE+FGS_fold-domain→??→??→ TM+TM+BaxI_1→?→ NUDIX→	134	Streptomyces sp. FxanaC1	GCF_000375625.1	actinobacteria
WP_018088837.1	EACC1	EACC1*→ CASPASE+DnaJ_ZnR+DnaJ_ZnR+DnaJ_C→	135	Streptomyces sp. FxanaC1	GCF_000375625.1	actinobacteria
WP_018089822.1	EACC1	-	155	Streptomyces sp. FxanaC1	-	actinobacteria
WP_018348269.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	123	Longispora albida	GCF_000379825.1	actinobacteria

acc	architecture	operon	len	species	gca	taxend
WP_018382060.1	EACC1	EACC1*→ CASPASE+TPRs→	121	Streptomyces vitaminophilus	GCA_001445835.1	actinobacteria
WP_018487316.1	EACC1	EACC1*→ CASPASE+TPRs??+GHKL_ATPase+TPRs??→	121	Streptomyces sp. CcalMP-8W	GCF_000373305.1	actinobacteria
WP_018537276.1	EACC1	??→ EACC1*→ CASPASE+TPRs→	126	Streptomyces sp. MspMP-M5	GCF_000373585.1	actinobacteria
WP_018538327.1	EACC1	EACC1*→ CASPASE+TM+Beta_rich→	116	Streptomyces sp. MspMP-M5	GCF_000373585.1	actinobacteria
WP_018540178.1	EACC1	EACC1*→ CASPASE+TM+??→	78	Streptomyces sp. MspMP-M5	GCF_000373585.1	actinobacteria
WP_018541940.1	EACC1	EACC1*→ CASPASE+TM+BetaPropeller→	117	Streptomyces sp. MspMP-M5	GCF_000373585.1	actinobacteria
WP_018549570.1	EACC1	-	149	Streptomyces sp. LaPpAH-108	-	actinobacteria
WP_018554561.1	EACC1	-	127	Streptomyces sp. ATexAB-D23	-	actinobacteria
WP_018558425.1	EACC1	EACC1*→ CASPASE+PBPB+vWA→	122	Streptomyces sp. BoleA5	GCF_000373665.1	actinobacteria
WP_018569469.1	EACC1	TPRs→ EACC1*→ CASPASE+TPRs→	114	Streptomyces sp. PsTaAH-124	GCF_000373685.1	actinobacteria
WP_018654763.1	EACC1	EACC1*→ CASPASE+SAD+HNH→	123	Actinomadura flavalba	GCF_000374305.1	actinobacteria
WP_018683317.1	EACC1	EACC1*→ CASPASE+TPRs→	139	Actinokineospora enzanensis	GCF_000374445.1	actinobacteria
WP_018842129.1	EACC1	-	135	Streptomyces sp. CNS335	-	actinobacteria
WP_018851576.1	EACC1	EACC1*→ CASPASE+??→	137	Streptomyces sp. CNY243	GCF_000377165.1	actinobacteria
WP_018895946.1	EACC1	TM+REase→ EACC1*→ CASPASE+??+SF1-helicase+Vsr(PDDEXK)?→	132	Streptomyces sp. CNY228	GCF_000377545.1	actinobacteria
WP_018956197.1	EACC1	Beta_rich?→ EACC1*→ CASPASE+TPRs→??→??→	133	Streptomyces sp. CNB091	GCF_000377965.1	actinobacteria
WP_019060213.1	EACC1	polar_lead?+TM+TM+TM+polar_tail?+low-complexity→??→ EACC1*→ CASPASE+TPRs→	159	Streptomyces prunicolor	GCF_000367365.1	actinobacteria
WP_019075768.1	EACC1	EACC1*→ CASPASE+STAND+BetaPropeller→	167	Streptomyces hokutonensis	GCF_000376565.1	actinobacteria
WP_019325097.1	EACC1	EACC1*→ CASPASE+TPRs→	138	Streptomyces sp. TOR3209	GCF_000259895.1	actinobacteria
WP_019329427.1	EACC1	Trypsin+HDxxH+VMAP-M0+CASPASE→ EACC1*→	-	-	GCF_000259895.1	-
WP_019608401.1	EACC1	EACC1*→ CASPASE+TM?+BetaPropeller→	126	Nocardiopsis	GCA_002260685.1	actinobacteria
WP_019750099.1	EACC1	EACC1*→ CASPASE+??→	128	Rhodococcus	GCF_000469645.1	actinobacteria
WP_019885900.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	204	Streptomyces purpureus	GCF_000384175.1	actinobacteria
WP_019927514.1	EACC1	EACC1*→ CASPASE+TM+BetaPropeller→ CASPASE+TM+TM+BetaPropeller→ CASPASE+TM+BetaPropeller→	191	Nocardia sp. BMG111209	GCF_000381925.1	actinobacteria
WP_019929385.1	EACC1	EACC1*→	96	Nocardia sp. BMG111209	GCF_000381925.1	actinobacteria
WP_019930719.1	EACC1	EACC1*→ CASPASE+TPRs→	116	Nocardia sp. BMG111209	GCF_000381925.1	actinobacteria
WP_019983234.1	EACC1	TPRs→ EACC1*→ CASPASE+TPRs→	114	Streptomyces sp. Amel2xE9	GCF_000383935.1	actinobacteria
WP_020115005.1	EACC1	EACC1*→ CASPASE+TPRs→	119	Streptomyces bottropensis	GCF_000340335.1	actinobacteria
WP_020117476.1	EACC1	low-complexity+HD+Tox-RelA+TGS+ACT→ Pkinase+TPRs→ EACC1*→ CASPASE+TPRs→	124	Streptomyces canus	GCF_000383615.1	actinobacteria
WP_020135550.1	EACC1	EACC1*→ CASPASE+TPRs→	151	Streptomyces sp. 351MFTsu5.1	GCF_000383655.1	actinobacteria
WP_020141601.1	EACC1	EACC1*→ CASPASE+??+TM+TM+TM+TM+TM+TM+TM+TM→	124	Terracoccus sp. 273MFTsu3.1	GCF_000383675.1	actinobacteria
WP_020419828.1	EACC1	Pkinase+TM+TM+DUF3298+PSBP→ EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→||←?||?→||←PSE←?←?←FAD_binding_4+??+BBE	125	Amycolatopsis sp. ATCC 39116	GCF_000231075.2	actinobacteria
WP_020464182.1	TIR+EACC1+EAD1	??+TM+BetaPropeller→ TIR+EACC1+EAD1*→	405	Frankia sp. EAN1pec	GCA_000018005.1	actinobacteria
WP_020509053.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	118	Actinoplanes globisporus	GCF_000379645.1	actinobacteria
WP_020629315.1	EACC1	EACC1*→ CASPASE+TPRs→	109	Amycolatopsis alba	GCA_002234385.1	actinobacteria
WP_020631088.1	EACC1	EACC1*→	74	Amycolatopsis alba	GCA_002234385.1	actinobacteria
WP_020642628.1	EACC1	GATase→ ABC-ATPase+DUF4162→ cNMP_cyclase+TM+TM+TM+TM+TM+TM→ EACC1*→	104	Amycolatopsis balhimycina	GCA_003947255.1	actinobacteria
WP_020663538.1	EACC1	GATase→ ABC-ATPase+DUF4162→ cNMP_cyclase+TM+TM+TM+TM+TM+TM→ EACC1*→	108	Amycolatopsis benzoatilytica	GCF_000383915.1	actinobacteria
WP_020666482.1	EACC1	??+TM+TM+??+TM→ PBPB→ EACC1*→ CASPASE+TPRs→ PknG_rubred+Pkinase+PknG_TPR→ ZnR+PP2C→ vWA+alpha-helical→	114	Amycolatopsis nigrescens	GCF_000384315.1	actinobacteria
WP_023539736.1	EACC1	EACC1*→ CASPASE+??+SF1-helicase+Vsr(PDDEXK)?→	138	Streptomyces niveus	GCA_000497425.1	actinobacteria
WP_023560335.1	EACC1	EACC1*→ CASPASE+??→	122	Actinoplanes friuliensis	GCA_000494755.1	actinobacteria
WP_024806583.1	EACC1	EACC1*→ CASPASE+??→	116	Nocardia sp. BMG51109	GCF_000526215.1	actinobacteria
WP_024934407.1	EACC1	EACC1*→ CASPASE+??+TM+TM+TM→	126	Actinomadura madurae	GCF_000468475.2	actinobacteria
WP_025327428.1	EACC1	EACC1*→	119	Aeromonas hydrophila	GCF_000512185.1	gammaproteobacteria
WP_025348143.1	EACC1	DUF2510(W3)+BicD+DUF4041+T5orf172→ EACC1*→ CASPASE+TPRs→	122	Nocardia nova	GCA_000523235.1	actinobacteria
WP_025357936.1	EACC1	polar_lead?+TM+TM+TM+polar_tail?+low-complexity→??→ EACC1*→ CASPASE+TPRs→?→ CASPASE+??+TPRs?→	116	Kutzneria albida	GCF_000525635.1	actinobacteria
WP_026047540.1	EACC1	EACC1*→ CASPASE+??+SF1-helicase+Vsr(PDDEXK)?→	138	Streptomyces	GCA_900116145.1	actinobacteria
WP_026469049.1	EACC1	PBPB→?→?→ Aminotran_5+PAS_6+HTH_22→ EACC1*→	126	Amycolatopsis balhimycina	GCA_003947255.1	actinobacteria
WP_026855269.1	EACC1	EACC1*→ CASPASE+TM+TM+TM+TM+TM+TM+TM+TM→	124	Geodermatophilaceae bacterium URHB0062	GCF_000620185.1	actinobacteria
WP_026931303.1	EACC1	EACC1*→	113	Glycomyces tenuis	GCF_000427885.1	actinobacteria
WP_027003174.1	EACC1	EACC1*→ CASPASE+??→	131	Hugenholtzia roseola	GCF_000422585.1	bacteroidetes

acc	architecture	operon	len	species	gca	taxend
WP_027746727.1	EACC1	EACC1*→ CASPASE+TPRs→	149	Streptomyces sp. CNT371	GCF_000514995.1	actinobacteria
WP_027770853.1	EACC1	EACC1*→ CASPASE+STAND+TPRs→	132	Streptomyces sp. CNQ329	GCF_000482585.1	actinobacteria
WP_027930057.1	EACC1	Pkinase+TM+TM+DUF3298+PSBP→ EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	125	Amycolatopsis thermoflava	GCF_000473265.1	actinobacteria
WP_028419166.1	EACC1	EACC1*→ CASPASE+TPRs??+GHKL_ATPase+TPRs??→	121	Streptomyces sp. SolWspMP-sol2th	GCF_000647875.1	actinobacteria
WP_028435836.1	EACC1	EACC1*→ CASPASE+TPRs→	119	Streptomyces sp. TAA486	GCF_000426165.1	actinobacteria
WP_028661367.1	EACC1	EACC1*→	128	Nocardioides insulae	GCF_000422825.1	actinobacteria
WP_029721226.1	EACC1	EACC1*→ CASPASE+??+SF1-helicase+Vsr(PDDEXK)?→	130	Saccharopolyspora rectivirgula	GCA_000710755.1	actinobacteria
WP_030029222.1	EACC1	-	118	Streptomyces flavotricini	-	actinobacteria
WP_030076799.1	EACC1	EACC1*→ CASPASE+DnaJ_ZnR+DnaJ_ZnR+DnaJ_C→	135	Streptomyces decoyicus	GCA_001270575.1	actinobacteria
WP_030116247.1	EACC1	low-complexity+HD+Tox-RelA+TGS+ACT→ Pkinase+TPRs→ EACC1*→ CASPASE+TPRs→	135	Streptomyces	GCF_000717015.1	actinobacteria
WP_030125864.1	EACC1	EACC1*→	118	[Kitasatospora] papulosa	GCF_000717245.1	actinobacteria
WP_030154375.1	EACC1	EACC1*→ CASPASE+??+SF1-helicase+Vsr(PDDEXK)?→	136	Streptomyces sp. NRRL S-244	GCF_000717915.1	actinobacteria
WP_030154700.1	EACC1	EACC1*→ CASPASE+TPRs→	112	Glycomyces sp. NRRL B-16210	GCA_004364985.1	actinobacteria
WP_030177526.1	EACC1	??→ EACC1*→	114	Streptomyces sp. NRRL S-813	GCF_000718945.1	actinobacteria
WP_030192630.1	EACC1	EACC1*→ CASPASE+Concanavalin?→	126	Streptomyces	GCA_900090135.1	actinobacteria
WP_030192767.1	EACC1	low-complexity+HD+Tox-RelA+TGS+ACT→ Pkinase+TPRs→ EACC1*→ CASPASE+TPRs→	134	Streptomyces sp. NRRL S-87	GCF_000719335.1	actinobacteria
WP_030195455.1	EACC1	low-complexity+HD+Tox-RelA+TGS+ACT→ Pkinase+TPRs→ EACC1*→ CASPASE+TPRs→	135	Streptomyces	GCA_002082175.1	actinobacteria
WP_030219435.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→ HTH+N6_Mtase+Methylase_S→	129	Streptomyces sp. NRRL WC-3626	GCF_000718785.1	actinobacteria
WP_030241573.1	EACC1	EACC1*→ CASPASE+STAND+??+TPRs+??→	78	Streptomyces	GCF_000717875.1	actinobacteria
WP_030253333.1	EACC1	EACC1*→ CASPASE+TM?+BetaPropeller→	139	Streptomyces violens	GCF_000717745.1	actinobacteria
WP_030294927.1	EACC1	EACC1*→ CASPASE+Concanavalin?→	126	Streptomyces	GCA_001279425.1	actinobacteria
WP_030312162.1	EACC1	EACC1*→ CASPASE+??+SF1-helicase+Vsr(PDDEXK)?→ REase+STAND→	138	Streptomycetaceae	GCA_000707945.1	actinobacteria
WP_030334374.1	EACC1	TM+TM+TM+Peptidase_M48+TM+DUF4864+??→ EACC1*→	130	Micromonospora parva	GCF_000718515.1	actinobacteria
WP_030338292.1	EACC1	EACC1*→ CASPASE+TM+TM+bPH_domain?→	109	Streptomyces sp. NRRL S-1022	GCF_000720135.1	actinobacteria
WP_030339067.1	EACC1	EACC1*→ CASPASE+Concanavalin?→	126	Streptomyces floridae	GCF_000717665.1	actinobacteria
WP_030348773.1	EACC1	EACC1*→	119	Streptomyces sp. NRRL S-1022	GCF_000720135.1	actinobacteria
WP_030398398.1	EACC1	EACC1*→ CASPASE+HSP70→	151	Kitasatospora purpeofusca	GCF_000718025.1	actinobacteria
WP_030411720.1	EACC1	EACC1*→ CASPASE+TM+PBPB+vWA→	147	Streptomyces sp. NRRL S-1448	GCF_000719365.1	actinobacteria
WP_030453461.1	EACC1	EACC1*→	156	Herbidospora cretacea	GCF_000719065.1	actinobacteria
WP_030489041.1	EACC1	TM+TM+TM+Peptidase_M48+TM+DUF4864+??→ EACC1*→	134	Micromonospora chokoriensis	GCF_000718555.1	actinobacteria
WP_030490635.1	EACC1	EACC1*→	105	Micromonospora chokoriensis	GCF_000718555.1	actinobacteria
WP_030494645.1	EACC1	HATPase_c_2→ EACC1*→ CASPASE+??+SF1-helicase+Vsr(PDDEXK)?→	141	Microtetraspora glauca	-	actinobacteria
WP_030498129.1	EACC1	EACC1*→ CASPASE+STAND+??+TPRs+??→	162	Microtetraspora glauca	-	actinobacteria
WP_030521461.1	EACC1	EACC1*→ CASPASE+TPRs→	114	Nocardia rhamnosiphila	GCF_001613485.1	actinobacteria
WP_030546253.1	EACC1	EACC1*→ CASPASE+PBPB+vWA→	129	Streptomyces albus	GCF_000719865.1	actinobacteria
WP_030546694.1	EACC1	EACC1*→ CASPASE+TPRs→??→??	118	Streptomyces albus	GCF_000719865.1	actinobacteria
WP_030575480.1	EACC1	EACC1*→??+vWA→?→ CASPASE+TPRs→	113	Streptomyces sclerotialus	-	actinobacteria
WP_030609229.1	EACC1	EACC1*→ CASPASE+??+SF1-helicase+Vsr(PDDEXK)?→	127	Streptomyces achromogenes	GCF_000720835.1	actinobacteria
WP_030629352.1	EACC1	EACC1*→ CASPASE+??+SF1-helicase+Vsr(PDDEXK)?→	138	Streptomyces	GCA_900090065.1	actinobacteria
WP_030639116.1	EACC1	EACC1*→	118	Streptomyces sp. NRRL B-24051	GCF_000720405.1	actinobacteria
WP_030648078.1	EACC1	EACC1*→ CASPASE+??+SF1-helicase+Vsr(PDDEXK)?→??	145	Streptomyces rimosus	GCF_000718675.1	actinobacteria
WP_030656920.1	EACC1	EACC1*→ CASPASE+TM?+BetaPropeller→ MDMPI_N+MDMPI_C→ META→	116	Streptomyces	GCA_001047335.1	actinobacteria
WP_030679573.1	EACC1	EACC1*→ CASPASE+TPRs→	119	Streptomyces cellulosae	GCF_000721105.1	actinobacteria
WP_030705286.1	EACC1	Beta_rich?→ EACC1*→ CASPASE+TPRs→??→??	133	Streptomyces	GCA_900090075.1	actinobacteria
WP_030715834.1	EACC1	EACC1*→ CASPASE+??+SF1-helicase+Vsr(PDDEXK)?→	135	Streptomyces sp. NRRL F-2580	GCF_000720115.1	actinobacteria
WP_030733252.1	EACC1	-	142	Streptomyces sp. NRRL F-2890	-	actinobacteria
WP_030738956.1	EACC1	EACC1*→ CASPASE+TPRs→??→??	117	Streptomyces sp. NRRL F-2890	GCF_000719915.1	actinobacteria
WP_030741736.1	EACC1	EACC1*→ CASPASE+TPRs→	112	Streptomyces griseus	GCF_000718235.1	actinobacteria
WP_030777398.1	EACC1	EACC1*→ CASPASE+??+SF1-helicase+Vsr(PDDEXK)?→	127	Streptomyces lavenduligriseus	GCF_000718625.1	actinobacteria
WP_030783977.1	EACC1	EACC1*→ CASPASE+TM?+BetaPropeller→	133	Streptomyces lavenduligriseus	GCF_000718625.1	actinobacteria
WP_030815966.1	EACC1	EACC1*→ CASPASE+TM?+BetaPropeller→	156	Streptomyces sp. NRRL S-337	GCF_000720175.1	actinobacteria
WP_030821552.1	EACC1	EACC1*→ CASPASE+??+SF1-helicase+Vsr(PDDEXK)?→	140	Streptomyces	GCA_000966965.1	actinobacteria

acc	architecture	operon	len	species	gca	taxend
WP_030833567.1	EACC1	EACC1*→ CASPASE+STAND+??+TPRs→	133	Streptomyces	GCA_001279005.1	actinobacteria
WP_030850288.1	EACC1	EACC1*→ CASPASE+TPRs→	119	Streptomyces sp. NRRL F-4474	GCF_000719855.1	actinobacteria
WP_030860065.1	EACC1	-	116	Streptomyces sp. NRRL F-2747	-	actinobacteria
WP_030874413.1	EACC1	EACC1*→ CASPASE+Pkinase+TM?+??→	121	Streptomyces varsoviensis	GCA_001270595.1	actinobacteria
WP_030882299.1	EACC1	EACC1*→ CASPASE+TPRs→	165	Streptomyces sp. NRRL S-1868	GCF_000721305.1	actinobacteria
WP_030892741.1	EACC1	EACC1*→ CASPASE+TPRs→	162	Streptomyces sp. NRRL F-5053	GCF_000721445.1	actinobacteria
WP_030924025.1	EACC1	polar_lead?+TM+TM+TM+polar_tail?+low-complexity→??→ EACC1*→ CASPASE+TPRs→	118	Streptomyces sp. NRRL S-384	GCF_000721625.1	actinobacteria
WP_030935869.1	EACC1	EACC1*→	118	Streptomyces sp. NRRL B-24720	GCF_000721715.1	actinobacteria
WP_030968235.1	EACC1	DUF262+DUF1524+DNA_binding_1+??→?→ polar_lead?+TM+TM+TM+polar_tail?+low-complexity→??→ EACC1*→	124	Streptomyces sp. NRRL S-1824	GCF_000719575.1	actinobacteria
WP_030987664.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	111	Streptomyces sp. NRRL S-1813	GCF_000719605.1	actinobacteria
WP_030991892.1	EACC1	EACC1*→ CASPASE+DnaJ_ZnR+DnaJ_ZnR+DnaJ_C→	135	Streptomyces sp. NRRL S-1813	GCF_000719605.1	actinobacteria
WP_031005419.1	EACC1	HATPase_c_2→ EACC1*→ CASPASE+??+SF1-helicase+Vsr(PDDEXK)?→	141	Streptomyces sp. NRRL F-5727	GCF_000719555.1	actinobacteria
WP_031014439.1	EACC1	EACC1*→ CASPASE+STAND+??+TPRs+??→	123	Streptomyces sp. NRRL F-5727	GCF_000719555.1	actinobacteria
WP_031080561.1	EACC1	EACC1*→ CASPASE+TPRs→ TPRs→	118	Streptomyces sp. NRRL WC-3549	GCF_000721935.1	actinobacteria
WP_031084685.1	EACC1	EACC1*→	134	Streptomyces sp. NRRL WC-3549	GCF_000721935.1	actinobacteria
WP_031146689.1	EACC1	EACC1*→ CASPASE+??+SF1-helicase+Vsr(PDDEXK)?→	140	Streptomyces erythrochromogenes	GCF_000725555.1	actinobacteria
WP_031160229.1	EACC1	EACC1*→ CASPASE+??+SF1-helicase+Vsr(PDDEXK)?→	126	Streptomyces durhamensis	GCF_000725475.1	actinobacteria
WP_031484390.1	EACC1	EACC1*→ CASPASE+TM?+BetaPropeller→ MDMPI_N+MDMPI_C→	117	Streptomyces bicolor	GCF_000725465.1	actinobacteria
WP_032291538.1	EACC1	EACC1*→	116	Enterobacteriaceae	GCA_004219385.1	gammaproteobacteria
WP_032773793.1	EACC1	-	118	Streptomyces griseus	-	actinobacteria
WP_032798005.1	EACC1	EACC1*→	131	Streptomyces filamentosus	GCF_000156455.1	actinobacteria
WP_033030163.1	EACC1	EACC1*→ CASPASE+??+SF1-helicase+Vsr(PDDEXK)?→??→	145	Streptomyces rimosus	GCA_003947585.1	actinobacteria
WP_033085337.1	EACC1	EACC1*→ CASPASE+STAND+TPRs→	125	Nocardia seriolae	GCA_000583715.2	actinobacteria
WP_033263563.1	EACC1	PBPB→?→?→ Aminotran_5+PAS_6+HTH_22→ EACC1*→ CASPASE+??+TM+TM→||←Glyco_trans_4_4+UDPGT	125	Amycolatopsis vancoresmycina	GCF_000388135.1	actinobacteria
WP_033263828.1	EACC1	EACC1*→ CASPASE+TPRs→	117	Streptomyces	GCA_002189675.1	actinobacteria
WP_033269153.1	EACC1	Glyoxalase→ EACC1*→ CASPASE+DnaJ_ZnR+DnaJ_ZnR+DnaJ_C→	135	Streptomyces lydicus	GCF_001984445.1	actinobacteria
WP_033291480.1	EACC1	EACC1→ CASPASE+TPRs→?→ EACC1*→	109	Amycolatopsis jejuensis	GCF_000717335.1	actinobacteria
WP_033314394.1	EACC1	EACC1*→ CASPASE+TM+TM+PBPB+vWA→	121	Streptomyces iakyrus	GCF_000717055.1	actinobacteria
WP_033355495.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	131	Kitasatospora aureofaciens	GCF_000716885.1	actinobacteria
WP_033946822.1	EACC1	EACC1*→ CASPASE+??→	154	Streptomyces sp. CNQ431	GCF_000797385.1	actinobacteria
WP_034092777.1	EACC1	EACC1*→ CASPASE+TPRs→ Pkinase+??→	116	Streptacidiphilus albus	GCF_000787755.1	actinobacteria
WP_034262749.1	EACC1	polar_lead?+TM+TM+TM+polar_tail?+low-complexity→??→ EACC1*→ CASPASE+TPRs→	149	Actinospica robiniae	GCF_000504285.1	actinobacteria
WP_034267997.1	EACC1	EACC1*→ CASPASE+??→	113	Actinospica robiniae	GCF_000504285.1	actinobacteria
WP_034484638.1	EACC1	EACC1*→ CASPASE+BetaPropeller→	111	Actinomadura oligospora	GCF_000518265.1	actinobacteria
WP_035279790.1	EACC1	EACC1*→ CASPASE+??+ART→	117	Actinokineospora spheciospongiae	GCA_003182415.1	actinobacteria
WP_035302986.1	EACC1	EACC1*→	118	Actinokineospora inagensis	GCF_000482865.1	actinobacteria
WP_036372545.1	EACC1	TM+TM+TM+Peptidase_M48+TM+DUF4864+??→ EACC1*→	140	Micromonospora sp. ATCC 39149	GCF_000158815.1	actinobacteria
WP_036514812.1	EACC1	EACC1*→ CASPASE+TPRs→	121	Nocardia rhamnosiphila	GCF_001613485.1	actinobacteria
WP_036538668.1	EACC1	RNR_N+Ribonuc_red_lgN+Ribonuc_red_lgC→ EACC1*→	119	Nocardia cyriacigeorgica	GCA_005863225.1	actinobacteria
WP_037320246.1	EACC1	EACC1*→	110	Amycolatopsis orientalis	GCF_000478275.1	actinobacteria
WP_037342923.1	EACC1	EACC1*→	101	Amycolatopsis sp. MJM2582	GCA_000754115.1	actinobacteria
WP_037367462.1	EACC1	EACC1*→	108	Amycolatopsis orientalis	GCF_000411975.1	actinobacteria
WP_037570982.1	EACC1	EACC1*→ CASPASE+TPRs→	122	Streptacidiphilus oryzae	GCF_000744815.1	actinobacteria
WP_037662633.1	EACC1	-	150	Streptomyces griseofuscus	-	actinobacteria
WP_037683222.1	EACC1	EACC1*→ CASPASE+Trypsin+STAND+??+TM→	134	Streptomyces griseus	GCF_000720255.1	actinobacteria
WP_037710889.1	EACC1	EACC1*→ CASPASE+STAND+PBPB→	138	Streptomyces sp. ATexAB-D23	GCF_000373645.1	actinobacteria
WP_037726786.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	147	Streptomyces scopuliridis	GCA_003073355.1	actinobacteria
WP_037735136.1	EACC1	??→ EACC1*→ CASPASE+TM+TM+PBPB+vWA→	126	Streptomyces mirabilis	GCF_000746395.1	actinobacteria
WP_037737687.1	EACC1	EACC1*→ CASPASE+Beta_rich_repeat→	135	Streptomyces sp. CNT371	GCF_000514995.1	actinobacteria
WP_037738220.1	EACC1	EACC1*→ CASPASE+Cpn60_TCP1→	128	Streptomyces mirabilis	GCF_000746395.1	actinobacteria
WP_037738505.1	EACC1	EACC1*→ CASPASE+Beta_rich_repeat→	135	Streptomyces sp. CNQ865	GCF_000424805.1	actinobacteria
WP_037743072.1	EACC1	EACC1*→ CASPASE+STAND+TPRs→	132	Streptomyces mirabilis	GCF_000746395.1	actinobacteria

acc	architecture	operon	len	species	gca	taxend
WP_037743851.1	EACC1	EACC1*→ CASPASE+TPRs→	144	Streptomyces sp. CNQ-525	GCA_004217635.1	actinobacteria
WP_037743995.1	EACC1	polar_lead?+TM+TM+TM+polar_tail?+low-complexity→??→ EACC1*→ CASPASE+TPRs→	150	Streptomyces mirabilis	GCF_000746395.1	actinobacteria
WP_037754092.1	EACC1	EACC1*→ CASPASE+Beta_rich_repeat→	135	Streptomyces sp. CNQ-525	GCF_000701285.1	actinobacteria
WP_037792010.1	EACC1	EACC1*→ CASPASE+??→	132	Streptomyces sp. CNS606	GCF_000426325.1	actinobacteria
WP_037809200.1	EACC1	GATase→ ABC-ATPase+DUF4162→ cNMP_cyclase+TM+TM+TM+TM+TM+TM→ EACC1*→	109	Streptomyces sp. NRRL F-3213	GCF_000720075.1	actinobacteria
WP_037811931.1	EACC1	EACC1*→ CASPASE+??+TM+TM→	189	Streptomyces sp. MspMP-M5	GCF_000373585.1	actinobacteria
WP_037873834.1	EACC1	EACC1*→	120	Streptomyces	GCF_000373685.1	actinobacteria
WP_037877852.1	EACC1	EACC1*→ CASPASE+STAND+PBPB→	127	Streptomyces sp. NTK 937	GCF_000698495.1	actinobacteria
WP_037879140.1	EACC1	EACC1*→ CASPASE+TPRs→	119	Streptomyces sp. NTK 937	GCA_000698495.1	actinobacteria
WP_037891842.1	EACC1	TPRs→ EACC1*→ CASPASE+TPRs→	114	Streptomyces sp. Tu 6176	GCA_000611795.1	actinobacteria
WP_037958524.1	EACC1	EACC1*→ CASPASE+STAND+TPRs→	144	Streptomyces sp. PRh5	GCA_000590515.1	actinobacteria
WP_038508877.1	EACC1	EACC1*→ CASPASE+??→	121	Amycolatopsis japonica	GCA_000732925.1	actinobacteria
WP_038516952.1	EACC1	EACC1*→ CASPASE+TPRs→	110	Amycolatopsis japonica	GCA_000732925.1	actinobacteria
WP_039656817.1	EACC1	HATPase_c_2→ EACC1*→ CASPASE+??+SF1-helicase+Vsr(PDDEXK)?→	127	Streptomyces	GCA_000802245.2	actinobacteria
WP_039795335.1	EACC1	EACC1*→ CASPASE+TM+TM→	124	Nocardia araoensis	GCF_000308435.1	actinobacteria
WP_040694361.1	EACC1	EACC1*→ CASPASE+TM+BetaPropeller→	122	Nocardia vinacea	GCF_000308835.1	actinobacteria
WP_040712577.1	EACC1	EACC1*→	120	Nocardia takedensis	GCF_000308695.1	actinobacteria
WP_040745697.1	EACC1	EACC1*→ CASPASE+TPRs→	119	Nocardia transvalensis	GCF_000308875.1	actinobacteria
WP_040815634.1	EACC1	EACC1*→ CASPASE+BetaPropeller→	139	Nocardia concava	GCF_000308815.1	actinobacteria
WP_040828294.1	EACC1	DUF262+DUF1524+DNA_binding_1+??→?→ EACC1*→ CASPASE+STAND+TPRs+OMPdecase→	128	Nocardia jiangxiensis	GCF_000308615.1	actinobacteria
WP_040836686.1	EACC1	EACC1*→ CASPASE+TM+TM+PBPB+vWA→	111	Streptomyces acidiscabies	GCF_000242715.1	actinobacteria
WP_040857178.1	EACC1	EACC1*→ CASPASE+STAND+TPRs→	132	Nocardia niigatensis	GCF_000308655.1	actinobacteria
WP_041840760.1	EACC1	EACC1*→	119	Actinoplanes friuliensis	GCF_000494755.1	actinobacteria
WP_042150750.1	EACC1	EACC1*→ CASPASE+Beta_rich_repeat→	133	Streptomyces sp. NBRC 110027	GCA_000829715.2	actinobacteria
WP_042157862.1	EACC1	EACC1*→ CASPASE→ TPRs→	114	Streptomyces sp. NBRC 110027	GCA_000829715.2	actinobacteria
WP_042254254.1	EACC1	EACC1*→ CASPASE+??→	122	Nocardia brasiliensis	GCA_000308475.2	actinobacteria
WP_043262060.1	EACC1	TPRs→ EACC1*→ CASPASE+TPRs→	114	Streptomyces sp. e14	GCF_000162775.1	actinobacteria
WP_043450256.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	127	Streptomyces nodosus	GCA_000819545.1	actinobacteria
WP_043453717.1	EACC1	-	149	Streptomyces fulvoviolaceus	-	actinobacteria
WP_043457436.1	EACC1	EACC1*→ CASPASE+TPRs→	120	Streptomyces fulvoviolaceus	GCF_000718165.1	actinobacteria
WP_043464872.1	EACC1	EACC1*→ CASPASE+PBPB+vWA→	129	Streptomyces	GCA_001190165.1	actinobacteria
WP_043631880.1	EACC1	EACC1*→ CASPASE+SAD+HNH→	121	Nonomuraea candida	GCF_000725485.1	actinobacteria
WP_043686591.1	EACC1	EACC1*→ CASPASE+TPRs→	118	Streptomyces xylophagus	GCF_000716435.1	actinobacteria
WP_043735402.1	EACC1	EACC1*→ CASPASE+STAND+BetaPropeller+BetaPropeller→	128	Nocardia asiatica	GCF_000308415.1	actinobacteria
WP_043775607.1	EACC1	PBPB→?→?→ Aminotran_5+PAS_6+HTH_22→ EACC1*→	125	Amycolatopsis rifamycinica	GCA_000695625.1	actinobacteria
WP_043787005.1	EACC1	GATase→ ABC-ATPase+DUF4162→ cNMP_cyclase+TM+TM+TM+TM+TM+TM→ EACC1*→	105	Amycolatopsis rifamycinica	GCA_000695625.1	actinobacteria
WP_043814231.1	EACC1	EACC1*→ CASPASE+DnaJ_ZnR+DnaJ_ZnR+DnaJ_C→	122	Allokutzneria albata	GCA_900103775.1	actinobacteria
WP_043831325.1	EACC1	GATase→ ABC-ATPase+DUF4162→ cNMP_cyclase+TM+TM+TM+TM+TM+TM→ EACC1*→	109	Amycolatopsis orientalis	GCF_000411995.1	actinobacteria
WP_043967418.1	EACC1	??+TM+TM+TM+Peptidase_M48+TM+DUF4864+??→ EACC1*→	141	Micromonospora carbonacea	GCA_000876225.1	actinobacteria
WP_044381661.1	EACC1	EACC1*→ CASPASE+TPRs→ Clp_N+Clp_N+ClpABN-AAA→	80	Streptomyces cyaneogriseus	GCA_000931445.1	actinobacteria
WP_044384776.1	EACC1	EACC1*→ CASPASE+Pkinase→	114	Streptomyces cyaneogriseus	GCF_000931445.1	actinobacteria
WP_044473271.1	EACC1	HTH+CASPASE→ EACC1*→	125	Streptomyces	GCF_000331005.1	actinobacteria
WP_044851652.1	EACC1	EACC1*→	110	Amycolatopsis orientalis	GCA_000943515.2	actinobacteria
WP_045318341.1	EACC1	EACC1*→	113	Lechevalieria aerocolonigenes	GCA_000955955.1	actinobacteria
WP_045558679.1	EACC1	EACC1*→ CASPASE+TM+TM+bPH_domain+TM+TM+bPH_domain+TM+TM→	125	Streptomyces sp. FxanaA7	GCF_000958545.1	actinobacteria
WP_045743884.1	EACC1	EACC1*→ CASPASE+TPRs→	107	Actinoplanes rectilineatus	GCF_000962825.1	actinobacteria
WP_046567869.1	EACC1	EACC1*→	134	Micromonospora sp. HK10	GCA_000982955.1	actinobacteria
WP_046569306.1	EACC1	TM+TM+TM+Peptidase_M48+TM+DUF4864+??→ EACC1*→	131	Micromonospora sp. HK10	GCA_000982955.1	actinobacteria
WP_046724302.1	EACC1	-	150	Streptomyces xiamenensis	-	actinobacteria
WP_046928395.1	EACC1	Phage_int_SAM_3+Phage_integrase→ EACC1*→ CASPASE+TPRs→	121	Streptomyces lydicus	-	actinobacteria
WP_047178561.1	EACC1	EACC1*→ CASPASE+STAND+??+TPRs+??→	119	Streptomyces sp. MNU77	-	actinobacteria
WP_047179412.1	EACC1	HATPase_c_2→ EACC1*→ CASPASE+Beta_rich_repeat→	143	Streptomyces sp. MNU77	-	actinobacteria

acc	architecture	operon	len	species	gca	taxend
WP_047400359.1	EACC1	EACC1*→	116	Enterobacteriaceae	GCA_003687835.1	gammaproteobacteria
WP_048818821.1	EACC1	EACC1*→ CASPASE+TM+TM+bPH_domain+TM+TM+bPH_domain+TM+TM→	124	Streptomyces turgidiscabies	GCF_000331005.1	actinobacteria
WP_048830083.1	EACC1	EACC1*→ CASPASE+FGS_fold-domain→??→??→ TM+TM+BaxI_1→?→ NUDIX→	136	Streptomyces decoyicus	GCA_001270575.1	actinobacteria
WP_048831498.1	EACC1	EACC1*→ CASPASE+Pkinase+TM?+??→	113	Streptomyces varsoviensis	GCF_000718635.1	actinobacteria
WP_048910577.1	EACC1	EACC1*→ PSE→ MDMPI_N+MDMPI_C→ META→	98	Streptomyces	GCA_001280045.1	actinobacteria
WP_049567493.1	EACC1	EACC1*→ CASPASE+low-complexity+BetaPropeller→	97	Nonomuraea sp. SBT364	GCF_001083785.1	actinobacteria
WP_049715171.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	127	Streptomyces caatingaensis	GCA_001187435.1	actinobacteria
WP_049715549.1	EACC1	EACC1*→ CASPASE+TPRs→	124	Streptomyces caatingaensis	GCA_001187435.1	actinobacteria
WP_050008892.1	EACC1	EACC1*→	118	Escherichia coli	GCF_900092705.1	gammaproteobacteria
WP_050360662.1	EACC1	EACC1*→ CASPASE+STAND+??+TPRs+??→	119	Streptomyces	GCA_001189025.1	actinobacteria
WP_050367089.1	EACC1	EACC1*→	133	Kitasatospora aureofaciens	GCF_000719175.1	actinobacteria
WP_050372991.1	EACC1	EACC1*→ CASPASE+TM+TM+PBPB+vWA→	120	Streptomyces acidiscabies	GCF_001189015.1	actinobacteria
WP_050375602.1	EACC1	EACC1*→ CASPASE+low-complexity+BetaPropeller→	120	Streptomyces acidiscabies	GCA_001189015.1	actinobacteria
WP_050500757.1	EACC1	-	172	Streptomyces rimosus	-	actinobacteria
WP_050503036.1	EACC1	EACC1*→	125	Streptomyces monomycini	GCF_000715845.1	actinobacteria
WP_050504262.1	EACC1	EACC1*→ CASPASE+TM?+BetaPropeller→	175	Streptomyces rimosus	GCF_000718675.1	actinobacteria
WP_050506763.1	EACC1	-	185	Streptomyces rimosus	-	actinobacteria
WP_050507927.1	EACC1	-	172	Streptomyces peucetius	-	actinobacteria
WP_050508826.1	EACC1	EACC1*→ CASPASE+TM?+BetaPropeller→	174	Streptomyces rimosus	GCF_000716515.1	actinobacteria
WP_050514958.1	EACC1	-	155	Streptomyces rimosus	-	actinobacteria
WP_050593059.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	122	Salinispora arenicola	GCF_000514555.1	actinobacteria
WP_050782610.1	EACC1	MglB→ DUF742→ sGTP-MglA→?→ Beta_rich?→ EACC1*→ CASPASE+TPRs→??→??→	129	Streptomyces griseoflavus	GCF_000158975.1	actinobacteria
WP_050791603.1	EACC1	low-complexity+HD+Tox-RelA+TGS+ACT→ Pkinase+TPRs→ EACC1*→ CASPASE+TPRs→	120	Streptomyces pristinaespiralis	GCF_000154945.1	actinobacteria
WP_050799858.1	EACC1	EACC1*→ CASPASE+TPRs→ Clp_N+Clp_N+Clp_N+Clp_N+ClpABN-AAA→	118	Streptomyces himastatinicus	GCF_001650215.1	actinobacteria
WP_050997167.1	EACC1+EAD1	FHA+??+low-complexity+FHA+ABC-ATPase+TM→ EACC1+EAD1*→||←CASPASE+STAND+polar_region+TM+BetaPropeller	227	Frankia alni	GCF_000058485.1	actinobacteria
WP_051022391.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	128	Nocardia pneumoniae	GCF_000308755.1	actinobacteria
WP_051042155.1	EACC1	EACC1*→ CASPASE+TPRs→	114	Actinoplanes missouriensis	GCF_000284295.1	actinobacteria
WP_051044348.1	EACC1	EACC1*→ CASPASE+TPRs→??→??→	129	Streptomyces viridosporus	GCF_000316095.1	actinobacteria
WP_051047444.1	EACC1	EACC1*→ CASPASE+STAND→ BetaPropeller→	107	Nocardia asiatica	GCF_000308415.1	actinobacteria
WP_051104136.1	EACC1	EACC1*→ CASPASE+Beta_rich_repeat→	133	Streptomyces sp. FxanaC1	GCF_000375625.1	actinobacteria
WP_051158321.1	EACC1	EACC1*→	123	Nocardia carnea	GCF_000308515.1	actinobacteria
WP_051169530.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	107	Nocardia abscessus	GCF_000308455.1	actinobacteria
WP_051175242.1	EACC1	Pkinase+TM+LppX_LprAFG→ CASPASE+TPRs→ EACC1*→	128	Nocardia exalbida	GCF_000308575.1	actinobacteria
WP_051182412.1	EACC1	EACC1*→ CASPASE+??→	115	Nocardia vinacea	GCF_000308835.1	actinobacteria
WP_051182843.1	EACC1	EACC1*→ CASPASE+EAL→	117	Nocardia vinacea	GCF_000308835.1	actinobacteria
WP_051274390.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	123	Cellulomonas sp. URHD0024	GCF_000426185.1	actinobacteria
WP_051338412.1	EACC1	EACC1*→ CASPASE+TM?+BetaPropeller→	177	Streptomyces flavidovirens	GCF_000429085.1	actinobacteria
WP_051362899.1	EACC1	EACC1*→ CASPASE+TM+TM+TM+TM→	116	Amycolatopsis thermoflava	GCA_003752125.1	actinobacteria
WP_051367990.1	EACC1	PBPB→?→?→?→?→?→ EACC1*→	111	Hamadaea tsunoensis	GCF_000428945.1	actinobacteria
WP_051436354.1	EACC1	EACC1*→ CASPASE→	128	Streptomyces sp. CNT371	GCF_000514995.1	actinobacteria
WP_051450489.1	EACC1	EACC1*→	177	Actinospica robiniae	GCF_000504285.1	actinobacteria
WP_051450899.1	EACC1	EACC1*→ CASPASE+Pkinase+TM?+??→	118	Actinospica robiniae	GCF_000504285.1	actinobacteria
WP_051450927.1	EACC1	EACC1*→ CASPASE+TPRs→	115	Actinospica robiniae	GCF_000504285.1	actinobacteria
WP_051467403.1	EACC1	EACC1*→ CASPASE+SAD+HNH→?→||←METHYLASE	126	Actinomadura oligospora	GCF_000518265.1	actinobacteria
WP_051467905.1	EACC1	EACC1*→ CASPASE+low-complexity+BetaPropeller→	140	Actinomadura oligospora	GCF_000518265.1	actinobacteria
WP_051572740.1	EACC1	EACC1*→	93	Streptomyces sp. PRh5	GCA_000590515.1	actinobacteria
WP_051581547.1	EACC1	EACC1*→ CASPASE+TM+TM+TM+TM→	133	Pseudonocardia acaciae	GCF_000620785.1	actinobacteria
WP_051581839.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	152	Pseudonocardia acaciae	GCF_000620785.1	actinobacteria
WP_051653552.1	EACC1	EACC1*→ CASPASE+??+ZnR+ZnR→	120	Kitasatospora cheerisanensis	GCA_000696185.1	actinobacteria
WP_051661499.1	EACC1	EACC1*→ CASPASE+TM+TM+bPH_domain?→	141	Streptomyces albulus	GCF_000695235.1	actinobacteria
WP_051661885.1	EACC1	EACC1*→	124	Streptomyces albulus	GCA_000695235.1	actinobacteria
WP_051673827.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	132	Streptomyces sp. NTK 937	GCA_000698495.1	actinobacteria

acc	architecture	operon	len	species	gca	taxend
WP_051674065.1	EACC1	EACC1*→ CASPASE+STAND+PBPB→	150	Streptomyces sp. NTK 937	GCA_000698495.1	actinobacteria
WP_051674712.1	EACC1	Pkinase+TPRs→ EACC1*→ CASPASE+TPRs→	172	Streptomyces sp. URHA0041	GCF_000701325.1	actinobacteria
WP_051698691.1	EACC1	EACC1*→ CASPASE+TPRs→	121	Streptomyces sp. NRRL F-5917	GCA_001294325.1	actinobacteria
WP_051707420.1	EACC1	-	133	Streptomyces sp. NRRL B-12105	-	actinobacteria
WP_051708894.1	EACC1	EACC1*→	118	Micromonospora parva	GCF_000718515.1	actinobacteria
WP_051711433.1	EACC1	-	124	Streptomyces sp. NRRL S-350	-	actinobacteria
WP_051715268.1	EACC1	EACC1*→ CASPASE+TPRs→	124	Nocardia rhamnosiphila	GCF_001613485.1	actinobacteria
WP_051715276.1	EACC1	EACC1*→ CASPASE+??+SF1-helicase+Vsr(PDDEXK)?→	138	Nocardia rhamnosiphila	GCF_001613485.1	actinobacteria
WP_051723090.1	EACC1	-	129	Streptomyces albus	-	actinobacteria
WP_051723267.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	138	Streptomyces albus	GCF_000719865.1	actinobacteria
WP_051724817.1	EACC1	EACC1*→ CASPASE+TPRs→ Pkinase+??→	131	Streptacidiphilus jeojiense	GCF_000719095.1	actinobacteria
WP_051727252.1	EACC1	EACC1*→ CASPASE+??→	137	Streptomyces griseus	GCF_000719495.1	actinobacteria
WP_051733700.1	EACC1	polar_lead?+TM+TM+TM+polar_tail?+low-complexity→??→ EACC1*→ CASPASE+TPRs→	126	Streptomyces	GCA_001729485.1	actinobacteria
WP_051737317.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	148	Pseudonocardia autotrophica	GCF_000717175.1	actinobacteria
WP_051740136.1	EACC1	FAD_binding_4+FAD-oxidase_C→ DAGK_cat+DAGK_acc→ EACC1*→ CASPASE+TPRs→?→ Clp_N+Clp_N+ClpABN-AAA→	122	Kitasatospora sp. MBT66	GCF_000710405.2	actinobacteria
WP_051747232.1	EACC1	EACC1*→	133	Streptomyces sp. NRRL B-5680	GCF_000719415.1	actinobacteria
WP_051747308.1	EACC1	EACC1*→ CASPASE+??→	137	Streptomyces sp. NRRL B-5680	GCF_000719415.1	actinobacteria
WP_051751250.1	EACC1	-	123	Streptomyces griseoluteus	-	actinobacteria
WP_051751806.1	EACC1	EACC1*→ BetaPropeller(fragment)→	121	Streptosporangium amethystogenes	GCF_000721075.1	actinobacteria
WP_051753396.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	127	Streptosporangium amethystogenes	GCF_000721075.1	actinobacteria
WP_051753712.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	125	Streptosporangium amethystogenes	GCF_000721075.1	actinobacteria
WP_051754873.1	EACC1	FAD_binding_4+FAD-oxidase_C→ DAGK_cat+DAGK_acc→ EACC1*→ CASPASE+TPRs→ Clp_N+Clp_N+ClpABN-AAA→	122	Kitasatospora purpeofusca	GCF_000718025.1	actinobacteria
WP_051769029.1	EACC1+CASPASE+TPR_repeats+low_complexity+TM_region	TM+TM+BPD_transp_1→ OppC_N+TM+TM+BPD_transp_1→ ABC-ATPase+ABC-ATPase→ PBPB→ TM+Beta_rich+TM+Beta_rich+TM+TM→ EACC1+CASPASE+TPR_repeats+low_complexity+TM_region*→	774	Lentzea albidocapillata	GCA_900176525.1	actinobacteria
WP_051771299.1	EACC1	FAD_binding_4+FAD-oxidase_C→ DAGK_cat+DAGK_acc→ EACC1*→ CASPASE+TPRs→ Clp_N+Clp_N+ClpABN-AAA→	117	Streptomyces sp. NRRL F-6131	GCF_000719695.1	actinobacteria
WP_051789358.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	132	Streptomyces sp. NRRL S-1022	GCF_000720135.1	actinobacteria
WP_051790042.1	EACC1	EACC1*→ CASPASE+low-complexity+BetaPropeller→	141	Streptomyces sp. NRRL S-1022	GCF_000720135.1	actinobacteria
WP_051791754.1	EACC1	EACC1*→ CASPASE+TPRs→?→ EACC1→	73	Amycolatopsis jejuensis	GCF_000717335.1	actinobacteria
WP_051797235.1	EACC1	METHYLASE→ EACC1*→ CASPASE+TM+TM+TM+TM→	122	Catenuloplanes japonicus	GCF_000717135.1	actinobacteria
WP_051797407.1	EACC1	EACC1*→ CASPASE+TM+Beta_rich→	138	Streptomyces sp. NRRL S-337	GCF_000720175.1	actinobacteria
WP_051817603.1	EACC1	EACC1*→ CASPASE+alpha-helical+TM+TM+??+TM+TM→	183	Kitasatospora sp. NRRL B-11411	GCF_000721345.1	actinobacteria
WP_051818683.1	EACC1	EACC1*→ CASPASE+FGS_fold-domain→??→??	146	Streptomyces sp. NRRL S-1813	GCF_000719605.1	actinobacteria
WP_051820037.1	EACC1	EACC1*→ CASPASE+GAF+PAS+GGDEF→	116	Streptomyces sp. NRRL S-920	GCF_000717945.1	actinobacteria
WP_051820891.1	EACC1	EACC1*→ CASPASE+TPRs+LysM+PG-binding→	120	Streptomyces flavochromogenes	GCF_000717595.1	actinobacteria
WP_051822893.1	EACC1	EACC1*→ CASPASE+TM+Beta_rich→	138	Streptomyces sp. NRRL S-1448	GCF_000719365.1	actinobacteria
WP_051825763.1	EACC1	EACC1*→	133	Kitasatospora aureofaciens	GCF_000716885.1	actinobacteria
WP_051826953.1	EACC1	EACC1*→ CASPASE+TM+TM+bPH_domain?→	129	Streptomyces violaceoruber	GCF_000720805.1	actinobacteria
WP_051827480.1	EACC1	EACC1*→ CASPASE+TM+PBPI→	133	Streptomyces bicolor	GCF_000725465.1	actinobacteria
WP_051828064.1	EACC1	EACC1*→ CASPASE+alpha-helical+TM+TM+??+TM+TM→	155	Streptomyces sp. NRRL S-384	GCF_000721625.1	actinobacteria
WP_051828389.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	143	Streptomyces bicolor	GCF_000725465.1	actinobacteria
WP_051830699.1	EACC1	EACC1*→ CASPASE+TPRs→	136	Streptomyces violens	GCF_000717745.1	actinobacteria
WP_051831085.1	EACC1	-	103	Streptomyces violens	-	actinobacteria
WP_051831682.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	103	Streptomyces violens	GCF_000717745.1	actinobacteria
WP_051832798.1	EACC1	EACC1*→ CASPASE+GAF+PAS→	149	Streptomyces	GCA_001513955.1	actinobacteria
WP_051833041.1	EACC1	EACC1*→ CASPASE+??+TM+??→	120	Streptomyces sp. NRRL S-646	GCF_000720765.1	actinobacteria
WP_051833578.1	EACC1	EACC1*→ CASPASE+??→	116	Streptomyces katrae	GCF_000717655.1	actinobacteria
WP_051837966.1	EACC1	EACC1*→ CASPASE+??+TPRs→	114	Streptomyces sp. NRRL WC-3742	GCF_000720635.1	actinobacteria
WP_051840661.1	EACC1	-	93	Streptomyces sp. NRRL F-5126	-	actinobacteria
WP_051843364.1	EACC1	EACC1*→ CASPASE+TPRs→	132	Streptomyces sp. NRRL S-623	GCF_000725705.1	actinobacteria
WP_051843551.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	130	Streptomyces	GCF_000718375.1	actinobacteria
WP_051850144.1	EACC1	EACC1*→	141	Streptomyces griseofuscus	GCF_000718315.1	actinobacteria
WP_051850290.1	EACC1	EACC1*→ CASPASE+GAF+PAS→	150	Streptomyces griseofuscus	GCA_003933295.1	actinobacteria

acc	architecture	operon	len	species	gca	taxend
WP_051853232.1	EACC1	EACC1*→ CASPASE+PBPB→	120	Streptomyces aureocirculatus	GCF_000720475.1	actinobacteria
WP_051860348.1	EACC1	Beta_rich?→ EACC1*→ CASPASE+TPRs→??→??→	125	Streptomyces anulatus	GCA_003846255.1	actinobacteria
WP_051860360.1	EACC1	-	150	Streptomyces anulatus	-	actinobacteria
WP_051865517.1	EACC1	??→ EACC1*→ CASPASE+TM+TM+PBPB+vWA→	108	Streptomyces griseus	GCF_000720255.1	actinobacteria
WP_051871299.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	141	Streptomyces sclerotialus	-	actinobacteria
WP_051872051.1	EACC1	EACC1*→ CASPASE+TM+PBPB+vWA→	143	Streptomyces sclerotialus	-	actinobacteria
WP_051872372.1	EACC1	EACC1*→ CASPASE+TM?+BetaPropeller→	122	Streptomyces sclerotialus	-	actinobacteria
WP_051874280.1	EACC1	EACC1*→ CASPASE+TPRs→ DUF664→	121	Streptomyces exfoliatus	GCF_000725545.1	actinobacteria
WP_051877232.1	EACC1	EACC1*→ CASPASE+low-complexity+BetaPropeller→	114	Streptomyces natalensis	GCF_000935125.1	actinobacteria
WP_051877321.1	EACC1	PAS+GAF+PP2C+HATPase_c_2→ EACC1*→ CASPASE+TM+Beta_rich→	133	Streptomyces natalensis	GCF_000935125.1	actinobacteria
WP_051919877.1	EACC1	EACC1*→ CASPASE+??→	126	Streptomyces sp. PAN_FS17	GCA_900105465.1	actinobacteria
WP_051927179.1	EACC1	EACC1*→ CASPASE+TM+TM+bPH_domain?→	163	Streptomyces durhamensis	GCF_000725475.1	actinobacteria
WP_051951601.1	EACC1	EACC1*→ CASPASE+TPRs→	123	Streptomyces yeochonensis	GCF_000745345.1	actinobacteria
WP_051969288.1	EACC1	EACC1*→ CASPASE+DnaJ_ZnR+DnaJ_C+DnaJ_C+TM+TM→	106	Kitasatospora azatica	GCF_000744785.1	actinobacteria
WP_052069324.1	EACC1	EACC1*→||←?←?||Pkinase+??→	119	Streptacidiphilus albus	GCF_000744705.1	actinobacteria
WP_052163187.1	EACC1	EACC1*→ CASPASE+??→	118	Actinoplanes utahensis	GCF_000785985.1	actinobacteria
WP_052281097.1	EACC1	DUF2510(W3)+BicD+DUF4041+T5orf172→ EACC1*→ CASPASE+TPRs→	125	Nocardia vulneris	GCF_001613425.1	actinobacteria
WP_052287016.1	EACC1	low-complexity+HD+Tox-RelA+TGS+ACT→ Pkinase+TPRs→ EACC1*→ CASPASE+TPRs→	131	Streptomyces sp. 769	GCA_000816025.1	actinobacteria
WP_052287199.1	EACC1	polar_lead?+TM+TM+TM+polar_tail?+low-complexity→??→ EACC1*→ CASPASE+TPRs→	126	Streptomyces	GCA_000816025.1	actinobacteria
WP_052359567.1	EACC1	EACC1*→ CASPASE+DUF179→ SIR2+??→??→	115	Actinoplanes friuliensis	GCF_000494755.1	actinobacteria
WP_052371933.1	EACC1	EACC1*→ CASPASE+CLP_protease→	120	Amycolatopsis taiwanensis	GCF_000519205.1	actinobacteria
WP_052392347.1	EACC1	-	132	Streptomyces roseoverticillatus	-	actinobacteria
WP_052397909.1	EACC1	EACC1*→ CASPASE+STAND+TPRs→	130	Streptomyces sp. NRRL F-5123	GCF_000721495.1	actinobacteria
WP_052398340.1	EACC1	EACC1*→ CASPASE+BetaPropeller→	93	Streptomyces sp. NRRL F-5123	GCF_000721495.1	actinobacteria
WP_052407300.1	EACC1	EACC1*→	121	Allokutzneria albata	GCA_900103775.1	actinobacteria
WP_052412073.1	EACC1	low-complexity+HD+Tox-RelA+TGS+ACT→ Pkinase+TPRs→ EACC1*→ CASPASE+TPRs→	138	Streptomyces luteus	GCF_000739045.1	actinobacteria
WP_052413571.1	EACC1	EACC1*→ AB_hydrolase→	142	Streptomyces glaucescens	GCA_000761215.1	actinobacteria
WP_052423238.1	EACC1	EACC1*→ CASPASE+low-complexity+BetaPropeller→	125	Nonomuraea candida	GCF_000725485.1	actinobacteria
WP_052423634.1	EACC1	EACC1*→ CASPASE+TM+TM+??→	119	Nonomuraea candida	GCF_000725485.1	actinobacteria
WP_052478239.1	EACC1	PALP→ Trp_syntA→ TM+LGT→ EACC1*→	120	Kibdelosporangium sp. MJ126-NF4	GCF_000826545.1	actinobacteria
WP_052482684.1	EACC1	low-complexity+HD+Tox-RelA+TGS+ACT→ Pkinase+TPRs→ EACC1*→ CASPASE+TPRs→	141	Streptomyces albus	GCA_000827005.1	actinobacteria
WP_052577225.1	EACC1	-	149	Actinosporangium sp. NRRL B-3428	-	actinobacteria
WP_052701361.1	EACC1	EACC1*→	67	Streptomyces iranensis	GCF_000938975.1	actinobacteria
WP_052701406.1	EACC1	EACC1*→ CASPASE+low-complexity+TM+PBPB→	130	Streptomyces iranensis	GCA_000938975.1	actinobacteria
WP_052701431.1	EACC1	EACC1*→ CASPASE+TM+??→	147	Streptomyces iranensis	GCA_000938975.1	actinobacteria
WP_052705912.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	89	Streptomyces sp. NRRL B-1568	GCF_000967025.1	actinobacteria
WP_052709520.1	EACC1	EACC1*→ CASPASE+TPRs→ Clp_N+Clp_N+ClpABN-AAA→	126	Streptomyces sp. NRRL S-495	GCF_000966955.1	actinobacteria
WP_052714810.1	EACC1	EACC1*→	113	Streptomyces	GCF_000720235.1	actinobacteria
WP_052720941.1	EACC1	EACC1*→||←CASPASE+STAND+TM+polar_region+TM+BetaPropeller	88	Actinoplanes rectilineatus	GCF_000962825.1	actinobacteria
WP_052731619.1	EACC1	low-complexity+HD+Tox-RelA+TGS+ACT→ Pkinase+TPRs→ EACC1*→ CASPASE+TPRs→	138	Streptomyces sp. MBT28	GCA_005490965.1	actinobacteria
WP_052742894.1	EACC1	EACC1*→ CASPASE+alpha-helical+TM+TM+??+TM+TM→	67	Streptomyces mangrovisoli	GCA_000974985.2	actinobacteria
WP_052743230.1	EACC1	Pkinase+TPRs→ EACC1*→ CASPASE+TPRs→	125	Streptomyces mangrovisoli	GCF_000974985.2	actinobacteria
WP_052770426.1	EACC1+CASPASE+BetaPropeller	EACC1+CASPASE+BetaPropeller*→ BetaPropeller→	703	Streptomyces sp. CNQ-509	GCF_001011035.1	actinobacteria
WP_052845486.1	EACC1	EACC1*→ CASPASE+TM+??→	78	Streptomyces sp. NRRL S-31	GCF_000718775.1	actinobacteria
WP_053048421.1	EACC1	EACC1*→ CASPASE+TM+??→	141	Streptomyces antioxidans	GCA_000968685.2	actinobacteria
WP_053048662.1	EACC1	EACC1*→ CASPASE+Peripla_BP_5→	127	Streptomyces antioxidans	-	actinobacteria
WP_053080830.1	EACC1	low-complexity+HD+Tox-RelA+TGS+ACT→ Pkinase+TPRs→ EACC1*→ CASPASE+TPRs→	138	Streptomyces roseus	GCF_001044425.1	actinobacteria
WP_053116041.1	EACC1	EACC1*→ CASPASE+TPRs→	109	Streptomyces xiamenensis	GCA_000993785.2	actinobacteria
WP_053164263.1	EACC1	-	134	Streptomyces ahygroscopicus	-	actinobacteria
WP_053164556.1	EACC1	EACC1*→ CASPASE+PBPB→	120	Streptomyces albulus	GCF_000935185.3	actinobacteria
WP_053271602.1	EACC1	EACC1*→	116	Enterobacteriaceae	GCA_002249075.1	gammaproteobacteria
WP_053626492.1	EACC1	EACC1*→ CASPASE+TPRs→	119	Streptomyces	GCA_001279445.1	actinobacteria

acc	architecture	operon	len	species	gca	taxend
WP_053634092.1	EACC1	EACC1*→ CASPASE+TPRs→	119	Streptomyces	GCA_001279855.1	actinobacteria
WP_053650957.1	EACC1	EACC1*→ CASPASE+TPRs→ Clp_N+Clp_N+ClpABN-AAA→	126	Streptomyces sp. XY431	GCF_001279805.1	actinobacteria
WP_053652889.1	EACC1	EACC1*→	117	Micromonospora sp. NRRL B-16802	GCA_001279555.1	actinobacteria
WP_053670302.1	EACC1	??→ EACC1*→ CASPASE+TM+TM+PBPB+vWA→	121	Streptomyces sp. NRRL B-1140	GCA_001280065.1	actinobacteria
WP_053674387.1	EACC1	EACC1*→ CASPASE→ TPRs→	117	Streptomyces sp. NRRL B-1140	GCA_001280065.1	actinobacteria
WP_053676249.1	EACC1	EACC1*→ CASPASE+??+SF1-helicase+Vsr(PDDEXK)?→	139	Streptomyces sp. WM4235	GCF_001279725.1	actinobacteria
WP_053683135.1	EACC1	EACC1*→ CASPASE+TM?+BetaPropeller→	123	Streptomyces sp. WM4235	GCA_001279725.1	actinobacteria
WP_053684084.1	EACC1	EACC1*→ CASPASE+??+SF1-helicase+Vsr(PDDEXK)?→	140	Streptomyces sp. XY593	GCF_001279885.1	actinobacteria
WP_053692927.1	EACC1	EACC1*→ CASPASE+??→	109	Streptomyces sp. WM6372	GCF_001279655.1	actinobacteria
WP_053694030.1	EACC1	low-complexity+HD+Tox-RelA+TGS+ACT→ Pkinase+TPRs→ EACC1*→ CASPASE+TPRs→	137	Streptomyces sp. WM6372	GCA_001279655.1	actinobacteria
WP_053694048.1	EACC1	EACC1*→ CASPASE+??→	116	Streptomyces sp. WM6372	GCA_001279655.1	actinobacteria
WP_053707259.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	147	Streptomyces sp. NRRL B-3648	GCF_001279545.1	actinobacteria
WP_053711694.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	130	Streptomyces sp. NRRL B-3648	GCA_001279545.1	actinobacteria
WP_053711828.1	EACC1	EACC1*→ CASPASE+low-complexity+BetaPropeller→	153	Streptomyces sp. NRRL B-3648	GCF_001279545.1	actinobacteria
WP_053733409.1	EACC1	EACC1*→ CASPASE+Cpn60_TCP1→	111	Nocardia sp. NRRL S-836	GCA_001279525.1	actinobacteria
WP_053751185.1	EACC1	EACC1*→	113	Streptomyces sp. MMG1533	GCA_001279775.1	actinobacteria
WP_053754404.1	EACC1	EACC1*→ CASPASE+STAND+TPRs→	133	Streptomyces sp. MMG1533	GCF_001279775.1	actinobacteria
WP_053763839.1	EACC1	-	116	Streptomyces sp. AS58	-	actinobacteria
WP_053764190.1	EACC1	EACC1*→ CASPASE+TM+TM+bPH_domain+TM+TM+bPH_domain+TM+TM→	76	Streptomyces sp. AS58	GCA_001279985.1	actinobacteria
WP_053790627.1	EACC1	EACC1*→ CASPASE+??→	116	Streptomyces sp. XY332	GCF_001280885.1	actinobacteria
WP_053802205.1	EACC1	EACC1*→	180	Streptomyces rimosus	GCF_001279345.1	actinobacteria
WP_053847006.1	EACC1	EACC1*→ CASPASE+BetaPropeller→	136	Streptomyces sp. NRRL B-24085	GCF_001282115.1	actinobacteria
WP_053923404.1	EACC1	TPRs→ EACC1*→ CASPASE+TPRs→	114	Streptomyces chattanoogensis	GCA_001294335.1	actinobacteria
WP_053926881.1	EACC1	EACC1*→ CASPASE+TM?+BetaPropeller→	156	Streptomyces chattanoogensis	GCA_001294335.1	actinobacteria
WP_053927196.1	EACC1	PAS+GAF+PP2C+HATPase_c_2→ EACC1*→	128	Streptomyces chattanoogensis	GCF_001294335.1	actinobacteria
WP_054001110.1	EACC1	EACC1*→ CASPASE+TM+??→	120	Shimia sp. SK013	GCA_001292625.1	alphaproteobacteria
WP_054048388.1	EACC1	EACC1*→ CASPASE+STAND+TPRs→	106	Alloactinosynnema sp. L-07	GCA_900070365.1	actinobacteria
WP_054066041.1	EACC1	EACC1*→	125	Comamonas kerstersii	GCA_002056725.1	betaproteobacteria
WP_054212290.1	EACC1	EACC1*→ CASPASE+low-complexity+BetaPropeller→	108	Actinobacteria bacterium OK074	GCF_001298575.1	actinobacteria
WP_054217804.1	EACC1	EACC1*→	141	Actinobacteria bacterium OK074	GCF_001298575.1	actinobacteria
WP_054294680.1	EACC1	PALP→ Trp_syntA→ TM+LGT→ EACC1*→	117	Kibdelosporangium phytohabitans	GCA_001302585.1	actinobacteria
WP_054812365.1	EACC1	EACC1*→	97	Nocardia arizonensis	GCF_001618405.1	actinobacteria
WP_055409063.1	EACC1+EAD1	CASPASE+STAND+polar_region+TM+BetaPropeller|EACC1+EAD1*→	291	Frankia sp. ACN1ag	GCA_001414035.1	actinobacteria
WP_055418791.1	EACC1	polar_lead?+TM+TM+TM+polar_tail?+low-complexity→??→ EACC1*→ CASPASE+TPRs→	145	Streptomyces pactum	GCA_002005225.1	actinobacteria
WP_055472090.1	EACC1	EACC1*→ CASPASE+Peripla_BP_5→	122	Streptomyces pathocidini	GCF_001418495.1	actinobacteria
WP_055519506.1	EACC1	EACC1*→	117	Streptomyces ossamyceticus	GCF_001418475.1	actinobacteria
WP_055520371.1	EACC1	EACC1*→ CASPASE→ TPRs→	117	Streptomyces ossamyceticus	GCF_001418475.1	actinobacteria
WP_055529698.1	EACC1	EACC1*→ CASPASE+PBPB→	113	Streptomyces graminilatus	GCF_001418565.1	actinobacteria
WP_055547602.1	EACC1	EACC1*→ CASPASE+TPRs→ Clp_N+Clp_N+Clp_N+Clp_N+ClpABN-AAA→	118	Streptomyces sp. NBRC 110028	GCF_001417735.1	actinobacteria
WP_055554425.1	EACC1	HATPase_c_2→ EACC1*→	118	Streptomyces sp. NBRC 110028	GCF_001417735.1	actinobacteria
WP_055555440.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	150	Streptomyces sp. NBRC 110028	GCF_001417735.1	actinobacteria
WP_055564004.1	EACC1	EACC1*→ CASPASE+TPRs→	138	Streptomyces atriruber	GCF_001418325.1	actinobacteria
WP_055574191.1	EACC1	??+CASPASE→ EACC1*→	132	Streptomyces prasinopilosus	GCA_900101585.1	actinobacteria
WP_055582923.1	EACC1	EACC1*→ CASPASE+TM+TM+bPH_domain?→	141	Streptomyces	GCF_000935185.3	actinobacteria
WP_055591440.1	EACC1	??→ EACC1*→ CASPASE+TPRs→	129	Streptomyces griseoplanus	GCF_001418575.1	actinobacteria
WP_055593759.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	167	Streptomyces hirsutus	GCF_001418415.1	actinobacteria
WP_055607204.1	EACC1	??→ EACC1*→ CASPASE+TPRs→	130	Streptomyces prasinus	-	actinobacteria
WP_055607684.1	EACC1	TIR+CASPASE→ EACC1*→	141	Streptomyces prasinus	GCF_001418165.1	actinobacteria
WP_055628150.1	EACC1	EACC1*→ CASPASE+TPRs→	118	Streptomyces hirsutus	GCF_001418175.1	actinobacteria
WP_055689145.1	EACC1	-	168	Streptomyces prasinus	-	actinobacteria
WP_055690018.1	EACC1	??→ EACC1*→ CASPASE+TPRs→	130	Streptomyces prasinus	GCF_001419705.1	actinobacteria
WP_055690138.1	EACC1	EACC1*→ CASPASE+??→	137	Streptomyces prasinus	GCF_001419705.1	actinobacteria

acc	architecture	operon	len	species	gca	taxend
WP_055693189.1	EACC1	??+CASPASE→ EACC1*→	132	Streptomyces prasinopilosus	GCF_001419695.1	actinobacteria
WP_055698908.1	EACC1	low-complexity+HD+Tox-RelA+TGS+ACT→ Pkinase+TPRs→ EACC1*→ CASPASE+TPRs→	138	Streptomyces	GCF_001748305.1	actinobacteria
WP_055704881.1	EACC1	EACC1*→ CASPASE+??+SF1-helicase+Vsr(PDDEXK)?→	126	Streptomyces puniciscabiei	-	actinobacteria
WP_055721366.1	EACC1	EACC1*→ CASPASE+TM+TM+PBPB+vWA→	105	Streptomyces	GCA_003129505.1	actinobacteria
WP_055751765.1	EACC1+EAD1	FHA+??+low-complexity+FHA+ABC-ATPase+TM→ EACC1+EAD1*→||←CASPASE+STAND+polar_region+TM+BetaPropeller	233	Frankia sp. AvcI1	GCF_001420875.1	actinobacteria
WP_056700872.1	EACC1	EACC1*→ CASPASE+STAND+??+TPRs+??→	119	Streptomyces	GCA_001426325.1	actinobacteria
WP_056780488.1	EACC1	EACC1*→ CASPASE+??+TM+TM+TM+TM+TM+TM+TM+TM→	124	Terrabacter sp. Soil811	GCA_001429655.1	actinobacteria
WP_056790650.1	EACC1	??+CASPASE→ EACC1*→	127	Streptomyces	GCA_001426615.1	actinobacteria
WP_056799763.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	139	Streptomyces sp. Root55	GCA_001427245.1	actinobacteria
WP_056823413.1	EACC1	EACC1*→ CASPASE+??+TM+TM+TM+TM+TM+TM+TM+TM→	124	Terrabacter sp. Root85	GCA_001429185.1	actinobacteria
WP_057235967.1	EACC1	EACC1*→ CASPASE+TPRs→	135	Kitasatospora sp. Root107	GCA_001424875.1	actinobacteria
WP_057238329.1	EACC1	EACC1*→ CASPASE+TPRs→	131	Kitasatospora	GCA_001424875.1	actinobacteria
WP_057240280.1	EACC1	polar_lead?+TM+TM+TM+polar_tail?+low-complexity→??→ EACC1*→ CASPASE+TPRs→	117	Kitasatospora	GCA_001424875.1	actinobacteria
WP_058081073.1	EACC1	EACC1*→ CASPASE+TM?+BetaPropeller→ MDMPI_N+MDMPI_C→ META→	116	Streptomyces hygroscopicus	GCA_001447075.1	actinobacteria
WP_058084346.1	EACC1	EACC1*→ CASPASE+low-complexity+TM+PBPB→	140	Streptomyces hygroscopicus	GCA_001447075.1	actinobacteria
WP_058228238.1	EACC1	EACC1*→ CASPASE+??→	122	Rhodococcus enclensis	GCA_900094765.1	actinobacteria
WP_059065682.1	EACC1	EACC1*→	82	Klebsiella pneumoniae	GCA_002903025.1	gammaproteobacteria
WP_059144748.1	EACC1	TetR_N+TetR_C_6→ EACC1*→	130	Streptomyces	GCA_001509775.1	actinobacteria
WP_059145485.1	EACC1	EACC1*→	133	Streptomyces	GCA_001509775.1	actinobacteria
WP_059193393.1	EACC1	EACC1*→ CASPASE+TM+TM+TM+TM+TM+TM→	136	Streptomyces antibioticus	GCA_001514065.1	actinobacteria
WP_059193417.1	EACC1	EACC1*→ CASPASE+STAND+BetaPropeller→	125	Streptomyces antibioticus	GCA_001514065.1	actinobacteria
WP_059195108.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	133	Streptomyces antibioticus	GCA_001514065.1	actinobacteria
WP_059195220.1	EACC1	EACC1*→ CASPASE+TPRs→	118	Streptomyces antibioticus	GCA_001514065.1	actinobacteria
WP_059249456.1	EACC1	-	133	Streptomyces reticuli	-	actinobacteria
WP_059253791.1	EACC1	AMP-binding+AMP-binding_C→ AMP-binding+AMP-binding_C→ EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	152	Streptomyces	GCA_002251155.1	actinobacteria
WP_059263747.1	EACC1	EACC1*→ CASPASE+TM?+BetaPropeller→ MDMPI_N+MDMPI_C→ META→	116	Streptomyces corchorusii	GCA_001514055.1	actinobacteria
WP_059265627.1	EACC1	EACC1*→ CASPASE+low-complexity+TM+PBPB→	140	Streptomyces corchorusii	GCA_001514055.1	actinobacteria
WP_059267207.1	EACC1	EACC1*→ CASPASE+TPRs→	119	Streptomyces corchorusii	GCA_001514055.1	actinobacteria
WP_060888019.1	EACC1	EACC1*→ CASPASE+TM+TM+bPH_domain+TM+TM+bPH_domain+TM+TM→	134	Streptomyces	GCA_900114955.1	actinobacteria
WP_060904615.1	EACC1	EACC1*→ CASPASE+TPRs→	127	Streptomyces scabiei	GCF_001550235.1	actinobacteria
WP_061446668.1	EACC1	-	153	Streptomyces sp. CCM_MD2014	-	actinobacteria
WP_061446671.1	EACC1	EACC1*→ CASPASE+TPRs→	119	Streptomyces sp. CCM_MD2014	GCA_000772045.1	actinobacteria
WP_061989687.1	EACC1	EACC1*→	120	Amycolatopsis regifaucium	GCA_001613935.1	actinobacteria
WP_062133880.1	EACC1	EACC1*→ CASPASE(fragment)→	117	Streptomyces sp. CC71	GCA_001595515.1	actinobacteria
WP_062205207.1	EACC1	-	186	Streptomyces sp. NBRC 109706	-	actinobacteria
WP_062208870.1	EACC1	TM+TM+TM+PP2C→ EACC1*→ CASPASE+PBPB+vWA→	135	Streptomyces sp. NBRC 109706	GCF_000974485.1	actinobacteria
WP_062331945.1	EACC1	EACC1*→	119	Herbidospora sakaeratensis	GCF_001570525.1	actinobacteria
WP_062707009.1	EACC1	TPRs→ EACC1*→ CASPASE+TPRs→	114	Streptomyces regalis	GCA_001509475.1	actinobacteria
WP_062720803.1	EACC1	-	135	Streptomyces caeruleatus	GCA_001514235.1	actinobacteria
WP_062752525.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	181	Streptomyces	GCA_002943895.1	actinobacteria
WP_062924605.1	EACC1	EACC1*→ CASPASE+RE_Eco29kI+??→	124	Streptomyces sp. S10(2016)	GCA_001611795.1	actinobacteria
WP_062928059.1	EACC1	TM+TM+TM+PP2C→??→ EACC1*→ CASPASE+TM+TM+PBPB+vWA→	121	Streptomyces sp. S10(2016)	GCA_001611795.1	actinobacteria
WP_062976308.1	EACC1	EACC1*→ CASPASE+TPRs→	147	Nocardia flavorosea	GCF_001613385.1	actinobacteria
WP_062989910.1	EACC1	EACC1*→ CASPASE+TPRs→	117	Nocardia anaemiae	GCF_001612725.1	actinobacteria
WP_063006009.1	EACC1	DUF2510(W3)+BicD+DUF4041+T5orf172→ EACC1→ CASPASE+TPRs→ EACC1*→ CASPASE+EAL→	128	Nocardia cummidelens	GCF_001612865.1	actinobacteria
WP_063006011.1	EACC1	DUF2510(W3)+BicD+DUF4041+T5orf172→ EACC1*→ CASPASE+TPRs→ EACC1→ CASPASE+EAL→	125	Nocardia cummidelens	-	actinobacteria
WP_063038312.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	125	Nocardia pseudovaccinii	GCF_001613225.1	actinobacteria
WP_063038929.1	EACC1	EACC1*→ CASPASE+TPRs→	114	Nocardia grenadensis	GCF_001613445.1	actinobacteria
WP_063044051.1	EACC1	EACC1*→ CASPASE+TPRs→	169	Nocardia pseudovaccinii	GCF_001613225.1	actinobacteria
WP_063047902.1	EACC1	EACC1*→ CASPASE+TPRs→	138	Nocardia pseudovaccinii	GCF_001613225.1	actinobacteria
WP_063057431.1	EACC1	EACC1*→ CASPASE+??+SF1-helicase+Vsr(PDDEXK)?→	138	Nocardia sienata	GCF_001613205.1	actinobacteria
WP_063273430.1	EACC1	EACC1*→	101	Amycolatopsis keratiniphila	-	actinobacteria

acc	architecture	operon	len	species	gca	taxend
WP_063276304.1	EACC1	MFS_1→ EACC1*→ CASPASE+DnaJ_ZnR+DnaJ_ZnR+DnaJ_C→	122	Amycolatopsis keratiniphila	-	actinobacteria
WP_063483685.1	EACC1	EACC1*→ CASPASE+GTP_EFTU+GTP_EFTU_D2+GTP_EFTU_D3→	127	Streptomyces ambofaciens	GCA_001632865.1	actinobacteria
WP_063792803.1	EACC1	EACC1*→	127	Streptomyces aurantiacus	GCF_001418335.1	actinobacteria
WP_063837497.1	EACC1	EACC1*→	98	Streptomyces sp. NRRL WC-3549	GCF_000721935.1	actinobacteria
WP_064068784.1	EACC1	HATPase_c_2→ EACC1*→ CASPASE+??+SF1-helicase+Vsr(PDDEXK)?→	141	Streptomyces albulus	GCA_001646665.1	actinobacteria
WP_064534223.1	EACC1	??→ EACC1*→ CASPASE+TM+TM+PBPB+vWA→	114	Streptomyces sp. SAT1	GCA_001654495.1	actinobacteria
WP_065003909.1	EACC1	??→ EACC1*→ CASPASE+TPRs→	130	Streptomyces sp. H-KF8	GCA_001672315.1	actinobacteria
WP_065479927.1	EACC1	EACC1*→ CASPASE+??+SF1-helicase+Vsr(PDDEXK)?→??→	143	Streptomyces sp. PTY087I2	GCA_001687325.1	actinobacteria
WP_065484169.1	EACC1	EACC1*→ CASPASE+TPRs→	118	Streptomyces sp. PTY087I2	GCF_001687325.1	actinobacteria
WP_065807622.1	EACC1	EACC1*→	93	Enterobacteriaceae	GCA_002844785.1	gammaproteobacteria
WP_066361324.1	EACC1	EACC1*→	81	Herbidospora mongoliensis	GCF_001570545.1	actinobacteria
WP_066890950.1	EACC1	-	131	Streptomyces thermoautotrophicus	-	actinobacteria
WP_066927619.1	EACC1	EACC1*→ CASPASE+TPRs→	114	Streptomyces sp. NBRC 110611	GCA_001590865.1	actinobacteria
WP_066927855.1	EACC1	-	138	Streptomyces sp. NBRC 110611	GCA_001590865.1	actinobacteria
WP_066954369.1	EACC1	EACC1*→	200	Streptomyces lushanensis	GCF_001700515.1	actinobacteria
WP_066956024.1	EACC1	Pkinase+TPRs→ EACC1*→ CASPASE+TPRs→	136	Streptomyces lushanensis	GCF_001700515.1	actinobacteria
WP_066985804.1	EACC1	low-complexity+HD+Tox-RelA+TGS+ACT→ Pkinase+TPRs→ EACC1*→ CASPASE+TPRs→	148	Streptomyces sp. NRRL F-4489	GCA_001509485.1	actinobacteria
WP_067008945.1	EACC1	EACC1*→ CASPASE+PBPB→	152	Streptomyces cellostaticus	GCA_001513965.1	actinobacteria
WP_067118993.1	EACC1	EACC1*→ CASPASE+TPRs→	114	Streptomyces yokosukanensis	GCA_001514035.1	actinobacteria
WP_067155823.1	EACC1	low-complexity+HD+Tox-RelA+TGS+ACT→ Pkinase+TPRs→ EACC1*→ CASPASE+TPRs→	125	Streptomyces sp. ERV7	GCA_001653515.1	actinobacteria
WP_067166979.1	EACC1	EACC1*→ CASPASE+BetaPropeller→||←DUF664	126	Streptomyces sp. ERV7	GCA_001653515.1	actinobacteria
WP_067237622.1	EACC1	EACC1*→ CASPASE+STAND+??→	119	Streptomyces longwoodensis	GCA_001514125.1	actinobacteria
WP_067253610.1	EACC1	EACC1*→ CASPASE+low-complexity+BetaPropeller→	108	Streptomyces sp. DSM 15324	GCA_001514285.1	actinobacteria
WP_067303920.1	EACC1	EACC1*→ CASPASE+wHTH+BetaPropeller→	127	Streptomyces griseochromogenes	GCA_001542625.2	actinobacteria
WP_067304265.1	EACC1	EACC1*→ CASPASE+TM+TM→ PBPB→	145	Micromonospora rifamycinica	GCA_001542325.1	actinobacteria
WP_067309664.1	EACC1	EACC1*→ CASPASE+low-complexity+BetaPropeller→	118	Streptomyces griseochromogenes	GCA_001542625.2	actinobacteria
WP_067312463.1	EACC1	low-complexity+HD+Tox-RelA+TGS+ACT→ Pkinase+TPRs→ EACC1*→ CASPASE+TPRs→	125	Streptomyces griseochromogenes	GCA_001542625.2	actinobacteria
WP_067315441.1	EACC1	TM+TM+TM+Peptidase_M48+TM+DUF4864+??→ EACC1*→	155	Micromonospora rifamycinica	GCA_001542325.1	actinobacteria
WP_067353812.1	EACC1	low-complexity+HD+Tox-RelA+TGS+ACT→ Pkinase+TPRs→ EACC1*→ CASPASE+TPRs→	131	Streptomyces noursei	GCA_001704275.1	actinobacteria
WP_067470360.1	low_complexity+EACC1	low_complexity+EACC1*→	315	Nocardia amamiensis	GCF_001612745.1	actinobacteria
WP_067487973.1	EACC1	EACC1*→ CASPASE+EAL→	122	Nocardia ignorata	GCA_004362495.1	actinobacteria
WP_067499062.1	EACC1	EACC1*→ CASPASE+SF1-helicase→	126	Actinoplanes sp. TFC3	GCF_001553785.1	actinobacteria
WP_067529228.1	EACC1	EACC1*→ CASPASE+??→	128	Nocardia uniformis	GCF_001613345.1	actinobacteria
WP_067578379.1	EACC1	GATase→ ABC-ATPase+DUF4162→ cNMP_cyclase+TM+TM+TM+TM+TM+TM→ EACC1*→	109	Amycolatopsis	GCA_001651785.1	actinobacteria
WP_067670342.1	EACC1	EACC1*→	80	Nocardia miyunensis	GCF_001613065.1	actinobacteria
WP_067690701.1	EACC1	EACC1*→ CASPASE+TPRs→	122	Nocardia jejuensis	GCF_001613145.1	actinobacteria
WP_067694339.1	EACC1	EACC1*→ CASPASE+STAND+BetaPropeller→	156	Nocardia jejuensis	GCF_001613145.1	actinobacteria
WP_067792914.1	EACC1	EACC1*→ CASPASE+TPRs→	75	Nocardia amikacinitolerans	GCF_001612615.1	actinobacteria
WP_067804861.1	EACC1	Pkinase+TM+LppX_LprAFG→ CASPASE+TPRs→ EACC1*→	128	Nocardia beijingensis	GCF_001612785.1	actinobacteria
WP_067806049.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	129	Nocardia beijingensis	GCF_001612785.1	actinobacteria
WP_067827015.1	EACC1	EACC1*→ CASPASE+??→	136	Nocardia inohanensis	GCF_001612945.1	actinobacteria
WP_067915216.1	EACC1	EACC1*→ CASPASE+??+NUDIX→	126	Actinomadura	GCF_001552235.1	actinobacteria
WP_067978771.1	EACC1	EACC1*→ CASPASE+TM+TM+TM+TM+TM+TM+TM+TM→	75	Nocardia caishijiensis	GCF_001612825.1	actinobacteria
WP_068032713.1	EACC1	EACC1*→	157	Nocardia mexicana	GCF_001613165.1	actinobacteria
WP_068902202.1	EACC1	EACC1*→ CASPASE+SAD+HNH→	120	Planomonospora sphaerica	GCF_001653075.1	actinobacteria
WP_068904454.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	119	Planomonospora sphaerica	GCF_001653075.1	actinobacteria
WP_068927089.1	EACC1	EACC1*→	90	Planobispora rosea	GCF_001696485.1	actinobacteria
WP_068928249.1	EACC1	EACC1*→ CASPASE+TM+TM+TM+TM+TM+TM+BetaPropeller→	129	Planobispora rosea	GCF_001696485.1	actinobacteria
WP_069571402.1	EACC1	Glyoxalase→ EACC1*→ CASPASE+DnaJ_ZnR+DnaJ_ZnR+DnaJ_C→	135	Streptomyces lydicus	GCA_001729485.1	actinobacteria
WP_069571866.1	EACC1	EACC1*→ CASPASE+??→	119	Streptomyces lydicus	GCA_001729485.1	actinobacteria
WP_069628874.1	EACC1	EACC1*→?→ PALP→	120	Streptomyces niveus	GCA_004563805.1	actinobacteria
WP_069734965.1	EACC1	EACC1*→ CASPASE+TPRs→	118	Streptomyces sp. EN27	GCA_003353555.1	actinobacteria

acc	architecture	operon	len	species	gca	taxend
WP_069755251.1	EACC1	EACC1*→ CASPASE+STAND+??+TPRs+??→	119	Streptomyces sp. EN16	GCF_001746285.1	actinobacteria
WP_069756375.1	EACC1	EACC1*→ CASPASE+Beta_rich_repeat→??+SUKH→	137	Streptomyces sp. EN16	GCF_001746285.1	actinobacteria
WP_069767498.1	EACC1	EACC1*→ CASPASE+??+SF1-helicase+Vsr(PDDEXK)?→	126	Streptomyces sp. LUP30	GCF_001746365.1	actinobacteria
WP_069768493.1	EACC1	-	119	Streptomyces sp. LUP30	-	actinobacteria
WP_069776394.1	EACC1	EACC1*→ CASPASE+Pkinase+TM?+??→	138	Streptomyces puniciscabiei	GCA_001735805.1	actinobacteria
WP_069864785.1	EACC1	TetR_N+TetR_C_6→ EACC1*→ CASPASE+low-complexity+TM+PBPB→	140	Streptomyces sp. SPMA113	-	actinobacteria
WP_069865414.1	EACC1	EACC1*→ CASPASE+TM+??→	122	Streptomyces	GCA_002812405.1	actinobacteria
WP_070017995.1	EACC1	EACC1*→ CASPASE+STAND+??+TPRs→	132	Streptomyces nanshensis	GCA_001751255.1	actinobacteria
WP_070025777.1	EACC1	EACC1*→ CASPASE+??+ZnR+ZnR→	119	Streptomyces	GCA_900104815.1	actinobacteria
WP_070029270.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	130	Streptomyces sp. F-1	GCA_900079405.3	actinobacteria
WP_070029920.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	162	Streptomyces sp. F-1	GCA_900079405.3	actinobacteria
WP_070205154.1	EACC1	EACC1*→ CASPASE+TPRs→	119	Streptomyces	GCA_001751305.1	actinobacteria
WP_071284407.1	EACC1	EACC1*→	118	Enterobacter cloacae complex 'Hoffmann cluster IV'	GCA_001858135.1	gammaproteobacteria
WP_071366246.1	EACC1	EACC1*→ CASPASE+??+TM+TM+??→	139	Streptomyces sp. MUSC 93	GCA_001866645.1	actinobacteria
WP_071386200.1	EACC1	Pkinase+TPRs→ EACC1*→ CASPASE+TPRs→	135	Streptomyces sp. MUSC 1	GCA_001866665.1	actinobacteria
WP_071655689.1	EACC1	DUF742→?→?→||←?←?||EACC1*→?→ CASPASE+PBPB+vWA→?→||←?||MFS_1→	156	Streptomyces gilvigriseus	GCA_001879105.1	actinobacteria
WP_071806911.1	EACC1	EACC1*→ CASPASE+DUF179→ SIR2+??→??→	117	Couchioplanes caeruleus	GCA_001884705.1	actinobacteria
WP_071967634.1	EACC1	EACC1*→ CASPASE+TM+TM+PBPB+vWA→	103	Streptomyces cinnamoneus	GCF_001885705.1	actinobacteria
WP_072475297.1	EACC1	MFS_1→||←?||GATase→ ABC-ATPase+DUF4162→ cNMP_cyclase+TM+TM+TM+TM+TM+TM→ EACC1→ CASPASE+TM+TM+TM+TM→ EACC1*→	105	Amycolatopsis australiensis	GCA_900119165.1	actinobacteria
WP_072475299.1	EACC1	MFS_1→||←?||GATase→ ABC-ATPase+DUF4162→ cNMP_cyclase+TM+TM+TM+TM+TM+TM→ EACC1*→ CASPASE+TM+TM+TM+TM→ EACC1→	109	Amycolatopsis australiensis	GCF_900119165.1	actinobacteria
WP_072480727.1	EACC1	EACC1*→ CASPASE+TPRs→	116	Amycolatopsis australiensis	GCA_900119165.1	actinobacteria
WP_072656118.1	EACC1	EACC1*→	151	Streptomyces viridifaciens	GCA_001888885.1	actinobacteria
WP_073215496.1	EACC1	Beta_rich?→ EACC1*→ CASPASE+TPRs→??→??→	105	Streptomyces sp. NBRC 110465	GCF_001895105.1	actinobacteria
WP_073384278.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	140	Nocardiopsis flavescens	GCA_900141985.1	actinobacteria
WP_073444062.1	EACC1	polar_lead?+TM+TM+TM+polar_tail?+low-complexity→??→ EACC1*→ CASPASE+TPRs→	126	Streptomyces yunnanensis	GCA_900142595.1	actinobacteria
WP_073445437.1	EACC1	low-complexity+HD+Tox-RelA+TGS+ACT→ Pkinase+TPRs→ EACC1*→ CASPASE+TPRs→	131	Streptomyces yunnanensis	GCA_900142595.1	actinobacteria
WP_073500553.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	146	Streptomyces paucisporeus	GCF_900142575.1	actinobacteria
WP_073500803.1	EACC1	EACC1*→ CASPASE+HSP70→	119	Streptomyces paucisporeus	GCF_900142575.1	actinobacteria
WP_073719518.1	EACC1	EACC1*→ CASPASE+??+SF1-helicase+Vsr(PDDEXK)?→	137	Streptomyces sp. TSRI0281	GCA_001905125.1	actinobacteria
WP_073727530.1	EACC1	EACC1*→ CASPASE+TPRs→	118	Streptomyces sp. CB02414	GCA_001905385.1	actinobacteria
WP_073729973.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	173	Streptomyces sp. CB02414	GCF_001905385.1	actinobacteria
WP_073748875.1	EACC1	EACC1*→ CASPASE+??→	119	Streptomyces sp. CB02058	GCA_001905505.1	actinobacteria
WP_073752659.1	EACC1	-	141	Streptomyces sp. CB02058	-	actinobacteria
WP_073753325.1	EACC1	EACC1*→ CASPASE+STAND+??+TPRs→	123	Streptomyces sp. CB02058	GCA_001905505.1	actinobacteria
WP_073760381.1	EACC1	EACC1*→	118	Streptomyces sp. CB03234	GCA_001905885.1	actinobacteria
WP_073762288.1	EACC1	SF2-helicase+RecQ_Zn_bind+RQC+HRDC→ EACC1*→	147	Streptomyces sp. CB02923	GCA_001905005.1	actinobacteria
WP_073781011.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	154	Streptomyces sp. MJM1172	GCA_001905425.1	actinobacteria
WP_073799165.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	154	Streptomyces	GCA_001905025.1	actinobacteria
WP_073800187.1	EACC1	EACC1*→ CASPASE+??+SF1-helicase+Vsr(PDDEXK)?→	138	Streptomyces sp. TSRI0261	GCA_001905485.1	actinobacteria
WP_073802404.1	EACC1	Beta_rich?→ EACC1*→ CASPASE+TPRs→??→??→	122	Streptomyces sp. TSRI0261	GCA_001905485.1	actinobacteria
WP_073803866.1	EACC1	EACC1*→ CASPASE+Beta_rich_repeat→??+SUKH→	143	Streptomyces sp. TSRI0261	GCA_001905485.1	actinobacteria
WP_073808816.1	EACC1	EACC1*→ CASPASE+TM+TM+TM+TM→	143	Kitasatospora sp. CB01950	GCA_001905465.1	actinobacteria
WP_073846533.1	EACC1	EACC1*→	101	Amycolatopsis sp. CB00013	GCA_001905755.1	actinobacteria
WP_073863288.1	EACC1	EACC1*→ CASPASE+TPRs→	121	Streptomyces sp. CB01249	GCA_001905735.1	actinobacteria
WP_073871277.1	EACC1	EACC1*→	153	Streptomyces sp. CB00072	GCA_001905575.1	actinobacteria
WP_073910694.1	EACC1	HATPase_c_2→ EACC1*→ CASPASE+??+SF1-helicase+Vsr(PDDEXK)?→	134	Streptomyces sp. CB00455	GCA_001905445.1	actinobacteria
WP_073920305.1	EACC1	low-complexity+HD+Tox-RelA+TGS+ACT→ Pkinase+TPRs→ EACC1*→ CASPASE+TPRs→	167	Streptomyces sp. CB00455	GCA_001905445.1	actinobacteria
WP_073931364.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→ HTH+N6_Mtase+Methylase_S→	156	Streptomyces sp. CB02400	GCF_001905725.1	actinobacteria
WP_073946764.1	EACC1	←CASPASE+HATPase_c_4+STAND+TPRs||EACC1*→	111	Streptomyces kebangsaanensis	GCF_001906585.1	actinobacteria
WP_074266816.1	EACC1	EACC1*→ CASPASE+TPRs→	116	Paraburkholderia phenazinium	GCA_900141745.1	betaproteobacteria
WP_074311352.1	EACC1	EACC1*→	93	Micromonospora cremea	GCF_900143515.1	actinobacteria

acc	architecture	operon	len	species	gca	taxend
WP_074474396.1	EACC1	TM+TM+TM+Peptidase_M48+TM+DUF4864+??→ EACC1*→	159	Micromonospora carbonacea	-	actinobacteria
WP_074475907.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	130	Micromonospora carbonacea	GCA_900091535.1	actinobacteria
WP_074990165.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	162	Streptomyces misionensis	GCA_900104815.1	actinobacteria
WP_074990255.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	130	Streptomyces misionensis	GCA_900104815.1	actinobacteria
WP_075136975.1	EACC1	EACC1*→ CASPASE+TM+TM→ TM+PBPB→	129	Actinophytocola xinjiangensis	GCA_001921215.1	actinobacteria
WP_075138181.1	EACC1	Beta_rich?→ EACC1*→ CASPASE+TPRs→??→??→	123	Actinophytocola xinjiangensis	GCA_001921215.1	actinobacteria
WP_075733352.1	EACC1	EACC1*→ CASPASE+TM+TM+PBPB+vWA→	111	Streptomyces acidiscabies	GCF_001941275.1	actinobacteria
WP_075735850.1	EACC1	EACC1*→ CASPASE+TPRs→	112	Streptomyces acidiscabies	GCF_001941275.1	actinobacteria
WP_075740780.1	EACC1	EACC1*→ CASPASE+??→	131	Actinoalloteichus	GCA_001941625.1	actinobacteria
WP_075976363.1	EACC1	EACC1*→ CASPASE+GTP_EFTU+GTP_EFTU_D2→	126	Actinokineospora bangkokensis	GCA_001940455.1	actinobacteria
WP_076086048.1	EACC1	EACC1*→ CASPASE+TM+TM+PBPB+vWA→	120	Streptomyces sp. IMTB 2501	GCA_001953885.1	actinobacteria
WP_076166549.1	EACC1	EACC1*→	110	Amycolatopsis coloradensis	GCA_001953865.1	actinobacteria
WP_076818503.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	156	Frankia asymbiotica	GCA_001983105.1	actinobacteria
WP_076978205.1	EACC1	EACC1*→ CASPASE+TPRs→	119	Streptomyces sp. M1013	GCA_001970135.1	actinobacteria
WP_076986698.1	EACC1	EACC1*→	132	Actinosynnema sp. ALI-1.44	GCA_001984155.1	actinobacteria
WP_076994204.1	EACC1	PALP→ Trp_syntA→ TM+LGT→ EACC1*→	117	Actinosynnema sp. ALI-1.44	GCA_001984155.1	actinobacteria
WP_077059651.1	EACC1	EACC1*→ CASPASE+JAB→?→ MFS_1→	128	Streptomyces sp. MP131-18	GCA_001984575.1	actinobacteria
WP_077939109.1	EACC1	??+TM+TM+TM+Peptidase_M48+TM+DUF4864+??→?→ EACC1*→	75	Micromonospora sp. Rc5	GCA_002006875.1	actinobacteria
WP_077964689.1	EACC1	low-complexity+HD+Tox-RelA+TGS+ACT→ Pkinase+TPRs→ EACC1*→ CASPASE+TPRs→	158	Streptomyces tsukubensis	GCA_002007125.1	actinobacteria
WP_077965477.1	EACC1	EACC1*→ CASPASE+TPRs→ Pkinase+??→	141	Streptomyces tsukubensis	GCA_002007125.1	actinobacteria
WP_078630203.1	EACC1	EACC1*→ CASPASE+TPRs→	120	Streptomyces roseochromogenus	GCF_000497445.1	actinobacteria
WP_078644979.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	147	Streptomyces hygroscopicus	GCA_002021875.1	actinobacteria
WP_078884333.1	EACC1	EACC1*→ CASPASE+TM+TM+PBPB+vWA→	114	Streptomyces sp. NRRL S-340	GCF_000720185.1	actinobacteria
WP_078974305.1	EACC1	EACC1*→	123	Streptomyces scabrisporus	GCA_002024165.1	actinobacteria
WP_079076561.1	EACC1	EACC1*→ CASPASE+TPRs→	116	Streptomyces	GCF_001572115.1	actinobacteria
WP_079129943.1	EACC1	EACC1*→ CASPASE+TM+TM+PBPB+vWA→	114	Streptomyces sp. F-3	GCA_001653115.1	actinobacteria
WP_079136578.1	EACC1	-	117	Streptomyces sp. MJM8645	-	actinobacteria
WP_079151662.1	EACC1	EACC1*→ CASPASE+low-complexity+TM+PBPB→	133	Streptomyces sp. RTd22	GCF_001650215.1	actinobacteria
WP_079161065.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	144	Streptomyces puniciscabiei	GCF_001735805.1	actinobacteria
WP_079172843.1	EACC1	EACC1*→	129	Streptomyces sp. MUSC 1	GCF_001866665.1	actinobacteria
WP_079178867.1	EACC1	EACC1*→ CASPASE+TPRs→	122	Streptomyces humi	GCF_001005085.2	actinobacteria
WP_079182070.1	EACC1	EACC1*→ CASPASE+TM+MFS_1+TM+TM+TM+TM+TM+TM+TM+TM→	90	Streptomyces yunnanensis	GCF_900142595.1	actinobacteria
WP_079186679.1	EACC1	-	130	Streptomyces sp. TSRI0107	-	actinobacteria
WP_079189196.1	EACC1	??→ EACC1*→ CASPASE+TM+TM+PBPB+vWA→	114	Streptomyces kebangsaanensis	GCF_001906585.1	actinobacteria
WP_079193145.1	EACC1	MglB→ DUF742→ sGTP-MglA→?→?→ EACC1*→ CASPASE+TPRs→||←?||?→?→ DUF664→	118	Streptomyces sp. CB02488	GCF_001905365.1	actinobacteria
WP_079258527.1	EACC1	EACC1*→ CASPASE+TM+??→	122	Streptomyces autolyticus	GCA_001983975.1	actinobacteria
WP_079273211.1	EACC1	EACC1*→ CASPASE+RE_Eco29kI+??→	119	Streptomyces sp. TN58	GCF_001941845.1	actinobacteria
WP_079277600.1	EACC1	FAD_binding_4+??+BBE→ EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	125	Streptomyces sp. CB03234	GCF_001905885.1	actinobacteria
WP_079310450.1	EACC1	EACC1*→	120	Streptomyces sp. GKU 895	GCF_002027195.1	actinobacteria
WP_079314406.1	EACC1+CASPASE+TPR_region	EACC1+CASPASE+TPR_region*→	511	Microbispora sp. GKU 823	GCA_002027145.1	actinobacteria
WP_079565090.1	EACC1	EACC1*→ CASPASE+??+TM→	124	Bradyrhizobium erythrophlei	GCA_900129505.1	alphaproteobacteria
WP_079659971.1	EACC1	EACC1*→ CASPASE+??→	137	Streptomyces	GCA_002754515.1	actinobacteria
WP_080042215.1	EACC1	ARSR-HTH+RHOD-CDC25→??→??→ EACC1*→	126	Nonomuraea sp. ATCC 55076	GCA_002057455.1	actinobacteria
WP_081238712.1	EACC1	EACC1*→ CASPASE+TPRs→??→??→	129	Streptomyces viridosporus	GCF_002078235.1	actinobacteria
WP_081546165.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	144	Streptomyces sp. B9173	-	actinobacteria
WP_081550423.1	EACC1	EACC1*→ CASPASE+TPRs→	148	Streptomyces sp. B9173	-	actinobacteria
WP_082310112.1	EACC1	EACC1*→	113	Nonomuraea sp. SBT364	GCF_001083785.1	actinobacteria
WP_082411107.1	EACC1	HATPase_c_2→ EACC1*→ CASPASE+??+SF1-helicase+Vsr(PDDEXK)?→	130	Actinobacteria bacterium OV450	GCA_001298555.1	actinobacteria
WP_082417613.1	low_complexity+EACC1	low_complexity+EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	255	Actinobacteria bacterium OK006	GCF_001298565.1	actinobacteria
WP_082553406.1	EACC1	EACC1*→ CASPASE+??+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM→	131	Phycicoccus	GCF_001426245.1	actinobacteria
WP_082857637.1	EACC1	EACC1*→	110	Amycolatopsis regifaucium	GCA_900113515.1	actinobacteria
WP_083103658.1	EACC1	EACC1*→ CASPASE+low-complexity+TM+PBPB→	152	Streptomyces gilvosporeus	GCA_002082195.1	actinobacteria

acc	architecture	operon	len	species	gca	taxend
WP_083108843.1	EACC1	PAS+GAF+PP2C+HATPase_c_2→ EACC1*→ CASPASE+TM+Beta_rich→	133	Streptomyces gilvosporeus	GCA_002082195.1	actinobacteria
WP_083971536.1	EACC1	EACC1*→ CASPASE+??→	125	Actinoplanes awajinensis	GCF_001509495.1	actinobacteria
WP_083976228.1	cNMP_cyclase+EACC1	cNMP_cyclase+EACC1*→ CASPASE+TPRs→	608	Kitasatospora azatica	GCF_000744785.1	actinobacteria
WP_083979002.1	EACC1	EACC1*→ CASPASE+TM+TM+TM+TM+TM+TM→	99	Micromonospora rosaria	GCA_001567585.1	actinobacteria
WP_084531937.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	137	Nocardia miyunensis	GCF_001613065.1	actinobacteria
WP_084747233.1	EACC1	EACC1*→ CASPASE+??+SF1-helicase+Vsr(PDDEXK)?→	138	Kitasatospora albolonga	GCA_002082585.1	actinobacteria
WP_084759454.1	EACC1	EACC1*→	130	Nocardia sp. Y48	GCF_001886715.1	actinobacteria
WP_084772597.1	EACC1	polar_lead?+TM+TM+TM+polar_tail?+low-complexity→??→ EACC1*→ CASPASE+TPRs→	126	Streptomyces sp. MOE7	GCA_002090335.1	actinobacteria
WP_084774643.1	EACC1	Glyoxalase→ EACC1*→ CASPASE+DnaJ_ZnR+DnaJ_ZnR+DnaJ_C→	135	Streptomyces sp. MOE7	GCA_002090335.1	actinobacteria
WP_084896276.1	EACC1	EACC1*→ CASPASE→	143	Streptomyces sp. CB03238	GCA_002099185.1	actinobacteria
WP_085565198.1	EACC1	EACC1*→ CASPASE+GAF+PAS→	150	Streptomyces griseofuscus	GCA_002114065.1	actinobacteria
WP_085570882.1	EACC1	EACC1*→ CASPASE+TPRs→	119	Streptomyces sp. 13-12-16	GCA_002114215.1	actinobacteria
WP_085571424.1	EACC1	??→ EACC1*→ CASPASE+TPRs→	169	Streptomyces sp. 13-12-16	GCA_002114215.1	actinobacteria
WP_085922372.1	EACC1	EACC1*→ CASPASE→ TPRs→	114	Streptomyces platensis	GCA_002119195.1	actinobacteria
WP_085924689.1	EACC1	-	127	Streptomyces platensis	-	actinobacteria
WP_086157994.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	128	Streptomyces sp. SCSIO 03032	GCA_002128305.1	actinobacteria
WP_086168353.1	EACC1	EACC1*→ CASPASE(fragment)→ CASPASE+STAND+polar_region+TM+BetaPropeller→	173	Streptomyces pharetrae	GCA_002128465.1	actinobacteria
WP_086172729.1	EACC1	EACC1*→?→ AB_hydrolase→	136	Streptomyces pharetrae	GCA_002128465.1	actinobacteria
WP_086577439.1	EACC1+??	EACC1+??*→	459	Streptosporangium minutum	GCA_002149035.1	actinobacteria
WP_086662191.1	EACC1+CASPASE+TPR_repeats+low_complexity+TM_region	TM+TM+BPD_transp_1→ OppC_N+TM+TM+BPD_transp_1→ ABC-ATPase+ABC-ATPase→ PBPB→ TM+Beta_rich+TM+Beta_rich+TM+TM→ EACC1+CASPASE+TPR_repeats+low_complexity+TM_region*→	984	Lentzea kentuckyensis	GCF_002150765.1	actinobacteria
WP_086676010.1	EACC1	GATase→ ABC-ATPase+DUF4162→ cNMP_cyclase+TM+TM+TM+TM+TM+TM→ EACC1*→	105	Amycolatopsis pretoriensis	GCA_900107925.1	actinobacteria
WP_086696600.1	EACC1	??→??→ EACC1*→ CASPASE+??→	129	Streptomyces tricolor	GCF_002155905.1	actinobacteria
WP_086697136.1	EACC1	AMP-binding+AMP-binding_C→ AMP-binding+AMP-binding_C→ EACC1*→	143	Streptomyces tricolor	GCF_002155905.1	actinobacteria
WP_086721557.1	EACC1	EACC1*→ CASPASE+TPRs→	121	Streptomyces angustmyceticus	GCF_002154415.1	actinobacteria
WP_086727347.1	EACC1	??→ EACC1*→	114	Streptomyces carpinensis	GCF_002154505.1	actinobacteria
WP_086729273.1	EACC1	EACC1*→ CASPASE+TM+TM+bPH_domain?→	128	Streptomyces carpinensis	GCF_002154505.1	actinobacteria
WP_086733927.1	EACC1	EACC1*→ PSE→ AB_hydrolase→	136	Streptomyces glaucescens	GCF_002154375.1	actinobacteria
WP_086735375.1	EACC1	EACC1*→ CASPASE+??+BsuPI→	99	Streptomyces glaucescens	GCF_002154375.1	actinobacteria
WP_086740326.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	173	Streptomyces glaucescens	GCF_002154375.1	actinobacteria
WP_086754885.1	EACC1	EACC1*→ CASPASE+??→	120	Streptomyces scabiei	GCF_002156075.1	actinobacteria
WP_086766728.1	EACC1	low-complexity+HD+Tox-RelA+TGS+ACT→ Pkinase+TPRs→ EACC1*→ CASPASE+TPRs→	143	Streptomyces bobili	GCF_002154575.1	actinobacteria
WP_086796440.1	EACC1	EACC1*→ CASPASE+TPRs→	124	Streptomyces scabiei	GCF_002155725.1	actinobacteria
WP_086816558.1	EACC1	EACC1*→ CASPASE+TPRs→	162	Streptomyces cacaoi	GCA_006539165.1	actinobacteria
WP_086819105.1	EACC1	EACC1*→	121	Allokutzneria sp. NRRL B-24872	GCF_002155965.1	actinobacteria
WP_086825751.1	EACC1	EACC1*→ CASPASE+TPRs→	128	Allokutzneria sp. NRRL B-24872	GCF_002155965.1	actinobacteria
WP_086839407.1	EACC1	EACC1*→	130	Amycolatopsis kentuckyensis	GCF_002155975.1	actinobacteria
WP_086844622.1	EACC1	PBPB→?→?→ Aminotran_5+PAS_6+HTH_22→ EACC1*→	125	Amycolatopsis kentuckyensis	GCF_002155975.1	actinobacteria
WP_086847557.1	EACC1	EACC1*→ CASPASE+TPRs→	110	Amycolatopsis kentuckyensis	GCF_002155975.1	actinobacteria
WP_086848657.1	EACC1	GATase→ ABC-ATPase+DUF4162→ cNMP_cyclase+TM+TM+TM+TM+TM+TM→ EACC1*→	105	Amycolatopsis kentuckyensis	GCF_002155975.1	actinobacteria
WP_086856190.1	EACC1	GATase→ ABC-ATPase+DUF4162→ cNMP_cyclase+TM+TM+TM+TM+TM+TM→ EACC1*→	105	Amycolatopsis lexingtonensis	GCA_003937945.1	actinobacteria
WP_086876208.1	EACC1	low-complexity+HD+Tox-RelA+TGS+ACT→ Pkinase+TPRs→ EACC1*→ CASPASE+TPRs→	138	Streptomyces rochei	GCF_002155895.1	actinobacteria
WP_086885313.1	EACC1	EACC1*→ CASPASE+STAND+TPRs→	144	Streptomyces rhizosphaericus	GCF_002155885.1	actinobacteria
WP_087684270.1	EACC1	TetR_N+TetR_C_6→ EACC1*→ CASPASE+low-complexity+TM+PBPB→	141	Streptomyces autolyticus	GCA_001983975.1	actinobacteria
WP_087764507.1	EACC1	EACC1*→ CASPASE+Beta_rich_repeat→	143	Streptomyces sp. CS057	GCA_002188345.1	actinobacteria
WP_087765136.1	EACC1	EACC1*→ CASPASE+STAND+??+TPRs+??→	119	Streptomyces sp. CS057	GCA_002188345.1	actinobacteria
WP_087765178.1	EACC1	EACC1*→	117	Streptomyces sp. CS057	GCA_002188345.1	actinobacteria
WP_087812330.1	EACC1	EACC1*→ CASPASE+TPRs→	119	Streptomyces sp. CS113	GCA_002188365.1	actinobacteria
WP_088574340.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	95	Streptomyces sp. PgraA7	GCA_900187925.1	actinobacteria
WP_088643096.1	EACC1	TM+TM+TM+Peptidase_M48+TM+DUF4864+??→ EACC1*→	132	Micromonospora wenchangensis	GCA_002210435.1	actinobacteria
WP_088646394.1	EACC1	EACC1*→ CASPASE+STAND+TPRs→||←TM+TM+TM	119	Micromonospora wenchangensis	GCA_002210435.1	actinobacteria
WP_088797080.1	EACC1	EACC1*→ CASPASE+TM+PBPB+vWA→	147	Streptomyces	GCA_002300315.1	actinobacteria

acc	architecture	operon	len	species	gca	taxend
WP_088800827.1	EACC1	EACC1*→	132	Streptomyces	GCA_002300315.1	actinobacteria
WP_088948769.1	EACC1	EACC1*→	126	Micromonospora zamorensis	GCA_900090275.1	actinobacteria
WP_088949309.1	EACC1	TM+TM+TM+Peptidase_M48+TM+DUF4864+??→ EACC1*→	138	Micromonospora zamorensis	GCA_900090275.1	actinobacteria
WP_088961186.1	EACC1	TM+TM+TM+Peptidase_M48+TM+DUF4864+??→ EACC1*→	130	Micromonospora purpureochromogenes	GCA_900091515.1	actinobacteria
WP_088982801.1	EACC1	EACC1*→ CASPASE+TM+TM+TM+TM+TM+TM→	137	Micromonospora echinospora	GCA_002266845.1	actinobacteria
WP_088988490.1	EACC1	TM+TM+TM+Peptidase_M48+TM+DUF4864+??→ EACC1*→	130	Micromonospora chokoriensis	GCA_900091505.1	actinobacteria
WP_088989057.1	EACC1	EACC1*→	126	Micromonospora chokoriensis	GCF_900091505.1	actinobacteria
WP_088992833.1	EACC1	TM+TM+TM+Peptidase_M48+TM+DUF4864+??→ EACC1*→ TPRs+CASPASE→	133	Micromonospora echinaurantiaca	GCA_900090235.1	actinobacteria
WP_089020355.1	EACC1	EACC1*→	128	Micromonospora coriariae	GCA_900091455.1	actinobacteria
WP_089158195.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	129	Micromonospora sp. NBS 11-29	GCF_002140155.1	actinobacteria
WP_089205289.1	EACC1	EACC1*→ CASPASE+??→	115	Streptosporangium subroseum	GCA_900188345.1	actinobacteria
WP_089209902.1	EACC1	EACC1*→	61	Streptosporangium subroseum	GCF_900188345.1	actinobacteria
WP_089222615.1	EACC1	EACC1*→ CASPASE+PBPB+vWA→	122	Streptomyces glauciniger	GCA_900188405.1	actinobacteria
WP_089290989.1	EACC1	EACC1*→ CASPASE+BetaPropeller→	127	Actinoplanes regularis	GCA_900188005.1	actinobacteria
WP_089293414.1	EACC1	EACC1*→ CASPASE+TPRs→	125	Actinoplanes regularis	GCF_900188005.1	actinobacteria
WP_089309665.1	EACC1	EACC1*→ CASPASE+TM+TM→	102	Actinomadura mexicana	GCF_900188105.1	actinobacteria
WP_089316989.1	??+EACC1	??+EACC1*→	227	Actinomadura mexicana	GCA_900188105.1	actinobacteria
WP_089335170.1	EACC1	EACC1*→ CASPASE+TM+TM+TM+TM+TM+TM+TM+TM→ Aminotran_5→	127	Blastococcus sp. DSM 44272	GCF_900188025.1	actinobacteria
WP_089404658.1	EACC1	EACC1*→	134	Geodermatophilus saharensis	-	actinobacteria
WP_089510392.1	EACC1	-	126	Streptomyces sp. NBS 14/10	-	actinobacteria
WP_089513739.1	EACC1	EACC1*→ CASPASE+TM+TM+??+TM+TM+??+TM+TM+??→	124	Streptomyces sp. NBS 14/10	GCA_002224125.1	actinobacteria
WP_089918135.1	EACC1	polar_lead?+TM+TM+TM+polar_tail?+low-complexity→??→ EACC1*→ CASPASE+TPRs→	115	Lentzea albida	GCA_900111005.1	actinobacteria
WP_089919256.1	EACC1+CASPASE+TPR_repeats+low_complexity+TM_region	TM+TM+BPD_transp_1→ OppC_N+TM+TM+BPD_transp_1→ ABC-ATPase+ABC-ATPase→ PBPB→ TM+Beta_rich+TM+Beta_rich+TM+TM→ EACC1+CASPASE+TPR_repeats+low_complexity+TM_region*→	794	Lentzea albida	GCA_900111005.1	actinobacteria
WP_089938606.1	EACC1	RVT_1→23S_rRNA_IVP→ EACC1*→	127	Candidatus Entotheonella palauensis	GCA_000522445.1	nitrospinae/tectomicrobia group
WP_089951186.1	EACC1+CASPASE+TPR_repeats+low_complexity+TM_region	TM+TM+BPD_transp_1→ OppC_N+TM+TM+BPD_transp_1→ ABC-ATPase+ABC-ATPase→ PBPB→ TM+Beta_rich+TM+Beta_rich+TM+TM→ EACC1+CASPASE+TPR_repeats+low_complexity+TM_region*→	817	Lechevalieria xinjiangensis	GCA_900110955.1	actinobacteria
WP_090011727.1	EACC1+CASPASE+TPR_repeats+low_complexity+TM_region	TM+TM+BPD_transp_1→ OppC_N+TM+TM+BPD_transp_1→ ABC-ATPase+ABC-ATPase→ PBPB→ TM+Beta_rich+TM+Beta_rich+TM+TM→ EACC1+CASPASE+TPR_repeats+low_complexity+TM_region*→	772	Lentzea violacea	GCA_900100275.1	actinobacteria
WP_090048966.1	EACC1+CASPASE+TPR_repeats+low_complexity+TM_region	TM+TM+BPD_transp_1→ OppC_N+TM+TM+BPD_transp_1→ ABC-ATPase+ABC-ATPase→ PBPB→ TM+Beta_rich+TM+Beta_rich+TM+TM→ EACC1+CASPASE+TPR_repeats+low_complexity+TM_region*→	828	Lechevalieria fradiae	GCA_900100955.1	actinobacteria
WP_090068728.1	EACC1+CASPASE+TPR_repeats+low_complexity+TM_region	TM+TM+BPD_transp_1→ OppC_N+TM+TM+BPD_transp_1→ ABC-ATPase+ABC-ATPase→ PBPB→ TM+Beta_rich+TM+Beta_rich+TM+TM→ EACC1+CASPASE+TPR_repeats+low_complexity+TM_region*→	895	Lentzea flaviverrucosa	GCA_003350445.1	actinobacteria
WP_090097831.1	EACC1+CASPASE+TPR_repeats+low_complexity+TM_region	TM+TM+BPD_transp_1→ OppC_N+TM+TM+BPD_transp_1→ ABC-ATPase+ABC-ATPase→ PSE→ TM+Beta_rich+TM+Beta_rich+TM+TM→ EACC1+CASPASE+TPR_repeats+low_complexity+TM_region*→	750	Lentzea jiangxiensis	GCA_900104175.1	actinobacteria
WP_090797923.1	EACC1	TPRs+CASPASE→?→?→ EACC1*→?→ CASPASE+TPRs→	128	Asanoa ishikariensis	GCA_900107455.1	actinobacteria
WP_090800042.1	EACC1	EACC1*→ CASPASE+PRTase→	113	Asanoa ishikariensis	GCA_900107455.1	actinobacteria
WP_091039878.1	EACC1	EACC1*→ CASPASE+TPRs→	109	Glycomyces harbinensis	GCF_900101745.1	actinobacteria
WP_091046058.1	EACC1	EACC1*→	121	Glycomyces sambucus	GCA_900102815.1	actinobacteria
WP_091088895.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	113	Nonomuraea wenchangensis	GCF_900111685.1	actinobacteria
WP_091092856.1	EACC1	TM+TM+vWA+TM→ TM+TM+vWA+TM→ EACC1*→ CASPASE+TPRs→	111	Nonomuraea wenchangensis	GCF_900111685.1	actinobacteria
WP_091237393.1	EACC1	TM+TM+TM+Peptidase_M48+TM+DUF4864+??→ EACC1*→	129	Micromonospora matsumotoense	GCA_900091525.1	actinobacteria
WP_091239083.1	EACC1	EACC1*→ CASPASE+STAND+TPRs→||←?←?←?←TM+TM+TM	119	Micromonospora matsumotoense	GCA_900091525.1	actinobacteria
WP_091280673.1	EACC1+EAD1	EACC1+EAD1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	234	Frankia sp. G2	GCA_001536285.1	actinobacteria
WP_091285508.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	126	Amycolatopsis xylanica	GCF_900107045.1	actinobacteria
WP_091288897.1	EACC1	GATase→ ABC-ATPase+DUF4162→ cNMP_cyclase+TM+TM+TM+TM+TM+TM→ EACC1*→	79	Amycolatopsis xylanica	GCA_900107045.1	actinobacteria
WP_091289305.1	EACC1	EACC1*→ CASPASE+DnaJ_ZnR+DnaJ_ZnR+DnaJ_C→	122	Amycolatopsis xylanica	GCA_900107045.1	actinobacteria
WP_091305099.1	EACC1	GATase→ ABC-ATPase+DUF4162→ cNMP_cyclase+TM+TM+TM+TM+TM+TM→ EACC1*→	105	Amycolatopsis tolypomycina	GCA_900105945.1	actinobacteria
WP_091306292.1	EACC1	EACC1*→	118	Amycolatopsis tolypomycina	GCA_900105945.1	actinobacteria
WP_091360655.1	EACC1	EACC1*→ CASPASE+low-complexity+DUF4190(has2TM)→	132	Frankineae bacterium MT45	GCF_900100325.1	actinobacteria
WP_091399541.1	EACC1	EACC1*→	121	Micromonospora saelicesensis	GCA_900091575.1	actinobacteria

acc	architecture	operon	len	species	gca	taxend
WP_091407867.1	EACC1	TM+TM+TM+Peptidase_M48+TM+DUF4864+??→ EACC1*→	130	Micromonospora saelicesensis	GCA_900091575.1	actinobacteria
WP_091435315.1	EACC1	EACC1*→ CASPASE+SF1-helicase→	125	Micromonospora yangpuensis	GCA_900091615.1	actinobacteria
WP_091447807.1	EACC1	EACC1*→	136	Alloactinosynnema iranicum	GCA_900101685.1	actinobacteria
WP_091453106.1	EACC1	EACC1*→ CASPASE+TPRs→	124	Alloactinosynnema iranicum	GCA_900101685.1	actinobacteria
WP_091516393.1	EACC1	EACC1*→ CASPASE+TM+TM+TM+TM→	120	Amycolatopsis sacchari	GCA_900114035.1	actinobacteria
WP_091597524.1	EACC1	EACC1*→	121	Amycolatopsis lurida	GCA_000749465.3	actinobacteria
WP_091624407.1	EACC1	EACC1*→	114	Amycolatopsis saalfeldensis	GCA_900110575.1	actinobacteria
WP_092380860.1	EACC1	EACC1*→ CASPASE+Pkinase→	67	Xiangella phaseoli	GCF_003253475.1	actinobacteria
WP_092555827.1	??+STAND+EACC1	??+STAND+??→??+STAND+EACC1*→	770	Actinoplanes derwentensis	GCA_900104725.1	actinobacteria
WP_092704916.1	EACC1	EACC1*→	108	Rhodanobacter glycinis	GCF_900114325.1	gammaproteobacteria
WP_092783696.1	EACC1	EACC1*→	113	Actinokineospora terrae	GCA_900111175.1	actinobacteria
WP_092783891.1	EACC1	EACC1*→ CASPASE+??+TM+TM+TM+TM+TM+TM+TM+TM→ CASPASE+??+TM+TM+TM+TM+TM+TM+TM+TM→	128	Actinokineospora terrae	GCF_900111175.1	actinobacteria
WP_093160608.1	EACC1	EACC1*→ CASPASE+FTSK+FTSK+FTSK+FTSK→	128	Saccharopolyspora antimicrobica	GCA_003635025.1	actinobacteria
WP_093258118.1	EACC1	EACC1*→ CASPASE+Astro_capsid_N→	84	Thermostaphylospora chromogena	-	actinobacteria
WP_093344959.1	EACC1	EACC1*→ CASPASE+FTSK+FTSK+FTSK+FTSK→	128	Saccharopolyspora	GCA_003053965.1	actinobacteria
WP_093345617.1	EACC1	EACC1*→ CASPASE+BetaPropeller→	125	Saccharopolyspora	GCF_900112555.1	actinobacteria
WP_093405879.1	EACC1	EACC1*→ CASPASE+TPRs→	123	Verrucosispora sediminis	GCA_900112325.1	actinobacteria
WP_093468834.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	129	Streptomyces melanosporofaciens	GCF_900105695.1	actinobacteria
WP_093485252.1	EACC1	EACC1*→ CASPASE+??→	119	Streptomyces	GCA_002797835.1	actinobacteria
WP_093491400.1	EACC1	EACC1*→	132	Streptomyces sp. 2112.3	GCA_003610145.1	actinobacteria
WP_093497024.1	EACC1	EACC1*→ CASPASE+TM+TM+BetaPropeller→	128	Streptomyces sp. Ag109_O5-10	GCA_900105755.1	actinobacteria
WP_093588272.1	EACC1+CASPASE+TPR_repeats+low_complexity+TM_region	TM+TM+BPD_transp_1→ OppC_N+TM+TM+BPD_transp_1→ ABC-ATPase+ABC-ATPase→ PBPB→ TM+Beta_rich+TM+Beta_rich+TM+TM→ EACC1+CASPASE+TPR_repeats+low_complexity+TM_region*→	831	Lentzea waywayandensis	GCA_900115955.1	actinobacteria
WP_093595983.1	EACC1	EACC1*→ CASPASE+TM+TM+bPH_domain?→	162	Streptomyces sp. MnatMP-M17	GCA_900091995.1	actinobacteria
WP_093598336.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	123	Lentzea waywayandensis	GCA_900115955.1	actinobacteria
WP_093604360.1	EACC1	EACC1*→	145	Streptomyces sp. MnatMP-M17	GCA_900091995.1	actinobacteria
WP_093615170.1	EACC1	EACC1*→ CASPASE+PBPB+vWA→ TM+PBPB→	118	Actinoplanes philippinensis	GCA_900113015.1	actinobacteria
WP_093641700.1	EACC1	EACC1*→ CASPASE+Beta_rich_repeat→	155	Streptomyces sp. SceaMP-e96	GCF_900090095.1	actinobacteria
WP_093643256.1	EACC1	Phage_int_SAM_3+Phage_integrase→ EACC1*→ CASPASE+TPRs→	119	Streptomyces sp. SceaMP-e96	GCF_900090095.1	actinobacteria
WP_093643475.1	EACC1	EACC1*→	135	Streptomyces	GCA_003173275.1	actinobacteria
WP_093647855.1	EACC1	EACC1*→ CASPASE+FGS_fold-domain→??→??→ TM+TM+BaxI_1→?→ NUDIX→	134	Streptomyces sp. SceaMP-e96	GCA_900090095.1	actinobacteria
WP_093700286.1	EACC1	TetR_N+TetR_C_6→ EACC1*→	140	Streptomyces sp. MnatMP-M27	-	actinobacteria
WP_093709954.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	135	Streptomyces sp. 2131.1	GCA_900105515.1	actinobacteria
WP_093715662.1	EACC1	EACC1*→	134	Streptomyces alni	GCF_900112845.1	actinobacteria
WP_093717772.1	EACC1	EACC1*→ CASPASE+low-complexity+BetaPropeller→	117	Streptomyces alni	GCA_900112845.1	actinobacteria
WP_093734734.1	EACC1	EACC1*→	127	Streptomyces sp. DvalAA-14	GCF_900091855.1	actinobacteria
WP_093737778.1	EACC1	EACC1*→ CASPASE+TPRs→	126	Streptomyces sp. DvalAA-14	GCA_900091855.1	actinobacteria
WP_093744297.1	EACC1	EACC1*→ CASPASE+TPRs→	121	Streptomyces sp. PAN_FS17	GCA_900105465.1	actinobacteria
WP_093749236.1	EACC1	EACC1*→	63	Streptomyces sp. PAN_FS17	GCA_900105465.1	actinobacteria
WP_093760390.1	EACC1	EACC1*→ CASPASE+??+SF1-helicase+Vsr(PDDEXK)?→	138	Streptomyces sp. BpilaLS-43	GCA_900091875.1	actinobacteria
WP_093764368.1	EACC1	TM+TM+TM+PP2C→??→ EACC1*→ CASPASE+TM+TM+PBPB+vWA→	114	Streptomyces sp. F-7	GCF_900079415.1	actinobacteria
WP_093782548.1	EACC1	EACC1*→ CASPASE+TPRs→	132	Streptomyces guanduensis	GCA_900103985.1	actinobacteria
WP_093799277.1	EACC1	EACC1*→ CASPASE+TM?+BetaPropeller→	152	Streptomyces sp. Wb2n-11	GCF_001049855.1	actinobacteria
WP_093859836.1	EACC1	FAD_binding_4+FAD-oxidase_C→ DAGK_cat+DAGK_acc→ EACC1*→ CASPASE+TPRs→ Clp_N+Clp_N+ClpABN-AAA→	135	Streptomyces sp. TLI_053	GCF_900105395.1	actinobacteria
WP_093863049.1	EACC1	EACC1*→ CASPASE+HSP70→	139	Streptomyces sp. TLI_053	GCA_900105395.1	actinobacteria
WP_093896825.1	EACC1	EACC1*→ CASPASE+??→	137	Streptomyces sp. Ncost-T10-10d	GCA_900091955.1	actinobacteria
WP_093897822.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	106	Streptomyces sp. Ncost-T10-10d	-	actinobacteria
WP_093905892.1	EACC1	EACC1*→ CASPASE+TPRs→	179	Streptomyces sp. cf386	GCF_900103585.1	actinobacteria
WP_093937741.1	EACC1	EACC1*→	109	Amycolatopsis thailandensis	GCA_002234405.1	actinobacteria
WP_093945735.1	EACC1	GATase→ ABC-ATPase+DUF4162→ cNMP_cyclase+TM+TM+TM+TM+TM+TM→ EACC1→ CASPASE+EAD2+TM+TM+TM+TM→ EACC1*→	104	Amycolatopsis sp. H5	GCA_002234595.1	actinobacteria
WP_093945737.1	EACC1	GATase→ ABC-ATPase+DUF4162→ cNMP_cyclase+TM+TM+TM+TM+TM+TM→ EACC1*→ CASPASE+EAD2+TM+TM+TM+TM→ EACC1→	118	Amycolatopsis sp. H5	GCA_002234595.1	actinobacteria
WP_093950342.1	EACC1	PBPB→?→?→ Aminotran_5+PAS_6+HTH_22→ EACC1*→ CASPASE+??+TM+TM→	126	Amycolatopsis sp. H5	GCA_002234595.1	actinobacteria

acc	architecture	operon	len	species	gca	taxend
WP_094006827.1	EACC1	EACC1*→ CASPASE+low-complexity+BetaPropeller→	113	Amycolatopsis sp. KNN50.9b	GCA_002234605.1	actinobacteria
WP_094103272.1	EACC1	low-complexity+HD+Tox-RelA+TGS+ACT→ Pkinase+TPRs→ EACC1*→ CASPASE+TPRs→	142	Streptomyces phaeoluteigriseus	GCA_001896135.2	actinobacteria
WP_094212107.1	EACC1	EACC1*→ CASPASE+TPRs+LysM+PG-binding→	118	Streptomyces sp. 2R	GCA_002242735.1	actinobacteria
WP_094214728.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→ TM+Acid_phosphat_B→	141	Streptomyces diastatochromogenes	GCF_002242805.1	actinobacteria
WP_094215070.1	EACC1	EACC1*→ CASPASE+low-complexity+TM+TM+TM+TM+TM+TM+TM+TM+TM+TM+BetaPropeller→	143	Streptomyces diastatochromogenes	GCF_002242805.1	actinobacteria
WP_094299657.1	EACC1	EACC1*→	120	Salmonella enterica	GCA_002234475.1	gammaproteobacteria
WP_094374006.1	EACC1	??→??→ EACC1*→ CASPASE+??→	129	Streptomyces sp. FBKL.4005	GCA_002251155.1	actinobacteria
WP_095709382.1	EACC1	EACC1*→ CASPASE+Trypsin+TPRs→	132	Streptomyces	GCA_003428925.1	actinobacteria
WP_095751376.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	133	Streptomyces sp. SA15	GCA_002291145.1	actinobacteria
WP_095757213.1	EACC1	EACC1*→ CASPASE+PBPB+vWA→	129	Streptomyces xinghaiensis	GCF_000220705.2	actinobacteria
WP_095853409.1	EACC1	EACC1*→ CASPASE+BetaPropeller→	139	Streptomyces sp. Ag82_O1-15	GCA_003633975.1	actinobacteria
WP_095854532.1	EACC1	EACC1*→ CASPASE+TM+PBPI→	108	Streptomyces	GCA_002300485.1	actinobacteria
WP_096058917.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	135	Streptomyces thermoautotrophicus	GCF_001543895.1	actinobacteria
WP_096302135.1	EACC1	EACC1*→ CASPASE+low-complexity+DUF4190(has2TM)→?→ Glyoxalase→	132	Jatrophihabitans sp. GAS493	GCF_900230215.1	actinobacteria
WP_096492710.1	EACC1	EACC1*→	121	Actinosynnema pretiosum	GCA_002354875.1	actinobacteria
WP_096901987.1	EACC1	EACC1*→	103	Klebsiella pneumoniae	GCA_002411735.1	gammaproteobacteria
WP_097190236.1	EACC1	EACC1→ Tnp_DNA_bind+DDE_Tnp_1+Dimer_Tnp_Tn5→ CASPASE+TPRs→ EACC1→ CASPASE(fragment)→ EACC1*→ CASPASE+CASPASE+TM+TPRs→ CASPASE(fragment)→	135	Burkholderia sp. OK806	GCA_900230245.1	betaproteobacteria
WP_097190238.1	EACC1	EACC1→ Tnp_DNA_bind+DDE_Tnp_1+Dimer_Tnp_Tn5→ CASPASE+TPRs→ EACC1*→ CASPASE(fragment)→ EACC1→ CASPASE+CASPASE+TM+TPRs→ CASPASE(fragment)→	138	Burkholderia sp. OK806	GCA_900230245.1	betaproteobacteria
WP_097190240.1	EACC1	EACC1*→ Tnp_DNA_bind+DDE_Tnp_1+Dimer_Tnp_Tn5→ CASPASE+TPRs→ EACC1→ CASPASE(fragment)→ EACC1→ CASPASE+CASPASE+TM+TPRs→ CASPASE(fragment)→	135	Burkholderia sp. OK806	GCF_900230245.1	betaproteobacteria
WP_097217245.1	EACC1	EACC1*→ CASPASE+??+TM+TM+TM→	125	Streptomyces sp. Ag82_G6-1	GCA_900215615.1	actinobacteria
WP_097229463.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	144	Streptomyces zhaozhouensis	GCA_900230195.1	actinobacteria
WP_097231130.1	EACC1	Pkinase+TPRs→ EACC1*→ CASPASE+TPRs→	149	Streptomyces zhaozhouensis	GCA_900230195.1	actinobacteria
WP_097233812.1	EACC1	EACC1*→ CASPASE+JAB→	130	Streptomyces zhaozhouensis	-	actinobacteria
WP_097244713.1	EACC1	EACC1*→ CASPASE+TPRs→	113	Nocardia amikacinitolerans	GCA_900215415.1	actinobacteria
WP_097255380.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→ TM+Acid_phosphat_B→	141	Streptomyces sp. Ag109_G2-15	GCF_900215565.1	actinobacteria
WP_097257754.1	EACC1	EACC1*→ CASPASE+??+TM+TM+TM+TPRs→	112	Streptomyces	GCA_002846295.1	actinobacteria
WP_097317403.1	EACC1	EACC1*→ CASPASE+Pentapeptide_repeats→	112	Actinoplanes atraurantiacus	GCA_900215205.1	actinobacteria
WP_097327188.1	EACC1	EACC1*→ CASPASE+TPRs→	108	Actinoplanes atraurantiacus	GCA_900215205.1	actinobacteria
WP_097478582.1	EACC1	EACC1*→	116	Escherichia coli	GCF_002518865.1	gammaproteobacteria
WP_097868186.1	EACC1	EACC1*→ CASPASE+??+SF1-helicase+Vsr(PDDEXK)?→	138	Streptomyces sp. rh34	GCF_002551245.1	actinobacteria
WP_097873431.1	EACC1	EACC1*→ CASPASE+TPRs→	118	Streptomyces sp. ms184	GCF_002551335.1	actinobacteria
WP_097883263.1	EACC1	EACC1*→ CASPASE+TPRs→	118	Streptomyces sp. st140	GCF_002551135.1	actinobacteria
WP_097932812.1	EACC1	EACC1*→ CASPASE+STAND+??+TPRs+??→	119	Streptomyces	GCF_002551215.1	actinobacteria
WP_097944194.1	EACC1	EACC1*→ CASPASE+TPRs→	121	Streptomyces sp. ms115	GCF_002551345.1	actinobacteria
WP_097965555.1	EACC1	HATPase_c_2→ EACC1*→ CASPASE+Beta_rich_repeat→	143	Streptomyces sp. or20	GCF_002551305.1	actinobacteria
WP_097984112.1	EACC1	EACC1*→ CASPASE+TPRs→	118	Streptomyces sp. fl50	GCF_002551435.1	actinobacteria
WP_098020341.1	EACC1	EACC1*→ CASPASE+TPRs→	118	Streptomyces sp. b62	GCF_002551475.1	actinobacteria
WP_098083203.1	EACC1	DUF2510(W3)+BicD+DUF4041+T5orf172→ EACC1*→ CASPASE+TPRs→	121	Nocardia sp. FDAARGOS_372	GCA_002554515.1	actinobacteria
WP_098512379.1	EACC1	GATase→ ABC-ATPase+DUF4162→ cNMP_cyclase+TM+TM+TM+TM+TM+TM+TM→ EACC1*→	110	Amycolatopsis sulphurea	GCA_003600245.1	actinobacteria
WP_098750929.1	EACC1	low-complexity+HD+Tox-RelA+TGS+ACT→ Pkinase+TPRs→ EACC1*→ CASPASE+TPRs→	130	Streptomyces sp. Ru87	GCA_002573955.1	actinobacteria
WP_098752253.1	EACC1	EACC1*→	141	Streptomyces sp. Ru87	GCA_002573955.1	actinobacteria
WP_098753503.1	EACC1	polar_lead?+TM+TM+TM+polar_tail?+low-complexity→??→ EACC1*→ CASPASE+TPRs→	159	Streptomyces sp. Ru87	GCA_002573955.1	actinobacteria
WP_098753773.1	EACC1	EACC1*→ CASPASE+TM?+BetaPropeller→||←DUF664	121	Streptomyces sp. Ru87	GCA_002573955.1	actinobacteria
WP_098891783.1	EACC1	EACC1*→ CASPASE+TPRs→	125	Streptomyces sp. or3	GCF_002551295.1	actinobacteria
WP_098897631.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	95	Streptomyces sp. st77	GCF_002551175.1	actinobacteria
WP_099014516.1	EACC1	EACC1*→ CASPASE+TM+??→	122	Streptomyces malaysiensis	GCA_002591335.1	actinobacteria
WP_099014682.1	EACC1	TetR_N+TetR_C_6→ EACC1*→ CASPASE+low-complexity+TM+PBPB→	137	Streptomyces malaysiensis	GCF_002591335.1	actinobacteria
WP_099127615.1	EACC1	EACC1→ *CASPASE+low-complexity+BetaPropeller___*__##→*	122	Streptomyces sp. ScaeMP-e48	GCA_900090155.1	actinobacteria
WP_099174769.1	EACC1	polar_lead?+TM+TM+TM+polar_tail?+low-complexity→??→ EACC1*→ CASPASE+TPRs→	130	Streptomyces sp. LamerLS-316	GCA_900090175.1	actinobacteria

acc	architecture	operon	len	species	gca	taxend
WP_099198034.1	EACC1	EACC1*→ CASPASE+TM+TM+PBPB+vWA→	99	Streptomyces cinnamoneus	GCA_002727115.1	actinobacteria
WP_099217477.1	EACC1	EACC1*→ CASPASE+??+SF1-helicase+Vsr(PDDEXK)?→	138	Streptomyces	GCA_003173635.1	actinobacteria
WP_099281823.1	EACC1	EACC1*→	129	Streptomyces sp. AmelKG-E11A	GCF_002705975.1	actinobacteria
WP_099502446.1	EACC1	EACC1*→ CASPASE+TPRs→	122	Streptomyces	GCA_002946835.1	actinobacteria
WP_099847282.1	EACC1	TM+TM+TM+Peptidase_M48+TM+DUF4864+??→ EACC1*→	136	Verrucosispora sp. CNZ293	GCA_002754655.1	actinobacteria
WP_099854647.1	EACC1	EACC1*→	120	Micromonospora sp. CNZ299	GCF_002754415.1	actinobacteria
WP_099855908.1	EACC1	TM+TM+TM+Peptidase_M48+TM+DUF4864+??→ EACC1*→	138	Micromonospora sp. CNZ299	GCA_002754415.1	actinobacteria
WP_099871303.1	EACC1	Glyoxalase→ EACC1*→ CASPASE+DnaJ_ZnR+DnaJ_ZnR+DnaJ_C→	136	Streptomyces sp. 76	GCA_002754435.1	actinobacteria
WP_099871939.1	EACC1	EACC1*→ CASPASE+??→	137	Streptomyces sp. 76	GCA_002754435.1	actinobacteria
WP_099892682.1	EACC1	EACC1*→ CASPASE+GAF+PAS+GGDEF→	120	Streptomyces sp. 61	GCF_002754535.1	actinobacteria
WP_099893747.1	EACC1	low-complexity+HD+Tox-RelA+TGS+ACT→ Pkinase+TPRs→ EACC1*→ CASPASE+TPRs→	131	Streptomyces sp. 61	GCF_002754535.1	actinobacteria
WP_099898397.1	EACC1	polar_lead?+TM+TM+TM+polar_tail?+low-complexity→??→ EACC1*→ CASPASE+TPRs→	118	Streptomyces sp. 1	GCA_002754615.1	actinobacteria
WP_099904499.1	EACC1	Pkinase+TPRs→ EACC1*→ CASPASE+TPRs→	148	Streptomyces sp. 1	GCA_002754615.1	actinobacteria
WP_099918141.1	EACC1	EACC1*→ CASPASE+TM+??→	90	Streptomyces sp. 94	GCF_002754555.1	actinobacteria
WP_099919284.1	EACC1	EACC1*→ CASPASE+TPRs+LysM+PG-binding→	127	Streptomyces sp. 94	GCF_002754555.1	actinobacteria
WP_099922540.1	EACC1	EACC1*→ CASPASE+TM+PBPI→	145	Streptomyces sp. 94	GCA_002754555.1	actinobacteria
WP_099943888.1	EACC1	EACC1*→	143	Streptomyces sp. 93	GCF_002754595.1	actinobacteria
WP_100047576.1	EACC1	low-complexity+HD+Tox-RelA+TGS+ACT→ Pkinase+TPRs→ EACC1*→ CASPASE+TPRs→	137	Streptomyces sp. Alain-F2R5	GCA_002277855.1	actinobacteria
WP_100568343.1	EACC1	EACC1*→ CASPASE+TM+TM+PBPB+vWA→	114	Streptomyces sp. CB01373	GCA_002803075.1	actinobacteria
WP_100579415.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	113	Streptomyces sp. CB01201	GCA_002803085.1	actinobacteria
WP_100590194.1	EACC1	EACC1*→ CASPASE+PBPB+vWA→	117	Kitasatospora sp. CB02891	GCA_002803145.1	actinobacteria
WP_100598629.1	EACC1	-	139	Streptomyces sp. CB01635	-	actinobacteria
WP_100602265.1	EACC1	low-complexity+HD+Tox-RelA+TGS+ACT→ Pkinase+TPRs→ EACC1*→ CASPASE+TPRs→	131	Streptomyces sp. CB02959	GCA_002803155.1	actinobacteria
WP_100605450.1	low_complexity+EACC1	low_complexity+EACC1*→ CASPASE+TM+TM+bPH_domain?→	229	Streptomyces sp. CB02959	GCA_002803155.1	actinobacteria
WP_100806405.1	EACC1	TetR_N+TetR_C_6→ EACC1*→ CASPASE+low-complexity+TM+PBPB→	142	Streptomyces sp. M56	GCF_002812405.1	actinobacteria
WP_100825534.1	EACC1	EACC1*→ CASPASE+STAND→ TM+BetaPropeller→ TM+Acid_phosphat_B→	135	Streptomyces sp. 69	GCF_002813405.1	actinobacteria
WP_100841017.1	EACC1	EACC1*→ CASPASE+TM+TM+??+TM+TM+??+TM+TM+??→	110	Streptomyces sp. 4121.5	GCA_002813165.1	actinobacteria
WP_101277357.1	EACC1	EACC1*→ CASPASE+TPRs→	126	Streptomyces sp. EAG2	GCA_002844215.1	actinobacteria
WP_101373080.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→ TM+Acid_phosphat_B→	141	Streptomyces sp. 59	GCF_002846295.1	actinobacteria
WP_101373258.1	EACC1	Pkinase+??→?→?→||←?←?||HATPase_c_2→ EACC1*→ CASPASE+??+SF1-helicase+Vsr(PDDEXK)?→	130	Streptomyces sp. 59	GCA_002846295.1	actinobacteria
WP_101378381.1	EACC1	EACC1*→ CASPASE+DnaJ_ZnR+DnaJ_C+DnaJ_C+TM+TM→	106	Streptomyces sp. GP55	GCA_002846355.1	actinobacteria
WP_101380473.1	EACC1	EACC1*→ CASPASE+??+STAND+??→	108	Streptomyces sp. GP55	GCF_002846355.1	actinobacteria
WP_101386063.1	EACC1	EACC1*→ CASPASE+low-complexity+BetaPropeller→	133	Streptomyces sp. TLI_146	GCF_002846415.1	actinobacteria
WP_101387394.1	EACC1	low-complexity+HD+Tox-RelA+TGS+ACT→ Pkinase+TPRs→ EACC1*→ CASPASE+TPRs→	128	Streptomyces sp. TLI_146	GCA_002846415.1	actinobacteria
WP_101407060.1	EACC1	EACC1*→ CASPASE+TPRs→ Pkinase+??→	135	Streptomyces sp. OK885	-	actinobacteria
WP_101417477.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	93	Streptomyces sp. 73	GCF_002846315.1	actinobacteria
WP_101422506.1	EACC1+CASPASE+BetaPropeller	EACC1+CASPASE+BetaPropeller*→ BetaPropeller→||←METHYLASE	703	Streptomyces sp. CMB-StM0423	GCA_002847285.1	actinobacteria
WP_101436672.1	EACC1	EACC1*→	109	Amycolatopsis niigatensis	GCA_002846615.1	actinobacteria
WP_101468971.1	EACC1	EACC1*→ CASPASE+FTSK+FTSK+FTSK→	118	Nocardia fluminea	GCA_002846365.1	actinobacteria
WP_101606153.1	EACC1	EACC1*→ TM+ZU5+??→	107	Amycolatopsis sp. BJA-103	GCF_002849735.1	actinobacteria
WP_101608477.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	128	Amycolatopsis sp. BJA-103	GCA_002849735.1	actinobacteria
WP_102005349.1	EACC1	EACC1*→	103	Klebsiella quasipneumoniae	GCA_002853675.1	gammaproteobacteria
WP_102923658.1	EACC1	low-complexity+HD+Tox-RelA+TGS+ACT→ Pkinase+TPRs→ EACC1*→ CASPASE+TPRs→	131	Streptomyces noursei	GCA_002891315.1	actinobacteria
WP_102937470.1	EACC1	TetR_N+TetR_C_6→ EACC1*→ CASPASE+low-complexity+TM+PBPB→	140	Streptomyces malaysiensis	GCA_002891865.1	actinobacteria
WP_103335469.1	EACC1	EACC1*→ CASPASE+HSP70→	118	Amycolatopsis sp. CA-126428	GCF_002904335.1	actinobacteria
WP_103335615.1	EACC1	PBPB→?→?→ Aminotran_5+PAS_6+HTH_22→ EACC1*→||←Glyco_trans_4_4+UDPGT	125	Amycolatopsis sp. CA-126428	GCF_002904335.1	actinobacteria
WP_103338162.1	EACC1	GATase→ ABC-ATPase+DUF4162→ cNMP_cyclase+TM+TM+TM+TM+TM+TM→ EACC1*→	105	Amycolatopsis sp. CA-126428	GCF_002904335.1	actinobacteria
WP_103353785.1	EACC1	GATase→ ABC-ATPase+DUF4162→ cNMP_cyclase+TM+TM+TM+TM+TM+TM→ EACC1*→	104	Amycolatopsis sp. CA-128772	GCF_002904295.1	actinobacteria
WP_103417476.1	EACC1	Beta_rich?→ EACC1*→ CASPASE+TPRs→??→??	105	Streptomyces sp. ZL-24	GCA_002907485.1	actinobacteria
WP_103490228.1	EACC1	EACC1*→ CASPASE+TPRs→	118	Streptomyces	GCA_002910775.2	actinobacteria
WP_103506858.1	EACC1	TM+REase→ EACC1*→ CASPASE+??+SF1-helicase+Vsr(PDDEXK)?→	132	Streptomyces	GCA_001577385.1	actinobacteria
WP_103509194.1	EACC1	EACC1*→ CASPASE+??+SF1-helicase+Vsr(PDDEXK)?→	127	Streptomyces sp. SM13	GCF_002910875.1	actinobacteria

acc	architecture	operon	len	species	gca	taxend
WP_103512661.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	157	Streptomyces sp. SM13	GCF_002910875.1	actinobacteria
WP_103780861.1	EACC1	EACC1*→ CASPASE+TPRs→ Clp_N+Clp_N+ClpABN-AAA→	74	Streptomyces sp. Ru71	GCF_002920535.1	actinobacteria
WP_103817220.1	EACC1	EACC1*→ CASPASE+TM?+BetaPropeller→ MDMPI_N+MDMPI_C→ META→	116	Streptomyces sp. Ru62	GCA_002920615.1	actinobacteria
WP_103832810.1	EACC1	EACC1*→	89	Streptomyces sp. Ru73	GCF_002920575.1	actinobacteria
WP_103908125.1	EACC1	EACC1*→ CASPASE+BetaPropeller→	121	Saccharopolyspora hirsuta	GCA_003053965.1	actinobacteria
WP_103922458.1	EACC1	RVT_1→?→ EACC1*→	138	Thiotrichales bacterium HS_08	GCA_900099115.2	gammaproteobacteria
WP_104380153.1	EACC1	EACC1*→ CASPASE+TPRs→	114	Nocardia nova	GCA_002933535.1	actinobacteria
WP_104477267.1	EACC1	EACC1*→ CASPASE+TPRs→	130	Actinokineospora auranticolor	GCA_002934265.1	actinobacteria
WP_104482422.1	EACC1	EACC1*→ CASPASE+TM+TM→ TM+PBPB→	115	Actinokineospora auranticolor	GCF_002934265.1	actinobacteria
WP_104482994.1	EACC1+CASPASE	EACC1+CASPASE*→?→ BetaPropeller→	201	Actinokineospora auranticolor	GCA_002934265.1	actinobacteria
WP_104790638.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	115	Streptomyces sp. QL37	GCA_002941025.1	actinobacteria
WP_105971700.1	EACC1	EACC1*→ CASPASE+STAND+??+TPRs→	123	Streptomyces geranii	GCF_002954775.1	actinobacteria
WP_105975684.1	TPR_region+EACC1	TPR_region+EACC1*→	355	Streptomyces geranii	GCF_002954775.1	actinobacteria
WP_106126014.1	EACC1	EACC1*→ CASPASE+DUF179→ SIR2+??→??→	117	Pseudosporangium ferrugineum	GCA_003002065.1	actinobacteria
WP_106127751.1	EACC1	EACC1*→ CASPASE+TPRs→	113	Pseudosporangium ferrugineum	GCA_003002065.1	actinobacteria
WP_106188106.1	EACC1	EACC1*→ CASPASE+TM+TM+TM+TM→	117	Umezawaea tangerina	GCA_003002815.1	actinobacteria
WP_106243198.1	EACC1	EACC1*→ CASPASE+PBPB→	123	Nonomuraea fuscirosea	GCF_003001935.1	actinobacteria
WP_106318500.1	EACC1	Glyco_trans_4_4+UDPGT→ EACC1*→ CASPASE+PBPB+vWA→ TM+PBPB→	130	Actinoplanes italicus	GCF_003001815.1	actinobacteria
WP_106331136.1	EACC1+CASPASE+TPR_repeats+low_complexity+TM_region	EACC1+CASPASE+TPR_repeats+low_complexity+TM_region*→ STAND+TPRs→	854	Actinoplanes italicus	GCF_003001815.1	actinobacteria
WP_106677146.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	139	Streptosporangium nondiastaticum	GCA_003011965.1	actinobacteria
WP_106956679.1	EACC1	EACC1*→ CASPASE+TM+TM+TM+TM→	116	Nocardia sp. MDA0666	GCA_003023875.1	actinobacteria
WP_106958984.1	EACC1	EACC1*→	138	Streptomyces	GCF_000156695.2	actinobacteria
WP_107079341.1	EACC1	EACC1*→	117	Micromonospora sp. MH33	GCA_003013775.1	actinobacteria
WP_107082547.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	152	Streptomyces sp. Mg1	GCF_000412265.2	actinobacteria
WP_107089790.1	EACC1	EACC1*→ CASPASE+??+SF1-helicase+Vsr(PDDEXK)?→	133	Streptomyces sp. WM6373	GCF_001279685.1	actinobacteria
WP_107096587.1	EACC1	EACC1*→ CASPASE+TPRs→	126	Actinobacteria bacterium OK006	GCF_001298565.1	actinobacteria
WP_107103604.1	low_complexity+EACC1	low_complexity+EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→||←MFS_1	277	Streptomyces	GCF_001426405.1	actinobacteria
WP_107256709.1	EACC1	EACC1*→ CASPASE+TPRs→	124	Plantactinospora sp. BB1	GCA_003030385.1	actinobacteria
WP_107267269.1	EACC1	EACC1*→ CASPASE+TPRs→	124	Plantactinospora sp. BC1	GCA_003030345.1	actinobacteria
WP_107288274.1	EACC1	EACC1*→	134	Streptomyces sp. NBRC 110611	GCF_001590865.1	actinobacteria
WP_107450456.1	EACC1	EACC1*→ CASPASE+TPRs→	113	Streptomyces sp. LUP30	GCF_001746365.1	actinobacteria
WP_107456389.1	EACC1	EACC1*→ CASPASE+TM+TM+PBPB+vWA→	121	Streptomyces sp. A244	GCA_003041235.1	actinobacteria
WP_107458939.1	EACC1	EACC1*→ CASPASE+??→	117	Streptomyces sp. A244	GCF_003041235.1	actinobacteria
WP_107471257.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	135	Streptomyces sp. MUSC 1	GCF_001866665.1	actinobacteria
WP_107475813.1	EACC1	EACC1*→ CASPASE+TM?+DUF3558+DUF3558→	145	Streptomyces sp. FBKL.4005	GCF_002251155.1	actinobacteria
WP_107657320.1	EACC1	EACC1*→ CASPASE+STAND+BetaPropeller+BetaPropeller→	128	Nocardia suismassiliense	GCF_900269665.1	actinobacteria
WP_108907227.1	EACC1	EACC1*→ CASPASE+STAND+??→	116	Streptomyces sp. HNM0039	GCA_003097515.1	actinobacteria
WP_109174941.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	95	Streptomyces sp. CS147	GCA_003116775.1	actinobacteria
WP_109185243.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	157	Streptomyces sp. CS081A	GCA_003116715.1	actinobacteria
WP_109279769.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	130	Streptomyces orinoci	GCF_003121295.1	actinobacteria
WP_109321412.1	EACC1	EACC1*→ CASPASE+PBPB+vWA→	149	Streptomyces xinghaiensis	GCF_001756925.1	actinobacteria
WP_109378190.1	EACC1	EACC1*→ CASPASE+STAND+polar_region+TM+BetaPropeller→	161	Streptomyces sp. NWU339	GCA_003143855.1	actinobacteria
WP_109494743.1	EACC1	EACC1*→ CASPASE+TPRs→	120	Streptomyces sp. Act143	GCA_003143935.1	actinobacteria
WP_109508239.1	EACC1	EACC1*→	121	Nocardioides sp. YIM ART13	GCF_003121585.1	actinobacteria
WP_109530806.1	EACC1+CASPASE	EACC1+CASPASE*→	475	Nocardia sp. SYSU K10002	GCF_003123685.1	actinobacteria
WP_109593304.1	EACC1	EACC1*→ CASPASE+PBPB+vWA→ TM+PBPB→	140	Actinoplanes xinjiangensis	GCA_003148685.1	actinobacteria
WP_109638580.1	EACC1+CASPASE+TPR_repeats+low_complexity+TM_region	TM+TM+BPD_transp_1→ OppC_N+TM+TM+BPD_transp_1→ ABC-ATPase+ABC-ATPase→ PBPB→ TM+Beta_rich+TM+Beta_rich+TM+TM→ EACC1+CASPASE+TPR_repeats+low_complexity+TM_region*→	802	Lechevalieria deserti	GCA_003148865.1	actinobacteria
WP_109815933.1	EACC1	TM+TM+TM+Peptidase_M48+TM+DUF4864+??→ EACC1*→	131	Micromonospora sp. 5R2A7	GCA_003172955.1	actinobacteria
WP_109818808.1	EACC1	EACC1*→	131	Micromonospora sp. 5R2A7	GCA_003172955.1	actinobacteria
WP_109867070.1	EACC1	EACC1*→	116	Escherichia coli	GCA_006471505.1	gammaproteobacteria

acc	architecture	operon	len	species	gca	taxend
WP_109888687.1	EACC1	EACC1*→ CASPASE+FGS_fold-domain→??→??→ TM+TM+BaxI_1→?→ NUDIX→	134	Streptomyces sp. NEAU-S7GS2	GCA_003173275.1	actinobacteria
WP_109891221.1	EACC1	EACC1*→ CASPASE+Beta_rich_repeat→	155	Streptomyces sp. NEAU-S7GS2	GCA_003173275.1	actinobacteria
WP_109893417.1	EACC1	EACC1*→ CASPASE+??+SF1-helicase+Vsr(PDDEXK)?→	138	Streptomyces sp. NEAU-S7GS2	GCA_003173275.1	actinobacteria
WP_109899578.1	EACC1	TM+TM+TM+Peptidase_M48+TM+DUF4864+??→ EACC1*→ TPRs+CASPASE→	133	Micromonospora sp. S4605	GCA_003176715.1	actinobacteria
WP_109914226.1	EACC1	EACC1*→ CASPASE+TPRs??+GHKL_ATPase+TPRs??→	107	Streptomyces sp. ZEA17I	GCA_003173635.1	actinobacteria
WP_110036763.1	EACC1	EACC1*→	78	Nocardia neocaledoniensis	GCF_003182135.1	actinobacteria
WP_110040833.1	EACC1	DUF742→ EACC1*→ CASPASE+??→	125	Nocardia neocaledoniensis	GCA_003182135.1	actinobacteria

III. Source data - profile-profile comparisons

Comparisons between poorly-understood components of the FtsH- and beta-propeller-containing systems. All comparisons involve construction of a multiple sequence alignment, which is used as the query for profile generation and subsequent comparison with profile databases (including pfam and pdb) using the hhpred program. All significant (< 0.05) hits are reported.

domain query	profile hit	e-value
bpX2	fvmNEFF1-Nterm	8.6e-19
bpX2	fvmX7	1.9e-06
bpX2	bpX5	0.0072
bpX3	fvmX7	0.00036
bpX3	fvmNEFF1-Nterm	0.0032
bpX3	bpX2	0.0051
bpX5	bpX2	0.021
bpX5	fvmNEFF1-Nterm	0.038
fvmX2	fvmX5	4.6e-38
fvmX7	fvmNEFF1-Nterm	2.5e-29
fvmX7	bpX2	0.00012
fvmX5	fvmX2	9.2e-07
fvmX3-analog	fvmX3	0.046
fvmNEFF1-Nterm	bpX2	9e-19
fvmNEFF1-Nterm	fvmX7	5.5e-12

Comparisons between distinct EAD domains and other domains of interest. See above for methodology.

domain query	profile hit	p-value
EAD7	EAD6	2.1e-07
EAD7	EAD1	8.9e-07
EAD7	bDLD2	0.00015
EAD6	EAD7	1.7e-09
EAD6	EAD1	2.3e-07
EAD6	CARD	5.2e-05
EAD1	EAD7	7.1e-09
EAD1	EAD8	1.6e-06
EAD1	bDLD1	8.8e-06
EAD1	EAD6	1.5e-05
EAD1	EAD2	0.00028
EAD8	EAD2	1.3e-06
EAD8	bDLD2	2.5e-06
EAD8	EAD5	4.3e-06
EAD8	EAD1	7.7e-06
EAD2	EAD8	1e-06
EAD2	EAD5	0.00045
EAD2	EAD7	0.00052
EAD5	EAD8	0.00026
EAD5	EAD1	0.00077
bDLD1	EAD1	2.1e-05
bDLD1	DEATH(3OQ9E)	0.00032
bDLD2	EAD8	1.6e-05
bDLD2	CARD(2NZ7B)	0.0005

IV. Source data - pairwise systems comparison in same genomes

system vs system	ov.lap #	fraction
VMAP vs iSTAND	13	0.0317
VMAP vs FtsH	16	0.0403
VMAP vs beta propeller	6	0.0144
VMAP vs GAP1-N1	8	0.0164
VMAP vs GAP1-N2	214	0.2642
VMAP vs NucA	1	0.0026
VMAP vs EACC1	305	0.4398
iSTAND vs FtsH	2	0.022
iSTAND vs beta propeller	4	0.0362
iSTAND vs GAP1-N1	4	0.0219
iSTAND vs GAP1-N2	1	0.002
iSTAND vs NucA	1	0.0135
iSTAND vs EACC1	2	0.0052
FtsH vs beta propeller	17	0.1726
FtsH vs GAP1-N1	2	0.0117
FtsH vs GAP1-N2	13	0.0264
FtsH vs NucA	0	0
FtsH vs EACC1	13	0.0347
beta propeller vs GAP1-N1	5	0.0263
beta propeller vs GAP1-N2	13	0.0254
beta propeller vs NucA	0	0
beta propeller vs EACC1	5	0.0127
GAP1-N1 vs GAP1-N2	4	0.0069
GAP1-N1 vs NucA	2	0.013
GAP1-N1 vs EACC1	8	0.0171
GAP1-N2 vs NucA	1	0.0021
GAP1-N2 vs EACC1	168	0.2133
NucA vs EACC1	0	0

V. Source data - organisms with multiple systems in same genomes

- **VMAP vs iSTAND**:

species	multicellularity
[Scytonema hofmanni] UTEX B 1581	TRUE
Aphanocapsa montana BDHKU210001	TRUE
Calothrix sp. NIES-2098	TRUE
Calothrix sp. PCC 6303	TRUE
Calothrix sp. PCC 7103	TRUE
Fischerella sp. PCC 9431	TRUE
Geitlerinema sp. PCC 7105	TRUE
Mastigocoleus testarum BC008	TRUE
Nostoc punctiforme PCC 73102	TRUE
Rivularia sp. PCC 7116	TRUE
Scytonema sp. HK-05	TRUE
Trichodesmium erythraeum	TRUE
Trichodesmium erythraeum IMS101	TRUE

- **VMAP vs FtsH**:

species	multicellularity
Actinoplanes globisporus	TRUE
Amycolatopsis balhimycina	TRUE
Archangium gephyra	TRUE
Calothrix parietina	TRUE
Frankia sp. QA3	TRUE
Gemmata sp. SH-PL17	FALSE
Moorea producens	TRUE
Streptomyces durhamensis	TRUE
Streptomyces griseus	TRUE
Streptomyces mirabilis	TRUE
Streptomyces puniciscabiei	TRUE
Streptomyces sp. GKU 895	TRUE
Streptomyces sp. MMG1121	TRUE
Streptomyces sp. MUSC 1	TRUE
Streptomyces sp. MUSC 14	TRUE
Streptomyces yokosukanensis	TRUE

- **VMAP vs beta propeller**:

species	multicellularity
Actinoplanes globisporus	TRUE
Frankia sp. QA3	TRUE
Gemmata sp. SH-PL17	FALSE
Streptomyces scabiei	TRUE
Streptomyces sp. MMG1121	TRUE
Streptomyces sp. NRRL F-6131	TRUE

- **VMAP vs GAP1-N1**:

species	multicellularity
Actinomadura sp. CNU-125	TRUE
Archangium violaceum	TRUE
Burkholderia cepacia	FALSE
Burkholderia pseudomallei	FALSE
Pseudomonas	FALSE
Pseudomonas fluorescens	FALSE
Streptomyces canus	TRUE
Streptomyces viridochromogenes	TRUE

- **VMAP vs GAP1-N2**:

species	multicellularity
Actinobacteria bacterium OV450	NA
Actinokineospora inagensis	TRUE
Actinokineospora terrae	TRUE
Actinomadura atramentaria	TRUE
Actinomadura chibensis	TRUE
Actinomadura echinospora	TRUE
Actinomadura formosensis	TRUE
Actinomadura kijaniata	TRUE
Actinomadura latina	TRUE
Actinomadura macra	TRUE
Actinomadura madurae	TRUE
Actinomadura rifamycini	TRUE
Actinoplanes globisporus	TRUE
Actinoplanes rectilineatus	TRUE
Actinoplanes subtropicus	TRUE
Actinoplanes utahensis	TRUE
Amycolatopsis alba	TRUE
Amycolatopsis coloradensis	TRUE
Amycolatopsis rifamycinica	TRUE
Amycolatopsis sp. CB00013	TRUE

species	multicellularity
Beggiatoa sp. 4572_84	TRUE
Frankia sp. CcI49	TRUE
Frankia sp. EAN1pec	TRUE
Frankia sp. EUN1f	TRUE
Frankia sp. G2	TRUE
Frankia sp. QA3	TRUE
Frankia sp. R43	TRUE
Gemmata sp. SH-PL17	FALSE
Hamadaea tsunoensis	TRUE
Kibdelosporangium aridum	TRUE
Kibdelosporangium phytohabitans	TRUE
Kitasatospora azatica	TRUE
Lamprocystis purpurea	TRUE
Lechevalieria aerocolonigenes	TRUE
Lentzea guizhouensis	TRUE
Microcystis sp. T1-4	TRUE
Micromonospora carbonacea	TRUE
Micromonospora echinofusca	TRUE
Micromonospora haikouensis	TRUE
Microtetraspora glauca	TRUE
Mycobacterium tuberculosis	FALSE
Nocardia sp. NRRL S-836	TRUE
Nocardiopsis dassonvillei	TRUE
Nocardiopsis flavescens	TRUE
Nocardiopsis ganjiahuensis	TRUE
Nocardiopsis halotolerans	TRUE
Nocardiopsis kunsanensis	TRUE
Nocardiopsis sinuspersici	TRUE
Nocardiopsis sp. CNS-639	TRUE
Nocardiopsis sp. TSRI0078	TRUE
Nocardiopsis synnemataformans	TRUE
Nocardiopsis xinjiangensis	TRUE
Nonomuraea solani	TRUE
Saccharopolyspora spinosa	TRUE
Saccharothrix sp. ALI-22-I	TRUE
Saccharothrix sp. CB00851	TRUE
Saccharothrix sp. NRRL B-16314	TRUE
Streptomyces	TRUE
Streptomyces albidoflavus	TRUE
Streptomyces albus	TRUE
Streptomyces albus J1074	TRUE
Streptomyces antibioticus	TRUE
Streptomyces anulatus	TRUE
Streptomyces atratus	TRUE

species	multicellularity
Streptomyces atroolivaceus	TRUE
Streptomyces aurantiacus	TRUE
Streptomyces aurantiacus JA 4570	TRUE
Streptomyces baarnensis	TRUE
Streptomyces bicolor	TRUE
Streptomyces bingchenggensis	TRUE
Streptomyces bingchenggensis BCW-1	TRUE
Streptomyces caatingaensis	TRUE
Streptomyces cellostaticus	TRUE
Streptomyces cellulosae	TRUE
Streptomyces curacoi	TRUE
Streptomyces europaeiscabiei	TRUE
Streptomyces filamentosus	TRUE
Streptomyces fulvoviolaceus	TRUE
Streptomyces globisporus	TRUE
Streptomyces griseus	TRUE
Streptomyces griseus subsp. griseus NBRC 13350	TRUE
Streptomyces himastatinicus ATCC 53653	TRUE
Streptomyces hokutonensis	TRUE
Streptomyces kanamyceticus	TRUE
Streptomyces katrae	TRUE
Streptomyces lavendulae	TRUE
Streptomyces lushanensis	TRUE
Streptomyces luteocolor	TRUE
Streptomyces mediolani	TRUE
Streptomyces mirabilis	TRUE
Streptomyces misionensis	TRUE
Streptomyces nanshensis	TRUE
Streptomyces niveus	TRUE
Streptomyces qinglanensis	TRUE
Streptomyces regensis	TRUE
Streptomyces reticuli	TRUE
Streptomyces rimosus	TRUE
Streptomyces roseochromogenus	TRUE
Streptomyces roseochromogenus subsp. oscitans DS 12.976	TRUE
Streptomyces sampsonii	TRUE
Streptomyces scopuliridis	TRUE
Streptomyces silaceus	TRUE
Streptomyces sp. 136MFCol5.1	TRUE
Streptomyces sp. 150FB	TRUE

species	multicellularity
Streptomyces sp. 2131.1	TRUE
Streptomyces sp. AA1529	TRUE
Streptomyces sp. AcH 505	TRUE
Streptomyces sp. ACT-1	TRUE
Streptomyces sp. ATexAB-D23	TRUE
Streptomyces sp. AW19M42	TRUE
Streptomyces sp. BF-3	TRUE
Streptomyces sp. BpilaLS-43	TRUE
Streptomyces sp. C	TRUE
Streptomyces sp. CB00072	TRUE
Streptomyces sp. CB00316	TRUE
Streptomyces sp. CB01249	TRUE
Streptomyces sp. CB01580	TRUE
Streptomyces sp. CB02009	TRUE
Streptomyces sp. CB02058	TRUE
Streptomyces sp. CB02115	TRUE
Streptomyces sp. CB02366	TRUE
Streptomyces sp. CB02460	TRUE
Streptomyces sp. CB02488	TRUE
Streptomyces sp. CB02923	TRUE
Streptomyces sp. CcalMP-8W	TRUE
Streptomyces sp. cf386	TRUE
Streptomyces sp. CFMR 7	TRUE
Streptomyces sp. Cmuel-A718b	TRUE
Streptomyces sp. CNB091	TRUE
Streptomyces sp. CNH099	TRUE
Streptomyces sp. CNQ431	TRUE
Streptomyces sp. CNQ-525	TRUE
Streptomyces sp. CNQ766	TRUE
Streptomyces sp. CNQ865	TRUE
Streptomyces sp. CNS335	TRUE
Streptomyces sp. CNT318	TRUE
Streptomyces sp. CNT371	TRUE
Streptomyces sp. CNY228	TRUE
Streptomyces sp. CNY243	TRUE
Streptomyces sp. DI166	TRUE
Streptomyces sp. DvalAA-19	TRUE
Streptomyces sp. DvalAA-43	TRUE
Streptomyces sp. EN16	TRUE
Streptomyces sp. EN23	TRUE
Streptomyces sp. EN27	TRUE
Streptomyces sp. F-1	TRUE
Streptomyces sp. FR-008	TRUE
Streptomyces sp. FXJ1.172	TRUE

species	multicellularity
Streptomyces sp. GBA 94-10	TRUE
Streptomyces sp. HGB0020	TRUE
Streptomyces sp. IMTB 2501	TRUE
Streptomyces sp. KE1	TRUE
Streptomyces sp. LaPpAH-202	TRUE
Streptomyces sp. M10	TRUE
Streptomyces sp. MnatMP-M17	TRUE
Streptomyces sp. MnatMP-M77	TRUE
Streptomyces sp. MNU77	TRUE
Streptomyces sp. MP131-18	TRUE
Streptomyces sp. MUSC 1	TRUE
Streptomyces sp. NBRC 110465	TRUE
Streptomyces sp. Ncost-T10-10d	TRUE
Streptomyces sp. Ncost-T6T-1	TRUE
Streptomyces sp. NRRL B-1347	TRUE
Streptomyces sp. NRRL B-24720	TRUE
Streptomyces sp. NRRL B-3253	TRUE
Streptomyces sp. NRRL F-2747	TRUE
Streptomyces sp. NRRL F-5053	TRUE
Streptomyces sp. NRRL F-5126	TRUE
Streptomyces sp. NRRL F-5193	TRUE
Streptomyces sp. NRRL F-5630	TRUE
Streptomyces sp. NRRL F-5727	TRUE
Streptomyces sp. NRRL F-6628	TRUE
Streptomyces sp. NRRL S-1824	TRUE
Streptomyces sp. NRRL S-1868	TRUE
Streptomyces sp. NRRL S-237	TRUE
Streptomyces sp. NRRL S-241	TRUE
Streptomyces sp. NRRL S-244	TRUE
Streptomyces sp. NRRL S-444	TRUE
Streptomyces sp. NRRL WC-3549	TRUE
Streptomyces sp. NRRL WC-3723	TRUE
Streptomyces sp. NRRL WC-3725	TRUE
Streptomyces sp. NRRL WC-3744	TRUE
Streptomyces sp. NTK 937	TRUE
Streptomyces sp. ok210	TRUE
Streptomyces sp. or20	TRUE
Streptomyces sp. OspMP-M43	TRUE
Streptomyces sp. OspMP-M45	TRUE
Streptomyces sp. PBH53	TRUE
Streptomyces sp. PTY087I2	TRUE
Streptomyces sp. PVA 94-07	TRUE
Streptomyces sp. RTd22	TRUE
Streptomyces sp. RV15	TRUE

species	multicellularity
Streptomyces sp. S4	TRUE
Streptomyces sp. SA3_actG	TRUE
Streptomyces sp. ScaeMP-6W	TRUE
Streptomyces sp. SCSIO 03032	TRUE
Streptomyces sp. SolWspMP-5a-2	TRUE
Streptomyces sp. TSRI0261	TRUE
Streptomyces sp. TSRI0281	TRUE
Streptomyces sp. TSRI0395	TRUE
Streptomyces sp. TSRI0445	TRUE
Streptomyces sp. Tu6071	TRUE
Streptomyces sp. TverLS-915	TRUE
Streptomyces sp. W007	TRUE
Streptomyces sp. XY332	TRUE
Streptomyces specialis	TRUE
Streptomyces tsukubensis	TRUE
Streptomyces violaceoruber	TRUE
Streptomyces virginiae	TRUE
Streptomyces vitaminophilus	TRUE
Streptomyces wadayamensis	TRUE
Streptomyces xylophagus	TRUE
Streptomyces yerevanensis	TRUE
Thermomonospora curvata	TRUE

- **VMAP vs NucA**:

species	multicellularity
Bradyrhizobium	TRUE

- **VMAP vs EACC1**:

species	multicellularity
Actinobacteria bacterium OK006	NA
Actinobacteria bacterium OK074	NA
Actinobacteria bacterium OV450	NA
Actinokineospora inagensis	TRUE
Actinokineospora terrae	TRUE
Actinomadura madurae	TRUE
Actinophytocola xinjiangensis	TRUE
Actinoplanes awajinensis subsp. mycoplanecinus	TRUE
Actinoplanes globisporus	TRUE
Actinoplanes philippinensis	TRUE

species	multicellularity
Actinoplanes rectilineatus	TRUE
Actinoplanes sp. SE50/110	TRUE
Actinoplanes utahensis	TRUE
Actinospica robiniae	TRUE
Actinosporangium sp. NRRL B-3428	TRUE
Actinosynnema sp. ALI-1.44	TRUE
Amycolatopsis alba	TRUE
Amycolatopsis australiensis	TRUE
Amycolatopsis azurea	TRUE
Amycolatopsis balhimycina	TRUE
Amycolatopsis coloradensis	TRUE
Amycolatopsis decaplanina	TRUE
Amycolatopsis japonica	TRUE
Amycolatopsis keratiniphila	TRUE
Amycolatopsis mediterranei	TRUE
Amycolatopsis orientalis	TRUE
Amycolatopsis pretoriensis	TRUE
Amycolatopsis regifaucium	TRUE
Amycolatopsis rifamycinica	TRUE
Amycolatopsis sp. CB00013	TRUE
Amycolatopsis sp. MJM2582	TRUE
Amycolatopsis tolypomycina	TRUE
Amycolatopsis vancoresmycina	TRUE
Amycolatopsis xylanica	TRUE
Catenulispora acidiphila	TRUE
Catenuloplanes japonicus	TRUE
Frankia alni	TRUE
Frankia inefficax	TRUE
Frankia sp. ACN1ag	TRUE
Frankia sp. AvcI1	TRUE
Frankia sp. EAN1pec	TRUE
Frankia sp. G2	TRUE
Hamadaea tsunoensis	TRUE
Kibdelosporangium phytohabitans	TRUE
Kibdelosporangium sp. MJ126-NF4	TRUE
Kitasatospora	TRUE
Kitasatospora azatica	TRUE
Kitasatospora cheerisanensis	TRUE
Kitasatospora sp. CB02891	TRUE
Kitasatospora sp. MBT66	TRUE
Kitasatospora sp. NRRL B-11411	TRUE
Kitasatospora sp. Root107	TRUE

species	multicellularity
Kutzneria albida	TRUE
Kutzneria albida DSM 43870	TRUE
Lechevalieria aerocolonigenes	TRUE
Lechevalieria fradiae	TRUE
Lechevalieria xinjiangensis	TRUE
Lentzea albida	TRUE
Lentzea albidocapillata	TRUE
Lentzea flaviverrucosa	TRUE
Lentzea violacea	TRUE
Lentzea waywayandensis	TRUE
Longispora albida	TRUE
Micromonospora carbonacea	TRUE
Micromonospora matsumotoense	TRUE
Micromonospora parva	TRUE
Micromonospora sp. HK10	TRUE
Micromonospora sp. NBS 11-29	TRUE
Micromonospora sp. NRRL B-16802	TRUE
Microtetraspora glauca	TRUE
Nocardia mexicana	TRUE
Nocardia sp. NRRL S-836	TRUE
Nocardiopsis dassonvillei	TRUE
Nocardiopsis flavescens	TRUE
Nocardiopsis potens	TRUE
Nocardiopsis salina	TRUE
Nocardiopsis sp. CNR-923	TRUE
Nonomuraea solani	TRUE
Pseudonocardia acaciae	TRUE
Saccharopolyspora spinosa	TRUE
Saccharothrix espanaensis	TRUE
Streptomyces	TRUE
Streptomyces acidiscabies	TRUE
Streptomyces agglomeratus	TRUE
Streptomyces albus	TRUE
Streptomyces albus subsp. albus	TRUE
Streptomyces alni	TRUE
Streptomyces ambofaciens	TRUE
Streptomyces antibioticus	TRUE
Streptomyces antioxidans	TRUE
Streptomyces anulatus	TRUE
Streptomyces atratus	TRUE
Streptomyces atriruber	TRUE
Streptomyces aurantiacus	TRUE
Streptomyces aurantiacus JA 4570	TRUE

species	multicellularity
Streptomyces autolyticus	TRUE
Streptomyces bicolor	TRUE
Streptomyces caatingaensis	TRUE
Streptomyces caeruleatus	TRUE
Streptomyces canus	TRUE
Streptomyces cattleya	TRUE
Streptomyces cellostaticus	TRUE
Streptomyces cellulosae	TRUE
Streptomyces chartreusis	TRUE
Streptomyces chattanoogensis	TRUE
Streptomyces clavuligerus	TRUE
Streptomyces coelicolor	TRUE
Streptomyces corchorusii	TRUE
Streptomyces cyaneogriseus	TRUE
Streptomyces cyaneogriseus subsp. noncyanogenus	TRUE
Streptomyces decoyicus	TRUE
Streptomyces diastatochromogenes	TRUE
Streptomyces durhamensis	TRUE
Streptomyces erythrochromogenes	TRUE
Streptomyces europaeiscabiei	TRUE
Streptomyces exfoliatus	TRUE
Streptomyces filamentosus	TRUE
Streptomyces flavidovirens	TRUE
Streptomyces flavochromogenes	TRUE
Streptomyces fradiae	TRUE
Streptomyces fulvoviolaceus	TRUE
Streptomyces gilvosporeus	TRUE
Streptomyces glaucescens	TRUE
Streptomyces griseochromogenes	TRUE
Streptomyces griseofuscus	TRUE
Streptomyces griseus	TRUE
Streptomyces guanduensis	TRUE
Streptomyces himastatinicus	TRUE
Streptomyces himastatinicus ATCC 53653	TRUE
Streptomyces hokutonensis	TRUE
Streptomyces humi	TRUE
Streptomyces hygroscopicus	TRUE
Streptomyces iakyrus	TRUE
Streptomyces incarnatus	TRUE
Streptomyces iranensis	TRUE
Streptomyces katrae	TRUE

species	multicellularity
Streptomyces longwoodensis	TRUE
Streptomyces lushanensis	TRUE
Streptomyces lydicus	TRUE
Streptomyces mangrovisoli	TRUE
Streptomyces melanosporofaciens	TRUE
Streptomyces mirabilis	TRUE
Streptomyces misionensis	TRUE
Streptomyces monomycini	TRUE
Streptomyces nanshensis	TRUE
Streptomyces natalensis	TRUE
Streptomyces niveus	TRUE
Streptomyces niveus NCIMB 11891	TRUE
Streptomyces nodosus	TRUE
Streptomyces olindensis	TRUE
Streptomyces pactum	TRUE
Streptomyces paucisporeus	TRUE
Streptomyces platensis	TRUE
Streptomyces pristinaespiralis	TRUE
Streptomyces pristinaespiralis ATCC 25486	TRUE
Streptomyces puniciscabiei	TRUE
Streptomyces purpureus	TRUE
Streptomyces rapamycinicus NRRL 5491	TRUE
Streptomyces regalis	TRUE
Streptomyces regensis	TRUE
Streptomyces reticuli	TRUE
Streptomyces rimosus	TRUE
Streptomyces roseochromogenus	TRUE
Streptomyces roseochromogenus subsp. oscitans DS 12.976	TRUE
Streptomyces roseosporus NRRL 15998	TRUE
Streptomyces roseus	TRUE
Streptomyces scabiei	TRUE
Streptomyces scabrisporus	TRUE
Streptomyces sclerotialus	TRUE
Streptomyces scopuliridis	TRUE
Streptomyces silvensis	TRUE
Streptomyces sp. 2112.3	TRUE
Streptomyces sp. 2131.1	TRUE
Streptomyces sp. 4F	TRUE
Streptomyces sp. ACT-1	TRUE

species	multicellularity
Streptomyces sp. Ag82_O1-15	TRUE
Streptomyces sp. AS58	TRUE
Streptomyces sp. ATexAB-D23	TRUE
Streptomyces sp. B9173	TRUE
Streptomyces sp. BoleA5	TRUE
Streptomyces sp. BpilaLS-43	TRUE
Streptomyces sp. CB00072	TRUE
Streptomyces sp. CB00455	TRUE
Streptomyces sp. CB01249	TRUE
Streptomyces sp. CB02058	TRUE
Streptomyces sp. CB02115	TRUE
Streptomyces sp. CB02400	TRUE
Streptomyces sp. CB02414	TRUE
Streptomyces sp. CB02488	TRUE
Streptomyces sp. CB02923	TRUE
Streptomyces sp. CB03234	TRUE
Streptomyces sp. CB03238	TRUE
Streptomyces sp. CC71	TRUE
Streptomyces sp. CcalMP-8W	TRUE
Streptomyces sp. CCM_MD2014	TRUE
Streptomyces sp. cf386	TRUE
Streptomyces sp. CNB091	TRUE
Streptomyces sp. CNQ329	TRUE
Streptomyces sp. CNQ431	TRUE
Streptomyces sp. CNQ-509	TRUE
Streptomyces sp. CNQ-525	TRUE
Streptomyces sp. CNQ865	TRUE
Streptomyces sp. CNS335	TRUE
Streptomyces sp. CNS606	TRUE
Streptomyces sp. CNT371	TRUE
Streptomyces sp. CNY228	TRUE
Streptomyces sp. CNY243	TRUE
Streptomyces sp. DSM 15324	TRUE
Streptomyces sp. DvalAA-14	TRUE
Streptomyces sp. EN16	TRUE
Streptomyces sp. EN27	TRUE
Streptomyces sp. ERV7	TRUE
Streptomyces sp. F-1	TRUE
Streptomyces sp. F-3	TRUE
Streptomyces sp. FxanaC1	TRUE
Streptomyces sp. GKU 895	TRUE
Streptomyces sp. HGB0020	TRUE
Streptomyces sp. IMTB 2501	TRUE
Streptomyces sp. LaPpAH-108	TRUE

species	multicellularity
Streptomyces sp. LUP30	TRUE
Streptomyces sp. M1013	TRUE
Streptomyces sp. MBT28	TRUE
Streptomyces sp. Mg1	TRUE
Streptomyces sp. MJM1172	TRUE
Streptomyces sp. MMG1533	TRUE
Streptomyces sp. MnatMP-M17	TRUE
Streptomyces sp. MNU77	TRUE
Streptomyces sp. MOE7	TRUE
Streptomyces sp. MP131-18	TRUE
Streptomyces sp. MspMP-M5	TRUE
Streptomyces sp. MUSC 1	TRUE
Streptomyces sp. MUSC 14	TRUE
Streptomyces sp. MUSC 93	TRUE
Streptomyces sp. NBRC 109706	TRUE
Streptomyces sp. NBRC 110027	TRUE
Streptomyces sp. NBRC 110028	TRUE
Streptomyces sp. NBRC 110465	TRUE
Streptomyces sp. NBRC 110611	TRUE
Streptomyces sp. Ncost-T10-10d	TRUE
Streptomyces sp. NRRL B-24720	TRUE
Streptomyces sp. NRRL B-3648	TRUE
Streptomyces sp. NRRL F-2580	TRUE
Streptomyces sp. NRRL F-2747	TRUE
Streptomyces sp. NRRL F-2890	TRUE
Streptomyces sp. NRRL F-4474	TRUE
Streptomyces sp. NRRL F-5053	TRUE
Streptomyces sp. NRRL F-5123	TRUE
Streptomyces sp. NRRL F-5126	TRUE
Streptomyces sp. NRRL F-5727	TRUE
Streptomyces sp. NRRL F-6131	TRUE
Streptomyces sp. NRRL S-1022	TRUE
Streptomyces sp. NRRL S-1448	TRUE
Streptomyces sp. NRRL S-1813	TRUE
Streptomyces sp. NRRL S-1824	TRUE
Streptomyces sp. NRRL S-1868	TRUE
Streptomyces sp. NRRL S-244	TRUE
Streptomyces sp. NRRL S-31	TRUE
Streptomyces sp. NRRL S-337	TRUE
Streptomyces sp. NRRL S-340	TRUE
Streptomyces sp. NRRL S-384	TRUE
Streptomyces sp. NRRL S-495	TRUE
Streptomyces sp. NRRL S-646	TRUE
Streptomyces sp. NRRL S-813	TRUE

species	multicellularity
Streptomyces sp. NRRL S-87	TRUE
Streptomyces sp. NRRL WC-3549	TRUE
Streptomyces sp. NRRL WC-3618	TRUE
Streptomyces sp. NRRL WC-3626	TRUE
Streptomyces sp. NRRL WC-3742	TRUE
Streptomyces sp. NTK 937	TRUE
Streptomyces sp. or20	TRUE
Streptomyces sp. OV198	TRUE
Streptomyces sp. PAN_FS17	TRUE
Streptomyces sp. PBH53	TRUE
Streptomyces sp. PpalLS-921	TRUE
Streptomyces sp. PRh5	TRUE
Streptomyces sp. PTY087I2	TRUE
Streptomyces sp. RTd22	TRUE
Streptomyces sp. Ru87	TRUE
Streptomyces sp. S10(2016)	TRUE
Streptomyces sp. SceaMP-e96	TRUE
Streptomyces sp. SCSIO 03032	TRUE
Streptomyces sp. SPMA113	TRUE
Streptomyces sp. TLI_053	TRUE
Streptomyces sp. TN58	TRUE
Streptomyces sp. TOR3209	TRUE
Streptomyces sp. TSRI0107	TRUE
Streptomyces sp. TSRI0261	TRUE
Streptomyces sp. TSRI0281	TRUE
Streptomyces sp. URHA0041	TRUE
Streptomyces sp. W007	TRUE
Streptomyces sp. WM4235	TRUE
Streptomyces sp. WM6372	TRUE
Streptomyces sp. WM6373	TRUE
Streptomyces sp. XY332	TRUE
Streptomyces sp. XY431	TRUE
Streptomyces sp. XY593	TRUE
Streptomyces tsukubensis	TRUE
Streptomyces varsoviensis	TRUE
Streptomyces violaceoruber	TRUE
Streptomyces violens	TRUE
Streptomyces vitaminophilus	TRUE
Streptomyces xiamenensis	TRUE
Streptomyces xylophagus	TRUE
Streptomyces yanglinensis	TRUE
Streptomyces yokosukanensis	TRUE

- **iSTAND vs FtsH**:

species	multicellularity
Candidatus Magnetoglobus multicellularis str. Araruama	TRUE
Gammaproteobacteria bacterium	NA

- **iSTAND vs beta propeller**:

species	multicellularity
Candidatus Magnetoglobus multicellularis str. Araruama	TRUE
Candidatus Thiomargarita nelsonii	TRUE
Gammaproteobacteria bacterium	NA
Haliscomenobacter hydrossis DSM 1100	TRUE

- **iSTAND vs GAP1-N1**:

species	multicellularity
Bradyrhizobium japonicum	TRUE
Candidatus Accumulibacter sp. SK-01	FALSE
Candidatus Magnetoglobus multicellularis str. Araruama	TRUE
Gammaproteobacteria bacterium	NA

- **iSTAND vs GAP1-N2**:

species	multicellularity
Candidatus Thiomargarita nelsonii	TRUE

- **iSTAND vs NucA**:

species	multicellularity
Bradyrhizobium japonicum	TRUE

- **iSTAND vs EACC1**:

species	multicellularity
Beggiatoa sp. PS	TRUE
Thiotrichales bacterium HS_08	TRUE

- **FtsH vs beta propeller**:

species	multicellularity
Actinoplanes derwentensis	TRUE
Actinoplanes globisporus	TRUE
Amycolatopsis sp. H5	TRUE
Candidatus Magnetoglobus multicellularis str. Araruama	TRUE
Dactylosporangium aurantiacum	TRUE
Fimbriiglobus ruber	TRUE
Frankia coriariae	TRUE
Frankia sp. QA3	TRUE
Gammaproteobacteria bacterium	NA
Gemmata sp. SH-PL17	FALSE
Haliangium ochraceum	TRUE
Nostoc sp. T09	TRUE
Sinosporangium album	TRUE
Streptomyces sp. GGCR-6	TRUE
Streptomyces sp. MMG1121	TRUE
Thiohalocapsa sp. ML1	TRUE
Zavarzinella formosa	TRUE

- **FtsH vs GAP1-N1**:

species	multicellularity
Candidatus Magnetoglobus multicellularis str. Araruama	TRUE
Gammaproteobacteria bacterium	NA

- **FtsH vs GAP1-N2**:

species	multicellularity
Actinoplanes globisporus	TRUE
Dactylosporangium aurantiacum	TRUE
Fimbriiglobus ruber	TRUE

species	multicellularity
Frankia sp. QA3	TRUE
Gemmata obscuriglobus	FALSE
Gemmata sp. SH-PL17	FALSE
Isosphaera pallida	TRUE
Streptomyces griseus	TRUE
Streptomyces mirabilis	TRUE
Streptomyces sp. MUSC 1	TRUE
Streptomyces sp. WM6386	TRUE
Thiohalocapsa sp. ML1	TRUE
Zavarzinella formosa	TRUE

- **FtsH vs NucA**:

species	**multicellularity**

- **FtsH vs EACC1**:

species	multicellularity
Actinoplanes derwentensis	TRUE
Actinoplanes globisporus	TRUE
Amycolatopsis balhimycina	TRUE
Amycolatopsis sp. H5	TRUE
Streptomyces durhamensis	TRUE
Streptomyces griseus	TRUE
Streptomyces mirabilis	TRUE
Streptomyces puniciscabiei	TRUE
Streptomyces sp. Act143	TRUE
Streptomyces sp. GKU 895	TRUE
Streptomyces sp. MUSC 1	TRUE
Streptomyces sp. MUSC 14	TRUE
Streptomyces yokosukanensis	TRUE

- **beta propeller vs GAP1-N1**:

species	multicellularity
Candidatus Magnetoglobus multicellularis str. Araruama	TRUE
Flavobacterium hydatis	FALSE
Gammaproteobacteria bacterium	NA
Lysobacter enzymogenes	FALSE

species	multicellularity
Singulisphaera sp. GP187	TRUE

- **beta propeller vs GAP1-N2**:

species	multicellularity
Actinoplanes globisporus	TRUE
Blastopirellula marina	TRUE
Candidatus Thiomargarita nelsonii	TRUE
Dactylosporangium aurantiacum	TRUE
Fimbriiglobus ruber	TRUE
Frankia sp. QA3	TRUE
Gemmata sp. SH-PL17	FALSE
Planctomicrobium piriforme	TRUE
Roseimaritima ulvae	TRUE
Schlesneria paludicola	TRUE
Singulisphaera sp. GP187	TRUE
Thiohalocapsa sp. ML1	TRUE
Zavarzinella formosa	TRUE

- **beta propeller vs NucA**:

species	**multicellularity**

- **beta propeller vs EACC1**:

species	multicellularity
Actinoplanes derwentensis	TRUE
Actinoplanes globisporus	TRUE
Amycolatopsis sp. H5	TRUE
Streptomyces scabiei	TRUE
Streptomyces sp. NRRL F-6131	TRUE

- **GAP1-N1 vs GAP1-N2**:

species	multicellularity
Achromatium sp. WMS3	FALSE
Candidatus Achromatium palustre	FALSE

species	multicellularity
Rhodococcus fascians	TRUE
Singulisphaera sp. GP187	TRUE

- **GAP1-N1 vs NucA**:

species	multicellularity
Bradyrhizobium japonicum	TRUE
Sinorhizobium meliloti	TRUE

- **GAP1-N1 vs EACC1**:

species	multicellularity
Bradyrhizobium erythrophlei	TRUE
Enterobacteriaceae	FALSE
Gluconobacter oxydans	FALSE
Klebsiella pneumoniae	FALSE
Pseudosporangium ferrugineum	TRUE
Rhodanobacter glycinis	FALSE
Salmonella enterica	FALSE
Streptomyces canus	TRUE

- **GAP1-N2 vs NucA**:

species	multicellularity
Methylobacterium aquaticum	TRUE

- **GAP1-N2 vs EACC1**:

species	multicellularity
Actinobacteria bacterium OV450	NA
Actinokineospora enzanensis	TRUE
Actinokineospora inagensis	TRUE
Actinokineospora terrae	TRUE
Actinomadura	TRUE
Actinomadura flavalba	TRUE
Actinomadura madurae	TRUE
Actinomadura mexicana	TRUE
Actinomadura oligospora	TRUE
Actinoplanes globisporus	TRUE

species	multicellularity
Actinoplanes rectilineatus	TRUE
Actinoplanes regularis	TRUE
Actinoplanes utahensis	TRUE
Alloactinosynnema iranicum	TRUE
Amycolatopsis alba	TRUE
Amycolatopsis coloradensis	TRUE
Amycolatopsis kentuckyensis	TRUE
Amycolatopsis rifamycinica	TRUE
Amycolatopsis sp. CB00013	TRUE
Candidatus Entotheonella palauensis	TRUE
Frankia asymbiotica	TRUE
Frankia sp. EAN1pec	TRUE
Frankia sp. G2	TRUE
Hamadaea tsunoensis	TRUE
Herbidospora cretacea	TRUE
Herbidospora mongoliensis	TRUE
Herbidospora sakaeratensis	TRUE
Kibdelosporangium phytohabitans	TRUE
Kitasatospora albolonga	TRUE
Kitasatospora azatica	TRUE
Kitasatospora sp. MMS16-BH015	TRUE
Lechevalieria aerocolonigenes	TRUE
Lentzea kentuckyensis	TRUE
Micromonospora carbonacea	TRUE
Micromonospora sp. Rc5	TRUE
Microtetraspora glauca	TRUE
Nocardia concava	TRUE
Nocardia jejuensis	TRUE
Nocardia niigatensis	TRUE
Nocardia seriolae	TRUE
Nocardia sp. NRRL S-836	TRUE
Nocardia takedensis	TRUE
Nocardiopsis dassonvillei	TRUE
Nocardiopsis flavescens	TRUE
Nonomuraea solani	TRUE
Rhodococcus	TRUE
Saccharopolyspora	TRUE
Saccharopolyspora antimicrobica	TRUE
Saccharopolyspora erythraea	TRUE
Saccharopolyspora rectivirgula	TRUE
Saccharopolyspora shandongensis	TRUE
Saccharopolyspora spinosa	TRUE
Streptomyces	TRUE

species	multicellularity
Streptomyces albus	TRUE
Streptomyces antibioticus	TRUE
Streptomyces anulatus	TRUE
Streptomyces atratus	TRUE
Streptomyces aurantiacus	TRUE
Streptomyces aurantiacus JA 4570	TRUE
Streptomyces bicolor	TRUE
Streptomyces caatingaensis	TRUE
Streptomyces cacaoi	TRUE
Streptomyces cellostaticus	TRUE
Streptomyces cellulosae	TRUE
Streptomyces cinnamoneus	TRUE
Streptomyces davaonensis	TRUE
Streptomyces europaeiscabiei	TRUE
Streptomyces filamentosus	TRUE
Streptomyces floridae	TRUE
Streptomyces fulvoviolaceus	TRUE
Streptomyces griseus	TRUE
Streptomyces himastatinicus ATCC 53653	TRUE
Streptomyces hokutonensis	TRUE
Streptomyces katrae	TRUE
Streptomyces lushanensis	TRUE
Streptomyces mirabilis	TRUE
Streptomyces misionensis	TRUE
Streptomyces mobaraensis	TRUE
Streptomyces nanshensis	TRUE
Streptomyces niveus	TRUE
Streptomyces prunicolor	TRUE
Streptomyces regensis	TRUE
Streptomyces reticuli	TRUE
Streptomyces rimosus	TRUE
Streptomyces roseochromogenus	TRUE
Streptomyces roseochromogenus subsp. oscitans DS 12.976	TRUE
Streptomyces scopuliridis	TRUE
Streptomyces sp. 2131.1	TRUE
Streptomyces sp. 2R	TRUE
Streptomyces sp. 61	TRUE
Streptomyces sp. ACT-1	TRUE
Streptomyces sp. ATexAB-D23	TRUE
Streptomyces sp. b62	TRUE
Streptomyces sp. BpilaLS-43	TRUE
Streptomyces sp. CB00072	TRUE

species	multicellularity
Streptomyces sp. CB01249	TRUE
Streptomyces sp. CB02058	TRUE
Streptomyces sp. CB02115	TRUE
Streptomyces sp. CB02488	TRUE
Streptomyces sp. CB02923	TRUE
Streptomyces sp. CcalMP-8W	TRUE
Streptomyces sp. cf386	TRUE
Streptomyces sp. CNB091	TRUE
Streptomyces sp. CNQ431	TRUE
Streptomyces sp. CNQ-525	TRUE
Streptomyces sp. CNQ865	TRUE
Streptomyces sp. CNS335	TRUE
Streptomyces sp. CNT371	TRUE
Streptomyces sp. CNY228	TRUE
Streptomyces sp. CNY243	TRUE
Streptomyces sp. CS057	TRUE
Streptomyces sp. EAG2	TRUE
Streptomyces sp. EN16	TRUE
Streptomyces sp. EN27	TRUE
Streptomyces sp. F-1	TRUE
Streptomyces sp. f150	TRUE
Streptomyces sp. FBKL.4005	TRUE
Streptomyces sp. HCCB10043	TRUE
Streptomyces sp. HGB0020	TRUE
Streptomyces sp. IMTB 2501	TRUE
Streptomyces sp. LamerLS-316	TRUE
Streptomyces sp. MBRL 601	TRUE
Streptomyces sp. MnatMP-M17	TRUE
Streptomyces sp. MNU77	TRUE
Streptomyces sp. MP131-18	TRUE
Streptomyces sp. ms115	TRUE
Streptomyces sp. ms184	TRUE
Streptomyces sp. MUSC 1	TRUE
Streptomyces sp. NBRC 110465	TRUE
Streptomyces sp. NBS 14/10	TRUE
Streptomyces sp. Ncost-T10-10d	TRUE
Streptomyces sp. Ncost-T6T-2b	TRUE
Streptomyces sp. NRRL B-24051	TRUE
Streptomyces sp. NRRL B-24720	TRUE
Streptomyces sp. NRRL F-2747	TRUE
Streptomyces sp. NRRL F-5053	TRUE
Streptomyces sp. NRRL F-5126	TRUE
Streptomyces sp. NRRL F-5727	TRUE
Streptomyces sp. NRRL S-1824	TRUE

species	multicellularity
Streptomyces sp. NRRL S-1868	TRUE
Streptomyces sp. NRRL S-244	TRUE
Streptomyces sp. NRRL S-623	TRUE
Streptomyces sp. NRRL S-920	TRUE
Streptomyces sp. NRRL WC-3549	TRUE
Streptomyces sp. NTK 937	TRUE
Streptomyces sp. or20	TRUE
Streptomyces sp. or3	TRUE
Streptomyces sp. PBH53	TRUE
Streptomyces sp. PgraA7	TRUE
Streptomyces sp. PTY087I2	TRUE
Streptomyces sp. rh34	TRUE
Streptomyces sp. RSD-27	TRUE
Streptomyces sp. RTd22	TRUE
Streptomyces sp. ScaeMP-e48	TRUE
Streptomyces sp. SCSIO 03032	TRUE
Streptomyces sp. SolWspMP-sol2th	TRUE
Streptomyces sp. st140	TRUE
Streptomyces sp. st77	TRUE
Streptomyces sp. Termitarium-T10T-6	TRUE
Streptomyces sp. TSRI0261	TRUE
Streptomyces sp. TSRI0281	TRUE
Streptomyces sp. W007	TRUE
Streptomyces sp. XY332	TRUE
Streptomyces tsukubensis	TRUE
Streptomyces violaceoruber	TRUE
Streptomyces vitaminophilus	TRUE
Streptomyces xylophagus	TRUE
Thermomonospora sp. CIF 1	TRUE

- **NucA vs EACC1**:

species	**multicellularity**

VI. Source data - genome identifiers and systems for all EAD1-containing organisms

- **GCA_000166135.1; Frankia inefficax; counts= 22; multicellularity status: TRUE**
  - ??+EAD1+cNMP_cyclase+TIR->cNMP_cyclase+EAD1+TIR*->
  - EAD1->EAD1+cNMP_cyclase+TIR*->
  - EAD1*->EAD1+cNMP_cyclase+TIR->
  - EAD1+APATPase+wHTH+TPRs*->
  - EAD1+APATPase+wHTH+TPRs*->
  - EAD1+APATPase+wHTH+TPRs*->
  - EAD1+APATPase+wHTH+TPRs*->
  - EAD1+APATPase+wHTH+TPRs*->
  - EAD1+APATPase+wHTH+TPRs*->
  - EAD1+APATPase+wHTH+TPRs*->
  - EAD1+APATPase+wHTH+TPRs*->
  - EAD1+APATPase+wHTH+TPRs*->
  - EAD1+BetaPropeller*->
  - EAD1+EAD1+TIR*->
  - EAD1+STAND_NTPase+TPRs*->
  - EAD1+TIR*->
  - EAD1+TM+Peripla_BP*->
  - EAD1+TM+TM+STAND_NTPase+TPRs*->
  - EAD1+TPRs->||<-?<-?||EAD1+APATPase+wHTH+TPRs*->
  - EAD2+VMAP-M0+VMAP-C->MoxR->vWA+STAND_NTPase+TPRs->EAD2+EAD1*->
  - HTH+HTH+STAND_NTPase+wHTH+TPRs->EAD1+TPRs*->||<-?<-?||EAD1+APATPase+wHTH+TPRs->
- **GCA_001456025.1; Mastigocoleus testarum BC008; counts= 19; multicellularity status: TRUE**
  - EAD1+??*->
  - EAD1+CASPASE*->
  - EAD1+CASPASE*->
  - EAD1+EAD1-unk4+Pentapeptide_repeats*->
  - EAD1+EAD1-unk4+Pentapeptide_repeats*->
  - EAD1+GUN4*->
  - EAD1+P-loop_NTPase*->
  - EAD1+Pentapeptide_repeats*->
  - EAD1+TIR*->

  - EAD1+TIR*->TIR+TM+GUN4->
  - EAD1+TIR+GUN4*->
  - EAD1+TIR+GUN4*->||<-?||EAD1+GUN4->
  - EAD1+TM+??*->
  - EAD1+TM+??*->
  - EAD1+TM+CHASE2+TM+TM+TM*->
  - EAD1+VMAP-M1+VMAP-C*->
  - EAD1+VMAP-M1+VMAP-C*->MoxR->
  - EAD8+EAD1+PNP_UDP_1*->
  - LRR_region+sGTP_APGTPase+COR+??+EAD1*->

- **GCA_000346485.2; Scytonema hofmannii PCC 7110; counts= 19; multicellularity status: TRUE**
  - ??+EAD1*->GUN4+EAD1->
  - EAD1*->
  - EAD1*->
  - EAD1+??*->
  - EAD1+CASPASE*->
  - EAD1+CASPASE+STAND_NTPase+GUN4*->||<-CASPASE<-STAND_NTPase+BetaPropeller
  - EAD1+EAD9*->
  - EAD1+P-loop_NTPase*->
  - EAD1+Pkinase+globin*->
  - EAD1+TerB+CASPASE+GUN4*->||<-?<-FGS-fold_domain
  - EAD1+TM+TM+TM+TM*->
  - EAD1+TPRs*->
  - EAD1+VMAP-C*->MoxR->
  - EAD1+VMAP-M1+VMAP-C*->MoxR->vWA+Beta-rich+FGS-fold_domain->
  - GUN4+EAD1*->
  - HTH+EAD1+STAND_NTPase+??*->
  - LRR_region+sGTP_APGTPase+COR+??+EAD1*->
  - PNP_UDP_1+EAD1*->
  - TCAD3+EAD1+EAD9*->EAD9+VMAP-M1+VMAP-C->MoxR->vWA+Beta-rich+FGS-fold_domain->

- **GCA_001854645.1; Frankia sp. EUN1h; counts= 18; multicellularity status: TRUE**
  - <-EAD1+EAD1||EAD1+STAND_NTPase+??*->
  - <-EAD1+STAND_NTPase+??||EAD1+EAD1*->
  - EAD1+??*->
  - EAD1+APATPase+wHTH+TPRs*->
  - EAD1+APATPase+wHTH+TPRs*->
  - EAD1+APATPase+wHTH+TPRs*->
  - EAD1+APATPase+wHTH+TPRs*->
  - EAD1+APATPase+wHTH+TPRs*->
  - EAD1+APATPase+wHTH+TPRs*->

  - EAD1+cNMP_cyclase+TIR->cNMP_cyclase+EAD1+TIR*->
  - EAD1+EACC2*->
  - EAD1+EAD1+BetaPropeller*->
  - EAD1+LGFP_repeat_region*->
  - EAD1+STAND_NTPase+TPRs*->
  - EAD1+STAND_NTPase+wHTH+TPRs+BetaPropeller*->
  - low_complexity+EAD1*->
  - pntlT4_fusion_domain+EAD1*->
  - pntlT4_fusion_domain+EAD1*->

- **GCF_000331305.1; Calothrix sp. PCC 7103; counts= 16; multicellularity status: TRUE**
  - DRHyd?+??+EAD1+??*->
  - EAD1*->
  - EAD1+??*->
  - EAD1+APATPase+wHTH+TPRs*->
  - EAD1+CASPASE*->||<-EAD1+TM+Peripla_BP
  - EAD1+LRR_region+sGTP_APGTPase+COR+??->??+Trypsin->?->EAD1+VMAP-M23+VMAP-C*->MoxR->
  - EAD1+LRR_region+sGTP_APGTPase+COR+??*->??+Trypsin->?->EAD1+VMAP-M23+VMAP-C->
  - EAD1+TIR->EAD1+VMAP-M11+VMAP-M1+VMAP-C*->
  - EAD1+TIR*->EAD1+VMAP-M11+VMAP-M1+VMAP-C->
  - EAD1+TM+Peripla_BP*->||<-EAD1+CASPASE
  - EAD1+TPRs*->
  - EAD1+Trypsin->EAD1*->
  - EAD1+Trypsin*->EAD1->
  - HTH+EAD1+FISNA?*->
  - LRR_region+sGTP_APGTPase+COR+EAD1->EAD1+TCAD4+CASPASE*->
  - LRR_region+sGTP_APGTPase+COR+EAD1*->EAD1+TCAD4+CASPASE->

- **GCA_000177675.1; Frankia sp. EUN1f; counts= 15; multicellularity status: TRUE**
  - ??+EAD1*->
  - <-EAD1+TIR||EAD1+P-loop_NTPase(i)*->MoxR->helical_region+vWA->??+EAD1+EAD1+cNMP_cyclase+TIR->
  - <-helical_region+vWA<-MoxR<-EAD1+P-loop_NTPase(i)||EAD1+TIR*->
  - EAD1+??*->
  - EAD1+APATPase+wHTH+TPRs*->
  - EAD1+cNMP_cyclase+TIR*->
  - EAD1+EAD1+TIR*->TIR+STAND_NTPase+BetaPropeller->
  - EAD1+P-loop_NTPase(i)->MoxR->helical_region+vWA->??+EAD1+EAD1+cNMP_cyclase+TIR*->
  - EAD1+PH?*->
  - EAD1+STAND_NTPase+??*->
  - EAD1+TIR*->
  - EAD1+TIR*->
  - EAD1+TIR*->||<-TIR

  - EAD2+EAD1*->
  - EAD2+EAD1*->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs->

- **GCA_001536285.1; Frankia sp. G2; counts= 14; multicellularity status: TRUE**
  - ??+EAD1+??*->?->vWA->
  - <-EAD1+TIR||EAD1+P-loop_NTPase(i)*->MoxR->helical_region+vWA->??+EAD1+EAD1+cNMP_cyclase+TIR->
  - <-helical_region+vWA<-MoxR<-EAD1+P-loop_NTPase(i)||EAD1+TIR*->
  - <-TIR+STAND_NTPase+wHTH+PRs||EACC2+EAD1*->CASPASE+STAND_NTPase+wHTH+BetaPropeller->
  - EAD1+??*->
  - EAD1+??*->
  - EAD1+APATPase+wHTH+TPRs*->
  - EAD1+APATPase+wHTH+TPRs*->
  - EAD1+cNMP_cyclase+TIR*->
  - EAD1+P-loop_NTPase(i)->MoxR->helical_region+vWA->??+EAD1+EAD1+cNMP_cyclase+TIR*->
  - EAD1+TIR*->
  - EAD1+TIR*->||<-TIR
  - EAD1+TIR+STAND_NTPase*->
  - EAD2+EAD1*->EAD2+VMAP-M0+VMAP-C->

- **GCA_002368435.1; Scytonema sp. NIES-4073; counts= 12; multicellularity status: TRUE**
  - EAD1+CASPASE->EAD1+STAND_NTPase+wHTH+TM+TM+TM+TM+TM+TM*->
  - EAD1+CASPASE*->EAD1+STAND_NTPase+wHTH+TM+TM+TM+TM+TM+TM->
  - EAD1+NACHT-like+FGS-fold_domain+GUN4*->
  - EAD1+P-loop_NTPase(i)*->MoxR->helical_region+vWA->
  - EAD1+STAND_NTPase+wHTH+TM+TM+TM+TM+TM+TM->EAD1+CASPASE*->
  - EAD1+STAND_NTPase+wHTH+TM+TM+TM+TM+TM+TM*->EAD1+CASPASE->
  - EAD1+TCAD4+CASPASE->?->EAD1+TerB-like?+GUN4*->
  - EAD1+TCAD4+CASPASE*->
  - EAD1+Trypsin->EAD1+VMAP-M1+VMAP-C*->MoxR->vWA+Beta-rich+FGS-fold_domain->
  - EAD1+Trypsin*->
  - TIR+EAD1*->
  - TIR+EAD1*->

- **GCA_000316665.1; Rivularia sp. PCC 7116; counts= 11; multicellularity status: TRUE**
  - EACC3+CASPASE+LRR_repeats+sGTP_APGTPase->LRR_region+sGTP_APGTPase+COR+??+EAD1*->
  - EAD1*->
  - EAD1+EAD1-unk4+GUN4*->
  - EAD1+EAD10+FGS-fold_domain*->
  - EAD1+GUN4*->
  - EAD1+Trypsin->EAD1+VMAP-M1+VMAP-C*->MoxR->vWA+Beta-rich+FGS-fold_domain->
  - EAD1+Trypsin*->EAD1+VMAP-M1+VMAP-C->MoxR->vWA+Beta-rich+FGS-fold_domain->
  - EAD1+VMAP-M1+VMAP-C*->MoxR->

  - LRR_region+sGTP_APGTPase+COR+??+EAD1*->
  - LRR_region+sGTP_APGTPase+COR+??+EAD1*->
  - LRR_region+sGTP_APGTPase+COR+??+EAD1*->

- **GCA_002368455.1; Calothrix sp. NIES-4071; counts= 11; multicellularity status: TRUE**
  - CASPASE+EAD1->EAD1+??+VMAP-C*->MoxR->vWA+Beta-rich+FGS-fold_domain->
  - CASPASE+EAD1*->EAD1+??+VMAP-C->MoxR->vWA+Beta-rich+FGS-fold_domain->
  - CASPASE+EAD1+CASPASE*->
  - EAD1+??*->
  - EAD1+CASPASE+GUN4*->
  - EAD1+EAD1-unk4+HTH+HTH*->
  - EAD1+TM+??*->
  - EAD1+Trypsin->EAD1+VMAP-M1+VMAP-C*->MoxR->
  - EAD1+Trypsin*->EAD1+VMAP-M1+VMAP-C->MoxR->
  - HTH+EAD1+STAND_NTPase+??*->
  - LRR_region+sGTP_APGTPase+COR+??+EAD1*->

- **GCA_900197875.1; Frankia sp. ARgP5; counts= 11; multicellularity status: NA**
  - *
  - EAD1+??*->
  - EAD1+APATPase+wHTH+TPRs*->
  - EAD1+BetaPropeller->EAD1+EAD1*->
  - EAD1+BetaPropeller*->EAD1+EAD1->
  - EAD1+cNMP_cyclase+extension*->
  - EAD1+cNMP_cyclase+TIR*->
  - EAD1+P-loop_NTPase+TPRs*->
  - EAD1+STAND_NTPase+??*->
  - EAD2+EAD1*->
  - pntlT4_fusion_domain+EAD1*->

- **GCA_001983215.1; Frankia sp. CcI49; counts= 11; multicellularity status: TRUE**
  - <-EAD1+TIR||EAD1+P-loop_NTPase(i)*->MoxR->helical_region+vWA->??+EAD1+EAD1+cNMP_cyclase+TIR->
  - <-helical_region+vWA<-MoxR<-EAD1+P-loop_NTPase(i)||EAD1+TIR*->
  - EAD1+??->EAD1+P-loop_NTPase+TPRs*->
  - EAD1+??*->
  - EAD1+APATPase+wHTH+TPRs*->
  - EAD1+cNMP_cyclase+TIR*->
  - EAD1+P-loop_NTPase(i)->MoxR->helical_region+vWA->??+EAD1+EAD1+cNMP_cyclase+TIR*->
  - EAD1+STAND_NTPase+wHTH*->
  - EAD1+TIR->?->?->EAD1+VMAP-C*->MoxR->
  - EAD1+TIR*->
  - EAD1+TIR*->?->?->EAD1+VMAP-C->

- **GCA_000948395.1; Frankia sp. CpI1-S; counts= 10; multicellularity status: TRUE**
  - ??+EAD1*->
  - ??+EAD1*->
  - EAD1+??*->
  - EAD1+BetaPropeller*->
  - EAD1+cNMP_cyclase+extension*->
  - EAD1+cNMP_cyclase+TIR*->
  - EAD2+EAD1*->
  - EAD2+EAD1*->
  - pntlT4_fusion_domain+EAD1*->
  - pntlT4_fusion_domain+EAD1*->
- **GCA_002368235.1; Scytonema sp. HK-05; counts= 9; multicellularity status: TRUE**
  - EAD1+CASPASE+P-loop_NTPase*->
  - EAD1+P-loop_NTPase(i)*->MoxR->helical_region+vWA->
  - EAD1+TCAD4+CASPASE->PSE->EAD1+TM+TM+STAND_NTPase+FGS-fold_domain+GUN4*->
  - EAD1+TCAD4+CASPASE*->PSE->EAD1+TM+TM+STAND_NTPase+FGS-fold_domain+GUN4->
  - EAD1+Trypsin->EAD1+FGS-fold_domain*->
  - EAD1+Trypsin*->EAD1+FGS-fold_domain->
  - MoxR->helical_region+vWA->PSE->?->TIR+EAD1*->
  - TCAD3+TCAD4+CASPASE+EAD1->EAD1+VMAP-M1+VMAP-C*->MoxR->vWA+Beta-rich+HTH+FGS-fold_domain->
  - TCAD3+TCAD4+CASPASE+EAD1*->EAD1+VMAP-M1+VMAP-C->MoxR->vWA+Beta-rich+HTH+FGS-fold_domain->
- **GCF_000235425.2; Frankia saprophytica; counts= 9; multicellularity status: NA**
  - <-EAD1+EAD1||?->EAD1+STAND_NTPase+??*->
  - EAD1+APATPase+wHTH+TPRs*->
  - EAD1+APATPase+wHTH+TPRs*->
  - EAD1+APATPase+wHTH+TPRs*->
  - EAD1+APATPase+wHTH+TPRs*->
  - EAD1+cNMP_cyclase+TIR*->cNMP_cyclase+EAD1+TIR->
  - EAD1+LGFP_repeat_region*->
  - EAD1+STAND_NTPase+TPRs*->
  - EAD1+TPRs*->
- **GCA_001027285.1; Archangium gephyra; counts= 8; multicellularity status: TRUE**
  - EAD1+STAND_NTPase->STAND_NTPase+wHTH+TPRs+EAD1+EAD5->EAD1+Trypsin*->
  - EAD1+STAND_NTPase->STAND_NTPase+wHTH+TPRs+EAD1+EAD5*->EAD1+Trypsin->
  - EAD1+STAND_NTPase*->STAND_NTPase+wHTH+TPRs+EAD1+EAD5->EAD1+Trypsin->
  - EAD1+TIR*->
  - EAD1+VMAP-M0+VMAP-C*->MoxR->vWA+CASPASE+SLOG+TPRs->
  - EAD1+VMAP-M0+VMAP-C*->vWA+SLOG+TPRs->
  - EAD1+VMAP-M1+VMAP-C*->MoxR->?->vWA+SLOG+SLOG+TPRs->

  - MoxR->?->vWA+SLOG+SLOG+TPRs->EAD1+Trypsin*->

- **GCF_000966285.1; Frankia sp. DC12; counts= 8; multicellularity status: NA**
  - ??+EAD1*->
  - EAD1*->
  - EAD1+??*->
  - EAD1+APATPase+wHTH+TPRs*->
  - EAD1+APATPase+wHTH+TPRs*->
  - EAD1+cNMP_cyclase+TIR*->
  - EAD1+VMAP-M2+VMAP-C*->
  - HTH+HTH+STAND_NTPase+wHTH+TPRs->EAD1+TPRs*->

- **GCA_001983105.1; Frankia asymbiotica; counts= 8; multicellularity status: TRUE**
  - EAD1+APATPase+wHTH+TPRs*->
  - EAD1+APATPase+wHTH+TPRs*->
  - EAD1+cNMP_cyclase+TIR*->
  - EAD1+P-loop_NTPase+TPRs*->
  - EAD1+Pentapeptide_repeats*->
  - EAD1+TM+Peripla_BP*->
  - EAD2+EAD1*->
  - pntlT4_fusion_domain+EAD1*->

- **GCA_001767235.1; Moorea producens PAL-8-15-08-1; counts= 7; multicellularity status: NA**
  - EAD1+STAND_NTPase+TM_region*->
  - EAD1+Trypsin->||<-?||PSE->EAD1+VMAP-M1+VMAP-C*->MoxR->vWA+Beta-rich+FGS-fold_domain->
  - EAD1+Trypsin*->||<-?||PSE->EAD1+VMAP-M1+VMAP-C->MoxR->
  - EAD1+VMAP-M1+FGS-fold_domain->EAD1+VMAP-M1+FGS-fold_domain->EAD1*->VMAP-M1+FGS-fold_domain->EAD1+VMAP-M1+FGS-fold_domain->
  - EAD1+VMAP-M1+FGS-fold_domain->EAD1+VMAP-M1+FGS-fold_domain*->EAD1->VMAP-M1+FGS-fold_domain->EAD1+VMAP-M1+FGS-fold_domain->
  - EAD1+VMAP-M1+FGS-fold_domain*->
  - EAD1+VMAP-M1+FGS-fold_domain*->EAD1+VMAP-M1+FGS-fold_domain->EAD1->VMAP-M1+FGS-fold_domain->

- **GCA_000058485.1; Frankia alni ACN14a; counts= 7; multicellularity status: TRUE**
  - ??+EAD1*->
  - EACC2+EAD1*->||<-CASPASE+STAND_NTPase+wHTH+BetaPropeller
  - EAD1*->
  - EAD1+cNMP_cyclase+extension*->
  - EAD1+cNMP_cyclase+TIR*->
  - EAD2+EAD1*->
  - TM+EAD1*->

- **GCA_000760695.2; Tolypothrix bouteillei VB521301; counts= 7; multicellularity status: NA**
  - EAD1*->
  - EAD1+??*->

  - EAD1+APATPase+wHTH+TPRs*->
  - EAD1+CASPASE*->
  - EAD1+STAND_NTPase+TM_region*->
  - EAD1+STAND_NTPase+TM_region*->
  - Pentapeptide_repeats+EAD1*->

- **GCA_000817735.2; Scytonema millei VB511283; counts= 7; multicellularity status: TRUE**
  - EAD1*->
  - EAD1+??*->
  - EAD1+??*->
  - EAD1+Trypsin->EAD1+FGS-fold_domain*->
  - EAD1+Trypsin*->EAD1+FGS-fold_domain->
  - TIR+EAD1->EAD1+STAND_NTPase+FGS-fold_domain+GUN4*->
  - TIR+EAD1*->EAD1+STAND_NTPase+FGS-fold_domain+GUN4->

- **GCA_001854805.1; Frankia sp. BMG5.36; counts= 7; multicellularity status: NA**
  - EAD1+APATPase+wHTH+TPRs*->
  - EAD1+APATPase+wHTH+TPRs*->
  - EAD1+BetaPropeller*->
  - EAD1+LGFP_repeat_region*->
  - EAD1+STAND_NTPase+TPRs*->
  - SP+TM+TM+TM+EAD1*->
  - TIR+TM+BetaPropeller->?->pntlT4_fusion_domain+EAD1*->CASPASE->

- **GCF_001456025.1; Mastigocoleus testarum; counts= 7; multicellularity status: TRUE**
  - EAD1+??+FGS-fold_domain*->
  - EAD1+APATPase+wHTH+TPRs*->
  - EAD1+FGS-fold_domain*->
  - EAD1+FGS-fold_domain*->
  - EAD1+GUN4*->
  - EAD1+GUN4*->
  - EAD1+TIR+GUN4->||<-?||EAD1+GUN4*->

- **GCF_001306465.1; Frankia sp. R43; counts= 7; multicellularity status: TRUE**
  - EAD1+APATPase+wHTH+TPRs*->
  - EAD1+APATPase+wHTH+TPRs*->
  - EAD1+APATPase+wHTH+TPRs*->
  - EAD1+cNMP_cyclase+TIR*->
  - EAD1+P-loop_NTPase(i)->MoxR->helical_region+vWA->??+EAD1+EAD1+cNMP_cyclase+TIR*->
  - EAD1+TIR*->
  - pntlT4_fusion_domain+EAD1*->?->Lon_C_protease(i)+TM+BetaPropeller->

- **GCA_001854205.1; Moorea producens JHB; counts= 6; multicellularity status: TRUE**

  - EAD1+low_complexity+TM+TM+TM*->
  - EAD1+Trypsin->EAD1+VMAP-M1+Calcineurin-like->EAD1+VMAP-M1+VMAP-C*->MoxR->vWA+FGS-fold_domain->
  - EAD1+Trypsin->EAD1+VMAP-M1+Calcineurin-like*->EAD1+VMAP-M1+VMAP-C->MoxR->vWA+FGS-fold_domain->
  - EAD1+Trypsin*->EAD1+VMAP-M1+Calcineurin-like->EAD1+VMAP-M1+VMAP-C->MoxR->
  - EAD1+VMAP-M1+FGS-fold_domain*->EAD1+VMAP-M1+FGS-fold_domain->
  - VMAP-M1+FGS-fold_domain->EAD1+VMAP-M1+FGS-fold_domain*->

- **GCA_002368195.1; Calothrix sp. NIES-2100; counts= 6; multicellularity status: NA**
  - EAD1+coiled_coil*->
  - EAD1+coiled_coil*->
  - EAD1+low_complexity*->
  - EAD1+TPRs*->
  - EAD1+Trypsin->TM+TM+TM->EAD1+VMAP-M1+VMAP-C*->MoxR->vWA+Beta-rich+FGS-fold_domain->
  - EAD1+Trypsin*->TM+TM+TM->EAD1+VMAP-M1+VMAP-C->MoxR->

- **GCA_000067165.1; Sorangium cellulosum So ce56; counts= 6; multicellularity status: TRUE**
  - bacHORMA->FtsH-like->SAVED+EAD1->EAD1+Trypsin*->
  - bacHORMA->FtsH-like->SAVED+EAD1*->EAD1+Trypsin->
  - EAD1+STAND_NTPase->STAND_NTPase+wHTH+TPRs+EAD1->EAD1+Trypsin*->
  - EAD1+STAND_NTPase*->STAND_NTPase+wHTH+TPRs+EAD1->EAD1+Trypsin->
  - STAND_NTPase+wHTH+TPRs+BetaPropeller+EAD1->EAD1+Trypsin*->
  - STAND_NTPase+wHTH+TPRs+BetaPropeller+EAD1*->EAD1+Trypsin->

- **GCA_001306465.1; Frankia sp. R43; counts= 6; multicellularity status: TRUE**
  - <-EAD1+TIR||EAD1+P-loop_NTPase(i)*->MoxR->helical_region+vWA->??+EAD1+EAD1+cNMP_cyclase+TIR->
  - <-helical_region+vWA<-MoxR<-EAD1+P-loop_NTPase(i)||EAD1+TIR*->
  - EAD1+APATPase+wHTH+TPRs*->
  - EAD1+PH?*->
  - EAD2+EAD1*->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs->
  - pntlT4_fusion_domain+EAD1*->?->Lon_C_protease(i)+TM+BetaPropeller->

- **GCA_001421075.1; Frankia sp. CpI1-P; counts= 6; multicellularity status: TRUE**
  - ??+EAD1*->
  - EAD1+??*->
  - EAD1+cNMP_cyclase+TIR*->
  - EAD2+EAD1*->
  - EAD2+EAD1*->
  - pntlT4_fusion_domain+EAD1*->

- **GCA_001589215.1; Sorangium cellulosum; counts= 6; multicellularity status: TRUE**
  - EAD1+Trypsin->EAD1+STAND_NTPase+TPRs*->
  - EAD1+Trypsin*->
  - EAD1+Trypsin*->?->MoxR->

  - EAD1+Trypsin*->EAD1+STAND_NTPase+TPRs->
  - STAND_NTPase+wHTH+TPRs+BetaPropeller+EAD1->EAD1+Trypsin*->
  - STAND_NTPase+wHTH+TPRs+BetaPropeller+EAD1*->EAD1+Trypsin->

- **GCA_001854655.1; Frankia sp. Cc1.17; counts= 6; multicellularity status: TRUE**
  - EAD1*->
  - EAD1+??*->||<-?<-TIR+STAND_NTPase+BetaPropeller
  - EAD1+BetaPropeller*->
  - EAD1+cNMP_cyclase+TIR*->
  - EAD1+TIR*->||<-TIR
  - MoxR->?->??+Pkinase+EAD1+TIR*->

- **GCA_900104725.1; Actinoplanes derwentensis; counts= 6; multicellularity status: TRUE**
  - CASPASE+STAND_NTPase+wHTH->?->AB_hydrolase+TIR->EAD1+TIR*->BetaPropeller+vWA->
  - EAD1+Trypsin->EAD1+P-loop_NTPase(i)*->MoxR->
  - Pkinase->EAD1+Trypsin->EAD1+STAND_NTPase*->?->||<-?<-??+Trypsin
  - Trypsin+EAD1*->BetaPropeller+vWA->
  - vWA->?->Pkinase->EAD1+Trypsin*->EAD1+STAND_NTPase->
  - ZnF->E1(active)+E1-ZnR_C->EAD1+YukDl-Nterm+UB+E2*->JAB-N+JAB->?->CDC48-like->

- **GCA_000018005.1; Frankia sp. EAN1pec; counts= 5; multicellularity status: TRUE**
  - EAD1+??*->
  - EAD1+cNMP_cyclase+TIR*->
  - EAD2+EAD1*->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs->
  - pntlT4_fusion_domain+EAD1*->
  - TM+BetaPropeller->TIR+EACC2+EAD1*->

- **GCA_001414035.1; Frankia sp. ACN1ag; counts= 5; multicellularity status: TRUE**
  - <-CASPASE+STAND_NTPase+wHTH+BetaPropeller||EACC2+EAD1*->
  - EAD1+cNMP_cyclase+TIR*->
  - EAD2+EAD1*->
  - EAD2+EAD1*->
  - pntlT4_fusion_domain+EAD1*->

- **GCA_001636565.1; Frankia sp. EI5c; counts= 5; multicellularity status: TRUE**
  - ??+EAD1*->
  - ??+EAD1*->
  - EAD1+cNMP_cyclase+extension*->
  - EAD1+TIR*->
  - pntlT4_fusion_domain+EAD1*->

- **GCA_001904745.1; Calothrix sp. HK-06; counts= 5; multicellularity status: NA**
  - CASPASE+EAD1->EAD1*->

  - EAD1*->
  - EAD1+??*->
  - EAD1+CASPASE+GUN4*->
  - EAD1+STAND_NTPase+TM_region*->

- **GCA_001942495.1; Moorea bouillonii PNG; counts= 5; multicellularity status: TRUE**
  - EAD1+low_complexity+TM+TM+TM*->
  - EAD1+Trypsin->EAD1+VMAP-M1+Calcineurin-like->EAD1+VMAP-M1+VMAP-C*->MoxR->vWA+Beta-rich+FGS-fold_domain->
  - EAD1+Trypsin->EAD1+VMAP-M1+Calcineurin-like*->EAD1+VMAP-M1+VMAP-C->MoxR->vWA+Beta-rich+FGS-fold_domain->
  - EAD1+Trypsin*->EAD1+VMAP-M1+Calcineurin-like->EAD1+VMAP-M1+VMAP-C->MoxR->
  - EAD1+VMAP-M1+FGS-fold_domain*->

- **GCF_000374165.1; Frankia elaeagni; counts= 5; multicellularity status: NA**
  - EAD1+??*->
  - EAD1+cNMP_cyclase+TIR*->
  - EAD1+TIR*->||<-TIR
  - pntlT4_fusion_domain+EAD1*->
  - pntlT4_fusion_domain+EAD1*->

- **GCF_000166135.1; Frankia inefficax; counts= 5; multicellularity status: TRUE**
  - ??+EAD1+cNMP_cyclase+TIR*->cNMP_cyclase+EAD1+TIR->
  - EAD1+APATPase+wHTH+TPRs*->
  - EAD1+APATPase+wHTH+TPRs*->
  - EAD1+APATPase+wHTH+TPRs*->
  - EAD1+STAND_NTPase+wHTH+TPRs+BetaPropeller*->

- **GCF_000760695.2; Tolypothrix bouteillei; counts= 5; multicellularity status: NA**
  - EAD1+APATPase+wHTH+TPRs*->
  - EAD1+CASPASE+GUN4*->
  - EAD1+GUN4*->
  - EAD1+STAND_NTPase+HEAT_repeat_region*->
  - Pentapeptide_repeats+EAD1*->

- **GCF_001420875.1; Frankia sp. AvcI1; counts= 5; multicellularity status: TRUE**
  - ??+EAD1*->
  - EACC2+EAD1*->||<-CASPASE+STAND_NTPase+wHTH+BetaPropeller
  - EAD1*->
  - EAD2+EAD1*->
  - TM+EAD1*->

- **GCA_000211815.1; Moorea producens 3L; counts= 4; multicellularity status: NA**
  - EAD1+Trypsin->EAD1+VMAP-M1+Calcineurin-like->EAD1+VMAP-M1+VMAP-C*->MoxR->vWA+TPRs+CASPASE->
  - EAD1+Trypsin->EAD1+VMAP-M1+Calcineurin-like*->EAD1+VMAP-M1+VMAP-C->MoxR->vWA+TPRs+CASPASE->

  - EAD1+Trypsin*->EAD1+VMAP-M1+Calcineurin-like->EAD1+VMAP-M1+VMAP-C->MoxR->
  - EAD1+VMAP-M1+FGS-fold_domain*->

- **GCA_000262465.1; Frankia sp. QA3; counts= 4; multicellularity status: TRUE**
  - E1(active)+E1_C_unk->EAD1+YukDl-Nterm+UB+E2*->JAB-N+JAB->
  - EAD1+??*->MoxR->
  - EAD1+cNMP_cyclase+extension*->
  - EAD1+cNMP_cyclase+TIR*->

- **GCA_001644415.1; Planctomycetaceae bacterium SCGC AG-212-F19; counts= 4; multicellularity status: NA**
  - EAD1+RRM+STAND_NTPase+FGS-fold_domain->?->EAD1+Trypsin*->
  - EAD1+RRM+STAND_NTPase+FGS-fold_domain*->?->EAD1+Trypsin->
  - EAD1+Trypsin*->
  - EAD1+Trypsin*->

- **GCA_001672105.1; Aphanizomenon flos-aquae WA102; counts= 4; multicellularity status: TRUE**
  - cNMP_cyclase+EAD1->EAD1*->MoxR->vWA+Beta-rich+HTH+FGS-fold_domain->
  - cNMP_cyclase+EAD1*->EAD1->MoxR->vWA+Beta-rich+HTH+FGS-fold_domain->
  - EAD1+Trypsin*->
  - Trypsin->TM+TM+TM->EAD1+P-loop_NTPase*->

- **GCA_001854695.1; Frankia sp. NRRL B-16219; counts= 4; multicellularity status: TRUE**
  - EAD1+cNMP_cyclase+TIR*->
  - EAD1+TM+??*->
  - EAD2+EAD1*->EAD2+VMAP-M0+VMAP-C->
  - pntlT4_fusion_domain+EAD1*->

- **GCF_000373365.1; Frankia discariae; counts= 4; multicellularity status: TRUE**
  - EAD1+??*->
  - EAD1+cNMP_cyclase+TIR*->
  - EAD1+TM+??*->
  - EAD2+EAD1*->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs->

- **GCA_001712795.1; Nostoc sp. KVJ20; counts= 4; multicellularity status: TRUE**
  - EAD1+Trypsin->EAD1+VMAP-M1+??*->MoxR->EB1_binding+vWA->
  - EAD1+Trypsin->TM+TM+TM->EAD1+coiled_coil*->
  - EAD1+Trypsin*->EAD1+VMAP-M1+??->MoxR->EB1_binding+vWA->
  - EAD1+Trypsin*->TM+TM+TM->EAD1+coiled_coil->

- **GCA_000970465.2; Devosia insulae; counts= 4; multicellularity status: FALSE**
  - EAD1+Phage_lysozyme->EAD1+Trypsin->EAD1+HExxH+helical_region*->TM+Endonuclease_NS(HNH)+LytR_C/SPOR->Trypsin+Endonuclease_NS(HNH)->
  - EAD1+Phage_lysozyme->EAD1+Trypsin*->EAD1+HExxH+helical_region->TM+Endonuclease_NS(HNH)+LytR_C/SPOR->Trypsin+Endonuclease_NS(HNH)->
  - EAD1+Phage_lysozyme*->EAD1+Trypsin->EAD1+HExxH+helical_region->TM+Endonuclease_NS(HNH)+LytR_C/SPOR->

  - EAD1+Trypsin*->

- **GCF_001870905.1; Geitlerinema sp. PCC 9228; counts= 4; multicellularity status: TRUE**
  - EAD1+??+VMAP-C*->MoxR->
  - EAD1+GUN4+??*->
  - EAD1+Trypsin->TM+TM+TM->EAD1+CASPASE+FGS-fold_domain*->
  - EAD1+Trypsin*->TM+TM+TM->EAD1+CASPASE+FGS-fold_domain->

- **GCA_001610855.1; Gemmata sp. SH-PL17; counts= 3; multicellularity status: FALSE**
  - EAD1+Trypsin->EAD1+HExxH+helical_region*->?->??+Trypsin->
  - EAD1+Trypsin*->EAD1+HExxH+helical_region->?->??+Trypsin->
  - VMAP-C->MoxR->EAD1+HD+vWA+NEFF1*->

- **GCA_000344805.1; Bradyrhizobium oligotrophicum S58; counts= 3; multicellularity status: TRUE**
  - EAD1+Trypsin->EAD1+??*->STAND_NTPase+wHTH+TM+TPRs->
  - EAD1+Trypsin*->EAD1+??->STAND_NTPase+wHTH+TM+TPRs->
  - Trypsin+EAD1+helical_region*->

- **GCA_001589195.1; Sorangium cellulosum; counts= 3; multicellularity status: TRUE**
  - bacHORMA->FtsH-like->SAVED+EAD1->EAD1+Trypsin*->
  - bacHORMA->FtsH-like->SAVED+EAD1*->EAD1+Trypsin->
  - EAD1+Trypsin*->

- **GCA_002148365.1; Litorilinea aerophila; counts= 3; multicellularity status: NA**
  - EAD1*->
  - EAD1+SIR2*->
  - EAD1+Trypsin*->

- **GCF_000426925.1; Dolichospermum circinale; counts= 3; multicellularity status: TRUE**
  - EAD1+Trypsin->TM+TM+TM->EAD1->EAD1+TM*->
  - EAD1+Trypsin->TM+TM+TM->EAD1*->EAD1+TM->
  - EAD1+Trypsin*->TM+TM+TM->EAD1->EAD1+TM->

- **GCF_000716715.1; Dactylosporangium aurantiacum; counts= 3; multicellularity status: TRUE**
  - EAD1+CASPASE->PSE->E1+E1-ZnR_C->EAD1+YukDl-Nterm+UB+E2*->JAB-N+JAB->?->CDC48-like->
  - EAD1+CASPASE*->PSE->E1+E1-ZnR_C->EAD1+YukDl-Nterm+UB+E2->JAB-N+JAB->
  - Trypsin+PDZ+STAND_NTPase+wHTH+TPRs->EAD1+Trypsin*->

- **GCF_000058485.1; Frankia alni; counts= 3; multicellularity status: TRUE**
  - EAD1*->
  - EAD2+EAD1*->
  - TM+EAD1*->

- **GCA_000733295.1; Archangium violaceum; counts= 3; multicellularity status: TRUE**

  - *
  - EAD1+Trypsin->EAD1+??+VMAP-C->MoxR->vWA+SLOG+TPRs+EAD1+TIR*->
  - EAD1+Trypsin*->EAD1+??+VMAP-C->MoxR->vWA+SLOG+TPRs+EAD1+TIR->

- **GCF_001983215.1; Frankia sp. CcI49; counts= 3; multicellularity status: TRUE**
  - EAD1+APATPase+wHTH+TPRs*->
  - EAD1+cNMP_cyclase+TIR*->?->STAND_NTPase+BetaPropeller->
  - EAD1+PNP_UDP_1+STAND_NTPase+wHTH*->

- **GCA_002603685.1; Leptospira phage vb_LkmZ_Bejolso9-LE1; counts= 2; multicellularity status: FALSE**
  - GAP2->ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->PNP_UDP_1+EAD1->
  - ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1->PNP_UDP_1+EAD1*->

- **GCA_000582515.1; Yersinia similis; counts= 2; multicellularity status: FALSE**
  - GAP2->ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->
  - ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1->CASPASE+EAD1*->

- **GCA_000739375.1; Comamonas testosteroni TK102; counts= 2; multicellularity status: FALSE**
  - CASPASE+EAD1*->
  - DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->

- **GCA_001610875.1; Pirellula sp. SH-Sr6A; counts= 2; multicellularity status: TRUE**
  - EAD1+Trypsin*->||<-GAP1-N1+GAP1-M+GAP1-C+EAD1<-DO-GTPase1<-ZnR+DO-GTPase2
  - ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->||<-EAD1+Trypsin

- **GCA_001931535.1; Minicystis rosea; counts= 2; multicellularity status: TRUE**
  - STAND_NTPase+BetaPropeller+EAD1->EAD1+Trypsin*->
  - STAND_NTPase+BetaPropeller+EAD1*->EAD1+Trypsin->

- **GCA_000959705.2; Aeromonas caviae; counts= 2; multicellularity status: NA**
  - GAP1-N1+GAP1-M+GAP1-C+EAD1->CASPASE+EAD1*->
  - GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->

- **GCA_000239775.2; Bradyrhizobium sp. ORS 375; counts= 2; multicellularity status: TRUE**
  - EAD1+Trypsin->EAD1+Lon_C_protease+STAND_NTPase*->
  - EAD1+Trypsin*->EAD1+Lon_C_protease+STAND_NTPase->

- **GCA_000982975.1; Halomonas sp. A3H3; counts= 2; multicellularity status: FALSE**
  - GAP2->ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->
  - ZnR+DO-GTPase2->PSE->GAP1-N1+GAP1-M+GAP1-C+EAD1->CASPASE+EAD1*->

- **GCA_900066015.1; Candidatus Promineofilum breve; counts= 2; multicellularity status: TRUE**
  - EAD1+STAND_NTPase+FGS-fold_domain*->
  - macroglobulin-like+EAD1*->

- **GCA_000244135.3; Leptospira interrogans serovar Grippotyphosa str. UI 08368; counts= 2; multicellularity status: FALSE**
  - EAD1*->PNP_UDP_1+EAD1->
  - PNP_UDP_1+EAD1*->
- **GCA_000316115.1; Leptolyngbya sp. PCC 7375; counts= 2; multicellularity status: TRUE**
  - EAD1+Trypsin*->TM+TM+TM->EAD1+??+VMAP-C->MoxR->
  - EAD1+VMAP-M1+VMAP-C*->MoxR->vWA+BetaPropeller+FGS-fold_domain->FGS-fold_domain->
- **GCA_000368445.1; Acinetobacter sp. CIP 56.2; counts= 2; multicellularity status: FALSE**
  - GAP2->ZnR+DO-GTPase2->DO-GTPase1->PSE->CASPASE+EAD1*->
  - ZnR+DO-GTPase2->DO-GTPase1->?->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->
- **GCA_000503035.1; Mesorhizobium sp. LSHC412B00; counts= 2; multicellularity status: TRUE**
  - EAD1+Trypsin+??+CarboxypepD-reg-IG+papain-like_peptidoglycan_hydrolase*->
  - Trypsin+Endonuclease_NS(HNH)->EAD1+Trypsin*->
- **GCA_000584955.2; Candidatus Accumulibacter sp. SK-01; counts= 2; multicellularity status: FALSE**
  - GAP2->ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->
  - ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1->CASPASE+EAD1*->
- **GCA_001047325.1; Streptomyces viridochromogenes; counts= 2; multicellularity status: TRUE**
  - GAP1-N1+GAP1-M+GAP1-C+EAD1->CASPASE+EAD1*->
  - GAP2->ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->
- **GCA_001314865.1; Phormidesmis priestleyi Ana; counts= 2; multicellularity status: TRUE**
  - EAD1+Trypsin->TM+TM+TM->EAD1+??+VMAP-C*->MoxR->vWA+FGS-fold_domain->FGS-fold_domain->
  - EAD1+Trypsin*->TM+TM+TM->EAD1+??+VMAP-C->MoxR->
- **GCA_001672155.1; Anabaena sp. WA113; counts= 2; multicellularity status: NA**
  - EAD1+Trypsin->TM+TM+TM->EAD1*->
  - EAD1+Trypsin*->TM+TM+TM->EAD1->
- **GCA_001672085.1; Anabaena sp. AL93; counts= 2; multicellularity status: TRUE**
  - EAD1+Trypsin->TM+TM+TM->EAD1*->
  - EAD1+Trypsin*->TM+TM+TM->EAD1->
- **GCA_001672075.1; Anabaena sp. CRKS33; counts= 2; multicellularity status: TRUE**
  - EAD1+Trypsin->TM+TM+TM->EAD1*->
  - EAD1+Trypsin*->TM+TM+TM->EAD1->
- **GCA_001672195.1; Anabaena sp. MDT14b; counts= 2; multicellularity status: TRUE**
  - EAD1+Trypsin->TM+TM+TM->EAD1*->
  - EAD1+Trypsin*->TM+TM+TM->EAD1->

- **GCA_001742065.1; Psychrobacter sp. B29-1; counts= 2; multicellularity status: NA**
  - PNP_UDP_1+EAD1*->?->ZnR+DO-GTPase2->DO-GTPase1->
  - ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->
- **GCA_001897835.1; Bacteroidetes bacterium 46-16; counts= 2; multicellularity status: FALSE**
  - ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1->PNP_UDP_1+EAD1*->
  - ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->PNP_UDP_1+EAD1->
- **GCA_001898665.1; Burkholderiales bacterium 68-20; counts= 2; multicellularity status: FALSE**
  - DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1->CASPASE+EAD1*->
  - DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->
- **GCA_001905545.1; Streptomyces sp. CB02056; counts= 2; multicellularity status: NA**
  - EAD1+Trypsin->EAD1+STAND_NTPase*->
  - EAD1+Trypsin*->||<-?||STAND_NTPase->STAND_NTPase+wHTH+TPRs+AB_hydrolase->
- **GCA_001921865.1; Pseudomonas chlororaphis; counts= 2; multicellularity status: FALSE**
  - GAP1-N1+GAP1-M+GAP1-C+EAD1->CASPASE+EAD1*->
  - GAP2->ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->
- **GCA_002280395.1; Flavobacteriales bacterium 32-35-8; counts= 2; multicellularity status: FALSE**
  - DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1->?->EAD1*->
  - GAP2->ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->?->EAD1->
- **GCA_002281555.1; Hydrogenophilales bacterium 28-61-23; counts= 2; multicellularity status: FALSE**
  - Calcineurin-like+EAD1*->
  - GAP1-N1+GAP1-M+GAP1-C+EAD1*->
- **GCA_002735705.1; Janthinobacterium sp. BJB426; counts= 2; multicellularity status: FALSE**
  - GAP1-N1+GAP1-M+GAP1-C+EAD1->CASPASE+EAD1*->
  - GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->
- **GCA_002746795.1; Chloroflexi bacterium; counts= 2; multicellularity status: TRUE**
  - EAD1+STAND_NTPase+FGS-fold_domain->?->?->EAD1+Trypsin*->
  - EAD1+STAND_NTPase+FGS-fold_domain*->?->?->EAD1+Trypsin->
- **GCA_002842665.1; Bacteroidetes bacterium HGW-Bacteroidetes-11; counts= 2; multicellularity status: FALSE**
  - GAP2->ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->PNP_UDP_1+EAD1->
  - ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1->PNP_UDP_1+EAD1*->
- **GCA_900111115.1; Giesbergeria anulus; counts= 2; multicellularity status: FALSE**
  - GAP2->ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->
  - ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1->CASPASE+EAD1*->

- **GCA_900115275.1; Pseudomonas syringae; counts= 2; multicellularity status: FALSE**
  - GAP2->ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->
  - ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1->CASPASE+EAD1*->
- **GCA_900215445.1; Serratia sp. JKS296; counts= 2; multicellularity status: FALSE**
  - CASPASE+EAD1*->
  - GAP2->ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->
- **GCA_000368665.1; Acinetobacter junii; counts= 2; multicellularity status: FALSE**
  - GAP2->ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->
  - ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1->CASPASE+EAD1*->
- **GCA_001896005.1; Acinetobacter; counts= 2; multicellularity status: FALSE**
  - PNP_UDP_1+EAD1*->?->ZnR+DO-GTPase2->DO-GTPase1->
  - ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->
- **GCA_000155555.1; Coleofasciculus chthonoplastes; counts= 2; multicellularity status: TRUE**
  - E1->?->EAD1+Trypsin->EAD1+GUN4*->
  - E1->?->EAD1+Trypsin*->EAD1+GUN4->
- **GCA_000190755.3; Methylobacter tundripaludum; counts= 2; multicellularity status: TRUE**
  - PNP_UDP_1+EAD1*->
  - ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->
- **GCA_000282095.2; Rhizobium sp. CF080; counts= 2; multicellularity status: TRUE**
  - GAP1-N1+GAP1-M+GAP1-C+EAD1->CASPASE+EAD1*->
  - GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->
- **GCA_000178855.1; Ktedonobacter racemifer; counts= 2; multicellularity status: TRUE**
  - EAD1+Trypsin->EAD1+STAND_NTPase+STAND_NTPase+wHTH+TPRs+EAD1+Trypsin(i)+PDZ*->
  - EAD1+Trypsin*->EAD1+STAND_NTPase+STAND_NTPase+wHTH+TPRs+EAD1+Trypsin(i)+PDZ->
- **GCF_000332095.2; Leptolyngbya sp. PCC 6406; counts= 2; multicellularity status: TRUE**
  - EAD1+Trypsin->TM+TM+TM->EAD1+VMAP-C*->MoxR->
  - EAD1+Trypsin*->TM+TM+TM->EAD1+VMAP-C->MoxR->
- **GCA_000296815.2; Fibrisoma limi; counts= 2; multicellularity status: TRUE**
  - DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1->PNP_UDP_1+EAD1*->
  - DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->PNP_UDP_1+EAD1->
- **GCA_000314635.1; Acinetobacter baumannii; counts= 2; multicellularity status: FALSE**
  - GAP2->ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->
  - ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1->CASPASE+EAD1*->

- **GCA_000014265.1; Trichodesmium erythraeum; counts= 2; multicellularity status: TRUE**
  - EAD1+Trypsin->TM+TM+TM->EAD1+VMAP-M0+VMAP-C*->MoxR->
  - EAD1+Trypsin*->TM+TM+TM->EAD1+VMAP-M0+VMAP-C->MoxR->
- **GCA_000017645.1; Xanthobacter autotrophicus; counts= 2; multicellularity status: FALSE**
  - GAP2->ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->
  - ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1->CASPASE+EAD1*->
- **GCA_000176855.2; Acidovorax avenae; counts= 2; multicellularity status: FALSE**
  - DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1->CASPASE+EAD1*->
  - DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->
- **GCA_000177615.2; Frankia symbiont of Datisca glomerata; counts= 2; multicellularity status: TRUE**
  - EAD1+PH?*->
  - TIR+EAD1*->
- **GCA_000092385.1; Streptomyces; counts= 2; multicellularity status: TRUE**
  - EAD1+Trypsin->EAD1+EAD7*->
  - EAD1+Trypsin*->EAD1+EAD7->
- **GCA_000284295.1; Actinoplanes missouriensis; counts= 2; multicellularity status: TRUE**
  - EAD1+P-loop_NTPase(i)->MoxR->?->EAD1+Trypsin*->
  - EAD1+P-loop_NTPase(i)*->MoxR->?->EAD1+Trypsin->
- **GCA_000317495.1; Crinalium epipsammum; counts= 2; multicellularity status: NA**
  - EAD1->?->EAD1+CASPASE*->
  - Trypsin->EAD1+P-loop_NTPase(i)*->MoxR->helical_region+vWA->
- **GCA_000317435.1; Calothrix parietina; counts= 2; multicellularity status: TRUE**
  - EAD8+EAD1->EAD1+YukDl-Nterm+UB+E2*->JAB-N+JAB->?->CDC48-like->
  - EAD8+EAD1*->EAD1+YukDl-Nterm+UB+E2->JAB-N+JAB->
- **GCA_000320385.2; Sinorhizobium meliloti; counts= 2; multicellularity status: TRUE**
  - GAP2->ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->
  - ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1->CASPASE+EAD1*->
- **GCA_002870665.1; Fischerella muscicola; counts= 2; multicellularity status: NA**
  - EAD1+CASPASE->EAD1*->
  - EAD1+CASPASE*->EAD1->
- **GCA_000287135.2; Vibrio ordalii; counts= 2; multicellularity status: FALSE**
  - GAP2->ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->
  - PNP_UDP_1+EAD1*->GAP2->ZnR+DO-GTPase2->DO-GTPase1->

- **GCA_000495775.1; Asticcacaulis benevestitus; counts= 2; multicellularity status: FALSE**
  - Trypsin+Endonuclease_NS(HNH)->?->EAD1+Trypsin->EAD1+Trypsin*->
  - Trypsin+Endonuclease_NS(HNH)->?->EAD1+Trypsin*->EAD1+Trypsin->
- **GCF_000383615.1; Streptomyces canus; counts= 2; multicellularity status: TRUE**
  - GAP1-N1+GAP1-M+GAP1-C+EAD1->CASPASE+EAD1*->
  - GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->
- **GCF_000383675.1; Terracoccus sp. 273MFTsu3.1; counts= 2; multicellularity status: TRUE**
  - EAD1+Trypsin->EAD1+STAND_NTPase*->STAND_NTPase+wHTH+TPRs->
  - EAD1+Trypsin*->EAD1+STAND_NTPase->STAND_NTPase+wHTH+TPRs->
- **GCF_000379645.1; Actinoplanes globisporus; counts= 2; multicellularity status: TRUE**
  - EAD1+CASPASE*->?->?->ZnF->
  - ZnF->E1(active)+E1_C_unk->EAD1+YukDl-Nterm+UB+E2*->JAB-N+JAB->?->CDC48-like->
- **GCA_002234385.1; Amycolatopsis alba; counts= 2; multicellularity status: TRUE**
  - EAD1+Trypsin->EAD1+STAND_NTPase*->STAND_NTPase+wHTH+TPRs+CASPASE->
  - EAD1+Trypsin*->EAD1+STAND_NTPase->STAND_NTPase+wHTH+TPRs+CASPASE->
- **GCA_003947255.1; Amycolatopsis balhimycina; counts= 2; multicellularity status: TRUE**
  - EAD1+CASPASE->E1(active)+E1_C_unk->EAD1+YukDl-Nterm+UB+E2*->
  - EAD1+CASPASE*->E1(active)+E1_C_unk->EAD1+YukDl-Nterm+UB+E2->
- **GCA_000418325.1; Sorangium cellulosum; counts= 2; multicellularity status: TRUE**
  - EAD1+APATPase+wHTH+TPRs+BetaPropeller+EAD7*->||<-EAD7+CASPASE
  - EAD1+Trypsin*->?->MoxR->
- **GCF_000412185.1; Euryhalocaulis caribicus; counts= 2; multicellularity status: FALSE**
  - ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+DNA-glycosylase+EAD1->CASPASE+EAD1*->
  - ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+DNA-glycosylase+EAD1*->CASPASE+EAD1->
- **GCA_000502815.1; Mesorhizobium; counts= 2; multicellularity status: NA**
  - EAD1+Trypsin*->?->STAND_NTPase+wHTH+TPRs->
  - Trypsin+Endonuclease_NS(HNH)->EAD1+Trypsin*->
- **GCF_000452605.1; Pseudomonas syringae; counts= 2; multicellularity status: FALSE**
  - GAP1-N1+GAP1-M+GAP1-C+EAD1->CASPASE+EAD1*->
  - GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->
- **GCF_000490295.1; Vibrio parahaemolyticus; counts= 2; multicellularity status: FALSE**
  - EAD1->CASPASE+EAD1*->
  - EAD1*->CASPASE+EAD1->

- **GCF_000425065.1; Actinomadura rifamycini; counts= 2; multicellularity status: TRUE**
  - <-EAD1+STAND_NTPase+TPRs||EAD1+Trypsin*->
  - <-EAD1+Trypsin||EAD1+STAND_NTPase+TPRs*->
- **GCF_000515315.1; Asinibacterium sp. OR53; counts= 2; multicellularity status: FALSE**
  - ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1->PNP_UDP_1+EAD1*->
  - ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->PNP_UDP_1+EAD1->
- **GCA_000769935.1; Flavobacterium subsaxonicum; counts= 2; multicellularity status: NA**
  - EAD1->?->EAD1+Trypsin*->Endonuclease_NS(HNH)->
  - EAD1*->?->EAD1+Trypsin->Endonuclease_NS(HNH)->
- **GCF_000686005.1; Phyllobacterium sp. UNC302MFCol5.2; counts= 2; multicellularity status: TRUE**
  - EAD1+Trypsin*->
  - SP+Ig-like+TM+EAD1*->
- **GCF_000718785.1; Streptomyces sp. NRRL WC-3626; counts= 2; multicellularity status: TRUE**
  - EAD1+Trypsin->EAD1+STAND_NTPase*->STAND_NTPase+wHTH+TPRs+AB_hydrolase->
  - EAD1+Trypsin*->EAD1+STAND_NTPase->STAND_NTPase+wHTH+TPRs+AB_hydrolase->
- **GCF_000719355.1; Streptomyces griseus; counts= 2; multicellularity status: TRUE**
  - EAD1+Trypsin->EAD1+STAND_NTPase*->STAND_NTPase+wHTH+TPRs+AB_hydrolase->
  - EAD1+Trypsin*->EAD1+STAND_NTPase->STAND_NTPase+wHTH+TPRs+AB_hydrolase->
- **GCF_000725475.1; Streptomyces durhamensis; counts= 2; multicellularity status: TRUE**
  - EAD1+CASPASE->ZnF->E1(active)+E1_C_unk->EAD1+YukDl-Nterm+UB+E2*->JAB-N+JAB->?->CDC48-like->
  - EAD1+CASPASE*->ZnF->E1(active)+E1_C_unk->EAD1+YukDl-Nterm+UB+E2->
- **GCF_000761035.1; Rhodococcus fascians; counts= 2; multicellularity status: TRUE**
  - DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1->PNP_UDP_1+EAD1*->
  - DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->PNP_UDP_1+EAD1->
- **GCA_000702925.2; Methylomonas sp. LW13; counts= 2; multicellularity status: FALSE**
  - GAP2->ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->
  - PNP_UDP_1+EAD1*->GAP2->ZnR+DO-GTPase2->DO-GTPase1->
- **GCA_001270515.1; Streptomyces; counts= 2; multicellularity status: TRUE**
  - EAD1+Trypsin->EAD1+STAND_NTPase*->STAND_NTPase+wHTH+TPRs->
  - EAD1+Trypsin*->EAD1+STAND_NTPase->STAND_NTPase+wHTH+TPRs->
- **GCF_000717055.1; Streptomyces iakyrus; counts= 2; multicellularity status: TRUE**
  - EAD1+Trypsin->EAD1+STAND_NTPase*->STAND_NTPase+wHTH+TPRs+AB_hydrolase->
  - EAD1+Trypsin*->EAD1+STAND_NTPase->STAND_NTPase+wHTH+TPRs+AB_hydrolase->

- **GCA_000696185.1; Kitasatospora cheerisanensis; counts= 2; multicellularity status: TRUE**
  - EAD1->Trypsin->EAD1+STAND_NTPase*->
  - EAD1*->Trypsin->EAD1+STAND_NTPase->
- **GCF_000262465.1; Frankia sp. QA3; counts= 2; multicellularity status: TRUE**
  - E1(active)+E1_C_unk->EAD1+YukDl-Nterm+UB+E2*->JAB-N+JAB->
  - MoxR->?->?->EAD1+??+YukD-like_Ub*->||<-E1(active)+E1-ZnR_C
- **GCF_000177675.1; Frankia sp. EUN1f; counts= 2; multicellularity status: TRUE**
  - EAD1*->
  - EAD1+APATPase+wHTH+TPRs*->
- **GCA_000695255.1; Photobacterium galatheae; counts= 2; multicellularity status: FALSE**
  - GAP2->ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->
  - PNP_UDP_1+EAD1*->GAP2->ZnR+DO-GTPase2->DO-GTPase1->
- **GCF_000746395.1; Streptomyces mirabilis; counts= 2; multicellularity status: TRUE**
  - EAD1+CASPASE->ZnF->E1(active)+E1_C_unk->EAD1+YukDl-Nterm+UB+E2*->JAB-N+JAB->?->CDC48-like->
  - EAD1+CASPASE*->ZnF->E1(active)+E1_C_unk->EAD1+YukDl-Nterm+UB+E2->
- **GCA_000788395.1; Pseudoalteromonas piratica; counts= 2; multicellularity status: FALSE**
  - GAP2->ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->
  - PNP_UDP_1+EAD1*->GAP2->ZnR+DO-GTPase2->DO-GTPase1->
- **GCA_000747525.1; Sphingobacterium sp. ML3W; counts= 2; multicellularity status: FALSE**
  - GAP1-N1+GAP1-M+GAP1-C+EAD1->?->?->EAD1+Trypsin*->Endonuclease_NS(HNH)->
  - GAP2->ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->?->?->EAD1+Trypsin->
- **GCA_000773415.1; Burkholderia pseudomallei; counts= 2; multicellularity status: FALSE**
  - ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1->CASPASE+EAD1*->
  - ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->
- **GCF_000813415.1; Plesiomonas shigelloides; counts= 2; multicellularity status: FALSE**
  - GAP2->ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->
  - PNP_UDP_1+EAD1*->GAP2->ZnR+DO-GTPase2->DO-GTPase1->
- **GCA_000746665.1; Vibrio vulnificus; counts= 2; multicellularity status: FALSE**
  - GAP2->ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->
  - PNP_UDP_1+EAD1*->GAP2->ZnR+DO-GTPase2->DO-GTPase1->
- **GCA_000830005.1; Streptomyces vietnamensis; counts= 2; multicellularity status: TRUE**
  - EAD1+Trypsin->EAD1+STAND_NTPase*->STAND_NTPase+wHTH+TPRs->
  - EAD1+Trypsin*->EAD1+STAND_NTPase->STAND_NTPase+wHTH+TPRs->

- **GCF_000018005.1; Frankia sp. EAN1pec; counts= 2; multicellularity status: TRUE**
  - EAD2+EAD1*->EAD2+VMAP-M0+VMAP-C->MoxR->vWA+APATPase+wHTH+TPRs->
  - pntlT4_fusion_domain+EAD1*->
- **GCF_000221965.1; Xanthomonas campestris; counts= 2; multicellularity status: FALSE**
  - ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1->CASPASE+EAD1*->
  - ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->
- **GCA_000601485.1; Chondromyces apiculatus; counts= 2; multicellularity status: NA**
  - STAND_NTPase+wHTH+TPRs+BetaPropeller+EAD1->EAD1+Trypsin*->
  - STAND_NTPase+wHTH+TPRs+BetaPropeller+EAD1*->EAD1+Trypsin->
- **GCF_000818475.1; Vibrio hyugaensis; counts= 2; multicellularity status: FALSE**
  - GAP2->ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->
  - PNP_UDP_1+EAD1*->GAP2->ZnR+DO-GTPase2->DO-GTPase1->
- **GCA_000938735.2; Sphingobacterium sp. PM2-P1-29; counts= 2; multicellularity status: FALSE**
  - DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1->?->EAD1+Trypsin*->Endonuclease_NS(HNH)->
  - DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->?->EAD1+Trypsin->Endonuclease_NS(HNH)->
- **GCA_000968575.1; Pseudomonas kilonensis; counts= 2; multicellularity status: FALSE**
  - ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1->CASPASE+EAD1*->
  - ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->
- **GCA_000974985.2; Streptomyces mangrovisoli; counts= 2; multicellularity status: TRUE**
  - EAD1+Trypsin->EAD1+STAND_NTPase*->STAND_NTPase+wHTH+TPRs+AB_hydrolase->
  - EAD1+Trypsin*->EAD1+STAND_NTPase->STAND_NTPase+wHTH+TPRs+AB_hydrolase->
- **GCA_000952035.2; Streptomyces lydicus; counts= 2; multicellularity status: TRUE**
  - *
  - EAD1+P-loop_helicase+??*->
- **GCA_001013325.1; Vibrio; counts= 2; multicellularity status: NA**
  - GAP2->ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->
  - PNP_UDP_1+EAD1*->GAP2->ZnR+DO-GTPase2->DO-GTPase1->
- **GCF_000798835.1; Shewanella sp. ZOR0012; counts= 2; multicellularity status: FALSE**
  - GAP2->ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->
  - ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1->CASPASE+EAD1*->
- **GCA_001028135.1; Xenorhabdus; counts= 2; multicellularity status: NA**
  - EAD1+P-loop_helicase->CASPASE+EAD1*->
  - EAD1+P-loop_helicase*->CASPASE+EAD1->

- **GCF_001044185.1; Streptomyces sp. HNS054; counts= 2; multicellularity status: NA**
  - EAD1+Trypsin->EAD1+STAND_NTPase*->STAND_NTPase+wHTH+TPRs+AB_hydrolase->
  - EAD1+Trypsin*->EAD1+STAND_NTPase->STAND_NTPase+wHTH+TPRs+AB_hydrolase->
- **GCA_001045445.1; Chryseobacterium sp. BLS98; counts= 2; multicellularity status: FALSE**
  - DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1->?->EAD1+Trypsin*->Endonuclease_NS(HNH)->
  - GAP2->ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->?->EAD1+Trypsin->Endonuclease_NS(HNH)->
- **GCA_001189295.1; Chondromyces crocatus; counts= 2; multicellularity status: TRUE**
  - STAND_NTPase+wHTH+TPRs+BetaPropeller+EAD1->EAD1+Trypsin*->
  - STAND_NTPase+wHTH+TPRs+BetaPropeller+EAD1*->EAD1+Trypsin->
- **GCF_000514395.1; Pseudomonas sp. URMO17WK12:I12; counts= 2; multicellularity status: NA**
  - GAP1-N1+GAP1-M+GAP1-C+EAD1->CASPASE+EAD1*->
  - GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->
- **GCF_000828075.2; Tolypothrix campylonemoides; counts= 2; multicellularity status: NA**
  - EAD1+low_complexity*->
  - TIR+EAD1*->
- **GCF_001273715.1; Vibrio alginolyticus; counts= 2; multicellularity status: FALSE**
  - GAP2->ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->
  - PNP_UDP_1+EAD1*->GAP2->ZnR+DO-GTPase2->DO-GTPase1->
- **GCA_001275735.1; Pseudomonas coronafaciens; counts= 2; multicellularity status: FALSE**
  - ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1->CASPASE+EAD1*->
  - ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->
- **GCA_001280885.1; Streptomyces sp. XY332; counts= 2; multicellularity status: TRUE**
  - EAD1+Trypsin->EAD1+STAND_NTPase*->STAND_NTPase+wHTH+TPRs->
  - EAD1+Trypsin*->EAD1+STAND_NTPase->STAND_NTPase+wHTH+TPRs->
- **GCF_001414035.1; Frankia sp. ACN1ag; counts= 2; multicellularity status: TRUE**
  - EAD1+cNMP_cyclase+TIR*->
  - pntlT4_fusion_domain+EAD1*->
- **GCF_000948395.1; Frankia sp. CpI1-P; counts= 2; multicellularity status: TRUE**
  - EAD1+BetaPropeller*->
  - EAD1+cNMP_cyclase+extension*->
- **GCA_001421665.1; Sphingobium sp. Leaf26; counts= 2; multicellularity status: FALSE**
  - GAP2->ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->
  - ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1->CASPASE+EAD1*->

- **GCA_001424875.1; Kitasatospora; counts= 2; multicellularity status: TRUE**
  - EAD1+Trypsin->EAD1+STAND_NTPase*->STAND_NTPase+wHTH+TPRs->
  - EAD1+Trypsin*->EAD1+STAND_NTPase->STAND_NTPase+wHTH+TPRs->
- **GCA_001444405.1; Pseudoalteromonas phenolica; counts= 2; multicellularity status: FALSE**
  - GAP2->ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->
  - PNP_UDP_1+EAD1*->GAP2->ZnR+DO-GTPase2->DO-GTPase1->
- **GCA_001458375.1; Tropicibacter naphthalenivorans; counts= 2; multicellularity status: FALSE**
  - GAP2->ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->
  - ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1->CASPASE+EAD1*->
- **GCA_001467105.1; Pseudomonas syringae; counts= 2; multicellularity status: FALSE**
  - ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1->CASPASE+EAD1*->
  - ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->
- **GCA_001425445.1; Devosia sp. Leaf420; counts= 2; multicellularity status: FALSE**
  - GAP2->ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->CASPASE+TPRs->
  - ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1->CASPASE+EAD1*->CASPASE+TPRs->
- **GCA_001611795.1; Streptomyces sp. S10(2016); counts= 2; multicellularity status: TRUE**
  - *
  - EAD1+Trypsin*->
- **GCF_900079515.1; Shewanella sp. Alg231_23; counts= 2; multicellularity status: FALSE**
  - GAP2->ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->
  - PNP_UDP_1+EAD1*->GAP2->ZnR+DO-GTPase2->DO-GTPase1->
- **GCA_001698815.1; Pseudomonas syringae; counts= 2; multicellularity status: FALSE**
  - ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1->CASPASE+EAD1*->
  - ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->
- **GCA_001969965.1; Streptomyces sparsogenes; counts= 2; multicellularity status: TRUE**
  - EAD1+Trypsin->EAD1+EAD7*->?->?->FGS-fold_domain->
  - EAD1+Trypsin*->EAD1+EAD7->
- **GCF_001685485.1; Formosa haliotis; counts= 2; multicellularity status: FALSE**
  - ??+EAD1->?->?->EAD1+Trypsin*->Endonuclease_NS(HNH)->
  - GAP2->PSE->PSE->?->??+EAD1*->?->?->EAD1+Trypsin->
- **GCF_001571225.1; Hydrogenophaga palleronii; counts= 2; multicellularity status: FALSE**
  - DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1->CASPASE+EAD1*->
  - DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->

- **GCF_000346485.2; Scytonema hofmannii; counts= 2; multicellularity status: TRUE**
  - ??+EAD1->GUN4+EAD1*->
  - PNP_UDP_1+EAD1*->
- **GCA_001548375.1; Nostoc sp. NIES-3756; counts= 2; multicellularity status: NA**
  - EAD1+Trypsin->TM+TM+TM->EAD1+STAND_NTPase+TPRs*->
  - EAD1+Trypsin*->TM+TM+TM->EAD1+STAND_NTPase+TPRs->
- **GCF_001746365.1; Streptomyces sp. LUP30; counts= 2; multicellularity status: TRUE**
  - EAD1+CASPASE->EAD1+P-loop_helicase*->
  - EAD1+CASPASE*->EAD1+P-loop_helicase->
- **GCA_001858125.1; Cylindrospermopsis raciborskii; counts= 2; multicellularity status: NA**
  - RHH->EAD1+Trypsin->TM+TM+TM->EAD1+P-loop_NTPase*->MoxR->helical_region+vWA->
  - RHH->EAD1+Trypsin*->TM+TM+TM->EAD1+P-loop_NTPase->MoxR->
- **GCA_900114875.1; Chryseobacterium limigenitum; counts= 2; multicellularity status: FALSE**
  - GAP2->ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->PNP_UDP_1+EAD1->
  - ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1->PNP_UDP_1+EAD1*->
- **GCA_001904715.1; Nostoc calcicola; counts= 2; multicellularity status: NA**
  - EAD1+Trypsin->EAD1+FGS-fold_domain*->||<-STAND_NTPase+FGS-fold_domain
  - EAD1+Trypsin*->EAD1+FGS-fold_domain->||<-STAND_NTPase+FGS-fold_domain
- **GCA_002217275.1; Flavobacterium; counts= 2; multicellularity status: FALSE**
  - GAP2->ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->PNP_UDP_1+EAD1->
  - ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1->PNP_UDP_1+EAD1*->
- **GCA_001939115.1; Leptolyngbya sp. 'hensonii'; counts= 2; multicellularity status: NA**
  - EAD1+Trypsin->TM+TM+TM->EAD1+??+VMAP-C*->MoxR->vWA+Beta-rich+FGS-fold_domain->
  - EAD1+Trypsin*->TM+TM+TM->EAD1+??+VMAP-C->MoxR->
- **GCF_001984055.1; Variovorax sp. KK3; counts= 2; multicellularity status: NA**
  - EAD1+Trypsin->EAD1+P-loop_NTPase(i)*->MoxR->helical_region+vWA->STAND_NTPase+TPRs+Lon-N+METALLOPORTEASE->
  - EAD1+Trypsin*->EAD1+P-loop_NTPase(i)->MoxR->helical_region+vWA->
- **GCA_004138325.1; Spirosoma sp. 209; counts= 2; multicellularity status: NA**
  - EAD1+Trypsin->EAD1+SIR2*->STAND_NTPase+wHTH+TM+BetaPropeller->
  - EAD1+Trypsin*->EAD1+SIR2->STAND_NTPase+wHTH+TM+BetaPropeller->
- **GCF_002009845.1; Leptospira alexanderi; counts= 2; multicellularity status: FALSE**
  - GAP2->ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->PNP_UDP_1+EAD1->
  - ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1->PNP_UDP_1+EAD1*->

- **GCA_900167465.1; Geobacter thiogenes; counts= 2; multicellularity status: FALSE**
  - ??+PNP_UDP_1+EAD1*->GAP2->ZnR+DO-GTPase2->DO-GTPase1->
  - GAP2->ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->
- **GCA_002027345.1; Cylindrospermopsis raciborskii; counts= 2; multicellularity status: NA**
  - RHH->EAD1+Trypsin->TM+TM+TM->EAD1+P-loop_NTPase*->MoxR->helical_region+vWA->
  - RHH->EAD1+Trypsin*->TM+TM+TM->EAD1+P-loop_NTPase->MoxR->
- **GCA_002027195.1; Streptomyces sp. GKU 895; counts= 2; multicellularity status: TRUE**
  - EAD1+CASPASE->E1+E1_C_unk->E1(active)+E1_C->EAD1+YukDl-Nterm+UB+E2*->JAB-N+JAB->?->CDC48-like->
  - EAD1+CASPASE*->E1+E1_C_unk->E1(active)+E1_C->EAD1+YukDl-Nterm+UB+E2->
- **GCF_001854645.1; Frankia sp. EUN1h; counts= 2; multicellularity status: TRUE**
  - EAD1+APATPase+wHTH+TPRs*->
  - EAD1+APATPase+wHTH+TPRs*->
- **GCF_001854655.1; Frankia sp. Cc1.17; counts= 2; multicellularity status: TRUE**
  - EAD1+BetaPropeller*->
  - EAD1+TIR*->
- **GCA_900155475.1; Methylomagnum ishizawai; counts= 2; multicellularity status: FALSE**
  - PNP_UDP_1+EAD1*->||<-?||?->ZnR+DO-GTPase2->
  - ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->
- **GCA_002151545.1; Sphingobacteriaceae bacterium GW460-11-11-14-LB5; counts= 2; multicellularity status: NA**
  - EAD1+Trypsin->EAD1+SIR2*->STAND_NTPase+wHTH+TM+BetaPropeller->
  - EAD1+Trypsin*->EAD1+SIR2->STAND_NTPase+wHTH+TM+BetaPropeller->
- **GCF_002150765.1; Lentzea kentuckyensis; counts= 2; multicellularity status: TRUE**
  - EAD1+Trypsin->EAD1+STAND_NTPase*->STAND_NTPase+wHTH+TPRs+CASPASE->
  - EAD1+Trypsin*->EAD1+STAND_NTPase->STAND_NTPase+wHTH+TPRs+CASPASE->
- **GCA_002154695.1; Nostoc sp. T09; counts= 2; multicellularity status: TRUE**
  - E1(active)+E1_C_unk->?->TCAD3+TCAD4+CASPASE+EAD1->EAD1+YukDl-Nterm+UB+E2*->JAB-N+JAB->?->CDC48-like->
  - ZnF->E1(active)+E1_C_unk->?->TCAD3+TCAD4+CASPASE+EAD1*->EAD1+YukDl-Nterm+UB+E2->JAB-N+JAB->
- **GCA_002157355.1; Variovorax sp. JS1663; counts= 2; multicellularity status: NA**
  - EAD1+Trypsin->EAD1+P-loop_NTPase(i)*->MoxR->helical_region+vWA->STAND_NTPase+TPRs+Lon-N+METALLOPORTEASE->
  - EAD1+Trypsin*->EAD1+P-loop_NTPase(i)->MoxR->helical_region+vWA->
- **GCF_900143175.1; Xanthomonas retroflexus; counts= 2; multicellularity status: FALSE**
  - *
  - ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1->CASPASE+EAD1*->

- **GCA_002209385.1; Methylovulum psychrotolerans; counts= 2; multicellularity status: FALSE**
  - GAP2->ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->
  - PNP_UDP_1+EAD1*->GAP2->ZnR+DO-GTPase2->DO-GTPase1->
- **GCA_002224125.1; Streptomyces sp. NBS 14/10; counts= 2; multicellularity status: TRUE**
  - EAD1+Trypsin->EAD1+EAD7*->
  - EAD1+Trypsin*->EAD1+EAD7->
- **GCA_900109175.1; Pseudomonas linyingensis; counts= 2; multicellularity status: FALSE**
  - ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1->CASPASE+EAD1*->
  - ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->
- **GCA_900113065.1; Aureimonas phyllosphaerae; counts= 2; multicellularity status: FALSE**
  - GAP1-N1+GAP1-M+GAP1-C+EAD1->CASPASE+EAD1*->
  - GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->
- **GCA_900115505.1; Geodermatophilus sp. DSM 44208; counts= 2; multicellularity status: NA**
  - EAD1+Trypsin->EAD1+P-loop_NTPase(i)*->MoxR->helical_region+vWA->
  - EAD1+Trypsin*->EAD1+P-loop_NTPase(i)->MoxR->helical_region+vWA->
- **GCA_900107105.1; Geodermatophilus africanus; counts= 2; multicellularity status: TRUE**
  - EAD1+Trypsin->EAD1+STAND_NTPase->STAND_NTPase+wHTH+TPRs+EAD1+Trypsin*->
  - EAD1+Trypsin*->EAD1+STAND_NTPase->STAND_NTPase+wHTH+TPRs+EAD1+Trypsin->
- **GCA_900116615.1; Algoriphagus locisalis; counts= 2; multicellularity status: FALSE**
  - GAP2->ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->EAD1+Trypsin->Endonuclease_NS(HNH)->
  - ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1->EAD1+Trypsin*->Endonuclease_NS(HNH)->
- **GCA_900113985.1; Phyllobacterium sp. CL33Tsu; counts= 2; multicellularity status: TRUE**
  - EAD1+Trypsin*->
  - SP+Ig-like+TM+EAD1*->
- **GCA_900111995.1; Collimonas sp. OK607; counts= 2; multicellularity status: FALSE**
  - ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1->CASPASE+EAD1*->
  - ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->
- **GCF_900104725.1; Actinoplanes derwentensis; counts= 2; multicellularity status: TRUE**
  - EAD1+Trypsin*->EAD1+P-loop_NTPase(i)->MoxR->
  - Trypsin+EAD1*->BetaPropeller+vWA->
- **GCA_002234595.1; Amycolatopsis sp. H5; counts= 2; multicellularity status: TRUE**
  - EAD1+CASPASE->ZnF->E1(active)+E1_C_unk->EAD1+YukDl-Nterm+UB+E2*->JAB-N+JAB->?->CDC48-like->
  - EAD1+CASPASE*->ZnF->E1(active)+E1_C_unk->EAD1+YukDl-Nterm+UB+E2->

- **GCA_002318995.1; Shewanella algae; counts= 2; multicellularity status: FALSE**
  - GAP2->ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->
  - PNP_UDP_1+EAD1*->GAP2->ZnR+DO-GTPase2->DO-GTPase1->
- **GCA_002356095.1; Pseudomonas putida; counts= 2; multicellularity status: FALSE**
  - ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1->CASPASE+EAD1*->
  - ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->
- **GCA_002368335.1; Nostoc sp. NIES-4103; counts= 2; multicellularity status: TRUE**
  - EAD1+CASPASE->EAD1+GUN4*->
  - EAD1+CASPASE*->EAD1+GUN4->
- **GCA_004296455.1; Calothrix sp. NIES-4101; counts= 2; multicellularity status: TRUE**
  - EAD1+Trypsin->TM+TM+TM->EAD1+VMAP-M1+VMAP-C*->
  - EAD1+Trypsin*->TM+TM+TM->EAD1+VMAP-M1+VMAP-C->
- **GCA_002368315.1; Fischerella sp. NIES-4106; counts= 2; multicellularity status: NA**
  - EAD1+Trypsin->TM+TM+TM->EAD1+??+VMAP-C*->MoxR->vWA+Beta-rich+FGS-fold_domain->
  - EAD1+Trypsin*->TM+TM+TM->EAD1+??+VMAP-C->MoxR->
- **GCA_900206255.1; Streptomyces sp. TLI_55; counts= 2; multicellularity status: TRUE**
  - EAD1+CASPASE->ZnF->E1(active)+E1_C_unk->EAD1+YukDl-Nterm+UB+E2*->
  - EAD1+CASPASE*->ZnF->E1(active)+E1_C_unk->EAD1+YukDl-Nterm+UB+E2->
- **GCA_002754245.1; Chryseobacterium sp. 52; counts= 2; multicellularity status: FALSE**
  - DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1->?->EAD1+Trypsin*->Endonuclease_NS(HNH)->
  - GAP2->ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->?->EAD1+Trypsin->Endonuclease_NS(HNH)->
- **GCF_002321945.1; Cylindrospermopsis raciborskii; counts= 2; multicellularity status: NA**
  - RHH->EAD1+Trypsin->TM+TM+TM->EAD1*->
  - RHH->EAD1+Trypsin*->TM+TM+TM->EAD1->
- **GCA_002795805.1; Mariprofundus aestuarium; counts= 2; multicellularity status: TRUE**
  - GAP2->ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->PNP_UDP_1+EAD1->
  - ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1->PNP_UDP_1+EAD1*->
- **GCA_002813455.1; Pseudomonas baetica; counts= 2; multicellularity status: NA**
  - EAD1+P-loop_helicase->CASPASE+EAD1*->
  - EAD1+P-loop_helicase*->CASPASE+EAD1->
- **GCA_000221965.1; Xanthomonas campestris pv. raphani 756C; counts= 1; multicellularity status: FALSE**
  - DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->
- **GCA_000418455.1; Streptomyces rapamycinicus NRRL 5491; counts= 1; multicellularity status: TRUE**

  - EAD1+CASPASE*->

- **GCA_001618865.1; Luteitalea pratensis; counts= 1; multicellularity status: NA**
  - CASPASE->EAD1+Trypsin+TM*->
- **GCA_003595545.1; Streptomyces sp. 11-1-2; counts= 1; multicellularity status: TRUE**
  - EAD1+CASPASE*->
- **GCA_000158915.1; Streptomyces himastatinicus ATCC 53653; counts= 1; multicellularity status: TRUE**
  - EAD1+Trypsin*->
- **GCA_000243895.3; Leptospira interrogans str. FPW2026; counts= 1; multicellularity status: FALSE**
  - helical_region+EAD1->PNP_UDP_1+EAD1*->
- **GCA_000516475.1; Candidatus Magnetoglobus multicellularis str. Araruama; counts= 1; multicellularity status: TRUE**
  - EAD1+??*->
- **GCA_000828085.2; Scytonema tolypothrichoides VB-61278; counts= 1; multicellularity status: NA**
  - EAD1*->
- **GCA_000961745.1; Rhodospirillaceae bacterium BRH_c57; counts= 1; multicellularity status: FALSE**
  - GAP1-N1+GAP1-M+GAP1-C+EAD1*->
- **GCA_001303105.1; Anaerolineae bacterium SG8_19; counts= 1; multicellularity status: NA**
  - EAD1*->
- **GCA_001589205.1; Sorangium cellulosum; counts= 1; multicellularity status: TRUE**
  - EAD1+APATPase+wHTH+TPRs+BetaPropeller+EAD7*->||<-EAD7+CASPASE
- **GCA_001589295.1; Sorangium cellulosum; counts= 1; multicellularity status: TRUE**
  - EAD1+Trypsin*->?->MoxR->
- **GCA_001640045.1; Candidatus Thiomargarita nelsonii; counts= 1; multicellularity status: TRUE**
  - E1(active)+E1_C->EAD1*->
- **GCA_001672255.1; Anabaena sp. AL09; counts= 1; multicellularity status: TRUE**
  - EAD1+CASPASE*->
- **GCA_001772385.1; candidate division WOR-1 bacterium RIFOXYA2_FULL_36_21; counts= 1; multicellularity status: NA**
  - EAD1+EAD1*->
- **GCA_001898145.1; Dyadobacter sp. 50-39; counts= 1; multicellularity status: NA**
  - Trypsin+Endonuclease_NS(HNH)->?->Trypsin(i)+STAND_NTPase+wHTH+TPRs->EAD1+Trypsin*->
- **GCA_001874765.1; Acinetobacter baumannii; counts= 1; multicellularity status: FALSE**

  - ZnR+DO-GTPase2->DO-GTPase1->?->??+EAD1*->

- **GCA_001983005.1; Frankia sp. BMG5.30; counts= 1; multicellularity status: TRUE**
  - TIR+EAD1*->
- **GCA_002200945.1; Mesorhizobium amorphae CCBAU 01583; counts= 1; multicellularity status: TRUE**
  - Endonuclease_NS(HNH)->EAD1*->Trypsin->EAD1->
- **GCA_002401655.1; Gammaproteobacteria bacterium; counts= 1; multicellularity status: NA**
  - GAP2->ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->
- **GCA_002858925.1; Caulobacter sp. 410; counts= 1; multicellularity status: NA**
  - EAD1+Trypsin*->
- **GCA_900101685.1; Alloactinosynnema iranicum; counts= 1; multicellularity status: TRUE**
  - EAD1+Trypsin*->STAND_NTPase+TPRs->
- **GCA_900106665.1; Paracoccus sanguinis; counts= 1; multicellularity status: NA**
  - EAD1+Trypsin*->
- **GCA_900169915.1; Acinetobacter baumannii; counts= 1; multicellularity status: FALSE**
  - ??+EAD1*->
- **GCA_000216135.3; Leptospira interrogans; counts= 1; multicellularity status: FALSE**
  - GAP2->ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->PNP_UDP_1+EAD1->
- **GCA_000306495.2; Leptospira interrogans; counts= 1; multicellularity status: FALSE**
  - GAP2->ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->PNP_UDP_1+EAD1->
- **GCA_000164015.3; Pseudomonas savastanoi; counts= 1; multicellularity status: FALSE**
  - ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->?->PSE->CASPASE+EAD1->
- **GCA_000280925.3; Myxococcus hansupus; counts= 1; multicellularity status: TRUE**
  - EAD1+Trypsin*->
- **GCA_002752655.1; Methylosinus; counts= 1; multicellularity status: TRUE**
  - EAD1+Trypsin*->?->STAND_NTPase+wHTH+TM+TPRs->
- **GCA_000368385.1; Acinetobacter sp. NIPH 899; counts= 1; multicellularity status: NA**
  - EAD1+??*->?->ZnR+DO-GTPase2->DO-GTPase1->
- **GCA_000369405.1; Acinetobacter; counts= 1; multicellularity status: FALSE**
  - EAD1+??*->?->ZnR+DO-GTPase2->DO-GTPase1->
- **GCA_000369745.1; Acinetobacter; counts= 1; multicellularity status: FALSE**

  - ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->

- **GCA_001686985.1; Mesorhizobium amorphae; counts= 1; multicellularity status: TRUE**
  - Trypsin+Endonuclease_NS(HNH)->EAD1+Trypsin*->
- **GCA_000350545.1; Desulfotignum phosphitoxidans; counts= 1; multicellularity status: FALSE**
  - ??+PNP_UDP_1+EAD1*->GAP2->ZnR+DO-GTPase2->DO-GTPase1->
- **GCA_000313875.1; Alcaligenes sp. EGD-AK7; counts= 1; multicellularity status: FALSE**
  - ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1->CASPASE+EAD1*->
- **GCF_000011365.1; Bradyrhizobium; counts= 1; multicellularity status: TRUE**
  - HNH+PNP_UDP_1+EAD1*->
- **GCA_000013345.1; Frankia; counts= 1; multicellularity status: TRUE**
  - EAD1+cNMP_cyclase+TIR*->
- **GCA_000012685.1; Myxococcus xanthus; counts= 1; multicellularity status: TRUE**
  - EAD1+Trypsin*->
- **GCA_000016405.1; Rhodobacter sphaeroides; counts= 1; multicellularity status: FALSE**
  - Trypsin->EAD1+Trypsin*->EAD1+HExxH+helical_region->TM+Endonuclease_NS(HNH)+LytR_C/SPOR->
- **GCA_000015165.1; Bradyrhizobium sp. BTAi1; counts= 1; multicellularity status: TRUE**
  - EAD1+Trypsin*->
- **GCA_000024805.1; Haliangium ochraceum; counts= 1; multicellularity status: TRUE**
  - ST_kinase+??+P-loop_NTPase+EAD1*->
- **GCA_000147335.1; Cyanothece sp. PCC 7822; counts= 1; multicellularity status: NA**
  - EAD1+TerB-like?+GUN4*->
- **GCA_000199675.1; Anaerolinea thermophila; counts= 1; multicellularity status: NA**
  - EAD1+Trypsin*->
- **GCA_000187705.1; Rahnella; counts= 1; multicellularity status: NA**
  - EAD1+??*->
- **GCA_000219105.1; Myxococcus fulvus; counts= 1; multicellularity status: TRUE**
  - EAD1+Trypsin*->
- **GCA_000147815.3; Streptomyces violaceusniger; counts= 1; multicellularity status: TRUE**
  - EAD1+CASPASE*->
- **GCA_000255295.1; Corallococcus coralloides; counts= 1; multicellularity status: NA**

  - EAD1+Trypsin*->

- **GCA_000807315.1; Bradyrhizobium japonicum; counts= 1; multicellularity status: TRUE**
  - Trypsin+EAD1+helical_region*->
- **GCA_000266905.1; Mycolicibacterium chubuense; counts= 1; multicellularity status: NA**
  - EAD1+Trypsin*->EAD1+STAND_NTPase->STAND_NTPase+wHTH+TPRs->
- **GCA_000331735.1; Myxococcus stipitatus; counts= 1; multicellularity status: TRUE**
  - EAD1+Trypsin*->
- **GCF_000427585.1; Sinorhizobium meliloti; counts= 1; multicellularity status: TRUE**
  - EAD1+Trypsin*->
- **GCA_000465875.3; Alcaligenes sp. EGD-AK7; counts= 1; multicellularity status: FALSE**
  - GAP2->ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->
- **GCA_000503155.1; Mesorhizobium; counts= 1; multicellularity status: NA**
  - Trypsin+Endonuclease_NS(HNH)->EAD1+Trypsin*->
- **GCA_000502795.1; Mesorhizobium; counts= 1; multicellularity status: NA**
  - EAD1+Trypsin*->
- **GCA_000502775.1; Mesorhizobium sp. LSJC265A00; counts= 1; multicellularity status: TRUE**
  - Trypsin+Endonuclease_NS(HNH)->EAD1+Trypsin*->
- **GCA_000502755.1; Mesorhizobium sp. LSJC264A00; counts= 1; multicellularity status: TRUE**
  - Trypsin+Endonuclease_NS(HNH)->EAD1+Trypsin*->
- **GCA_000502695.1; Mesorhizobium; counts= 1; multicellularity status: NA**
  - Trypsin+Endonuclease_NS(HNH)->EAD1+Trypsin*->
- **GCA_000503075.1; Mesorhizobium sp. LSHC422A00; counts= 1; multicellularity status: TRUE**
  - EAD1+Trypsin+??+CarboxypepD-reg-IG+papain-like_peptidoglycan_hydrolase*->
- **GCA_000502615.1; Mesorhizobium sp. LNJC405B00; counts= 1; multicellularity status: TRUE**
  - Trypsin+Endonuclease_NS(HNH)->EAD1+Trypsin*->
- **GCA_000502995.1; Mesorhizobium; counts= 1; multicellularity status: NA**
  - Trypsin+Endonuclease_NS(HNH)->EAD1+Trypsin*->
- **GCA_000502555.1; Mesorhizobium; counts= 1; multicellularity status: NA**
  - Trypsin+Endonuclease_NS(HNH)->EAD1+Trypsin*->
- **GCA_000502475.1; Mesorhizobium; counts= 1; multicellularity status: NA**

  - Trypsin+Endonuclease_NS(HNH)->EAD1+Trypsin*->

- **GCA_000502295.1; Mesorhizobium sp. L103C565B0; counts= 1; multicellularity status: TRUE**
  - Trypsin+Endonuclease_NS(HNH)->EAD1+Trypsin*->
- **GCA_000502255.1; Mesorhizobium sp. L103C120A0; counts= 1; multicellularity status: TRUE**
  - Trypsin+Endonuclease_NS(HNH)->EAD1+Trypsin*->
- **GCA_000502235.1; Mesorhizobium sp. L103C119B0; counts= 1; multicellularity status: TRUE**
  - Trypsin+Endonuclease_NS(HNH)->EAD1+Trypsin*->
- **GCF_000301755.1; Acinetobacter; counts= 1; multicellularity status: FALSE**
  - PNP_UDP_1+EAD1*->?->ZnR+DO-GTPase2->DO-GTPase1->
- **GCF_000428945.1; Hamadaea tsunoensis; counts= 1; multicellularity status: TRUE**
  - vWA->?->Pkinase->EAD1+Trypsin*->EAD1+STAND_NTPase->cNMP_cyclase+STAND_NTPase+wHTH->TM+TM+TM->
- **GCF_000521175.1; Aphanizomenon flos-aquae; counts= 1; multicellularity status: NA**
  - cNMP_cyclase+EAD1*->
- **GCA_004001485.1; Sinorhizobium meliloti; counts= 1; multicellularity status: TRUE**
  - GAP2->ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->
- **GCF_000510665.1; Sinorhizobium meliloti; counts= 1; multicellularity status: TRUE**
  - ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1->CASPASE+EAD1*->
- **GCA_001560865.1; Pseudomonas; counts= 1; multicellularity status: FALSE**
  - ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1->CASPASE+EAD1*->
- **GCF_000717715.1; Streptomyces sp. NRRL B-24484; counts= 1; multicellularity status: TRUE**
  - EAD1+Trypsin->EAD1+STAND_NTPase*->
- **GCF_000760995.1; Rhodococcus fascians; counts= 1; multicellularity status: TRUE**
  - DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->PNP_UDP_1+EAD1->
- **GCA_000737695.1; Flavobacterium hydatis; counts= 1; multicellularity status: FALSE**
  - GAP2->ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->?->EAD1+Trypsin->Endonuclease_NS(HNH)->
- **GCA_000732115.1; Frankia sp. CeD; counts= 1; multicellularity status: NA**
  - EAD1+cNMP_cyclase+TIR*->
- **GCF_000316115.1; Leptolyngbya sp. PCC 7375; counts= 1; multicellularity status: TRUE**
  - EAD1+Trypsin->TM+TM+TM->EAD1+??+VMAP-C*->MoxR->vWA+BetaPropeller+FGS-fold_domain->FGS-fold_domain->
- **GCF_000720255.1; Streptomyces griseus; counts= 1; multicellularity status: TRUE**

  - CASPASE->?->E1(active)+E1_C_unk->EAD1+YukDl-Nterm+UB+E2*->?->?->CDC48-like->

- **GCA_000738695.1; Streptomyces scabiei; counts= 1; multicellularity status: TRUE**
  - EAD1+TM+??+TM*->
- **GCA_000590515.1; Streptomyces sp. PRh5; counts= 1; multicellularity status: TRUE**
  - EAD1+CASPASE*->
- **GCA_000812465.1; Cupriavidus sp. IDO; counts= 1; multicellularity status: FALSE**
  - ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->
- **GCA_000789435.1; Aphanizomenon flos-aquae; counts= 1; multicellularity status: NA**
  - EAD1+Trypsin*->TM+TM+TM->EAD1+BetaPropeller->
- **GCF_000350545.1; Desulfotignum phosphitoxidans; counts= 1; multicellularity status: FALSE**
  - DO-GTPase1->?->?->GAP1-C+EAD1*->
- **GCF_000317495.1; Crinalium epipsammum; counts= 1; multicellularity status: NA**
  - EAD1*->?->EAD1+CASPASE->
- **GCA_000773865.1; Bradyrhizobium japonicum; counts= 1; multicellularity status: TRUE**
  - Trypsin+EAD1+helical_region*->
- **GCA_000826545.1; Kibdelosporangium sp. MJ126-NF4; counts= 1; multicellularity status: TRUE**
  - EAD1+Trypsin*->EAD1+STAND_NTPase->STAND_NTPase+wHTH+TPRs+CASPASE->
- **GCF_000344805.1; Bradyrhizobium oligotrophicum; counts= 1; multicellularity status: TRUE**
  - EAD1+Trypsin->EAD1+??*->STAND_NTPase+wHTH+TM+TPRs->
- **GCA_000834545.1; Pseudomonas fluorescens; counts= 1; multicellularity status: FALSE**
  - ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1->CASPASE+EAD1*->
- **GCA_000685765.2; Frankia sp. BMG5.23; counts= 1; multicellularity status: NA**
  - EAD1+cNMP_cyclase+TIR*->
- **GCA_000935305.1; Pseudomonas oryzihabitans; counts= 1; multicellularity status: FALSE**
  - ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->
- **GCA_001990805.2; Mastigocladus laminosus; counts= 1; multicellularity status: NA**
  - EAD1+CASPASE*->
- **GCA_000938975.1; Streptomyces iranensis; counts= 1; multicellularity status: TRUE**
  - EAD1+CASPASE*->
- **GCA_000943515.2; Amycolatopsis orientalis; counts= 1; multicellularity status: TRUE**

  - EAD1+Trypsin*->EAD1+STAND_NTPase->STAND_NTPase+wHTH+TPRs+CASPASE->
- **GCF_000818715.1; Vibrio jasicida; counts= 1; multicellularity status: FALSE**
  - ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->
- **GCA_000972385.1; Streptomyces sp. WM6386; counts= 1; multicellularity status: TRUE**
  - EAD1+CASPASE->ZnF->E1(active)+E1_C_unk->EAD1+YukDl-Nterm+UB+E2*->JAB-N+JAB->?->CDC48-like->
- **GCF_000981895.1; Streptomyces odonnellii; counts= 1; multicellularity status: TRUE**
  - EAD1+Pkinase*->
- **GCF_000985995.1; Neorhizobium galegae; counts= 1; multicellularity status: FALSE**
  - EAD1+Trypsin*->
- **GCA_000988565.1; Myxococcus fulvus; counts= 1; multicellularity status: TRUE**
  - EAD1+Trypsin*->
- **GCF_001182915.1; Kitasatospora sp. MY 5-36; counts= 1; multicellularity status: NA**
  - EAD1+Trypsin*->||<-?||STAND_NTPase->STAND_NTPase+wHTH+TPRs+AB_hydrolase->
- **GCF_000472985.1; Bradyrhizobium japonicum; counts= 1; multicellularity status: TRUE**
  - Trypsin+EAD1+helical_region*->
- **GCF_000739635.1; Verrucomicrobium sp. BvORR034; counts= 1; multicellularity status: FALSE**
  - VMAP-C->MoxR->vWA+sGTP_APGTPase+COR+EAD1+Trypsin*->
- **GCF_000158915.1; Streptomyces himastatinicus; counts= 1; multicellularity status: TRUE**
  - EAD1+Trypsin*->
- **GCF_000261805.1; Bradyrhizobium yuanmingense; counts= 1; multicellularity status: TRUE**
  - EAD1+Trypsin*->||<-EAD5+Trypsin<-STAND_NTPase+wHTH+TPRs
- **GCA_002217335.1; Flavobacterium hydatis; counts= 1; multicellularity status: FALSE**
  - DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1->?->EAD1+Trypsin*->Endonuclease_NS(HNH)->
- **GCF_000763825.1; Paracoccus sanguinis; counts= 1; multicellularity status: NA**
  - EAD1+Trypsin*->
- **GCA_003387095.1; Archangium gephyra; counts= 1; multicellularity status: TRUE**
  - EAD1+TIR*->
- **GCF_001043915.1; Methylobacterium aquaticum; counts= 1; multicellularity status: TRUE**
  - EAD1+Trypsin+??*->TM+Endonuclease_NS(HNH)->
- **GCA_001277295.1; Anabaena sp. WA102; counts= 1; multicellularity status: TRUE**

  - EAD1+Trypsin->TM+TM+TM->EAD1+TPRs*->

- **GCA_001280015.1; Streptomyces sp. MMG1121; counts= 1; multicellularity status: TRUE**
  - EAD1+CASPASE->ZnF->E1(active)+E1_C_unk->EAD1+YukDl-Nterm+UB+E2*->JAB-N+JAB->?->CDC48-like->
- **GCF_001421075.1; Frankia sp. CpI1-P; counts= 1; multicellularity status: TRUE**
  - EAD2+EAD1*->
- **GCA_001422775.1; Methylobacterium sp. Leaf87; counts= 1; multicellularity status: TRUE**
  - GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->
- **GCA_001424165.1; Massilia sp. Leaf139; counts= 1; multicellularity status: NA**
  - EAD1+Trypsin->EAD1+P-loop_NTPase*->STAND_NTPase+wHTH+TPRs->
- **GCA_001422925.1; Microbacterium sp. Leaf288; counts= 1; multicellularity status: NA**
  - EAD1+Trypsin*->?->STAND_NTPase+wHTH+TPRs->
- **GCA_001426195.1; Sphingomonas sp. Leaf339; counts= 1; multicellularity status: FALSE**
  - Trypsin+Endonuclease_NS(HNH)->EAD1+Trypsin*->?->STAND_NTPase+TM+Endonuclease_NS(HNH)->
- **GCA_001428505.1; Terrabacter; counts= 1; multicellularity status: NA**
  - EAD1+Trypsin->EAD1+STAND_NTPase*->STAND_NTPase+wHTH+TPRs->
- **GCA_001429185.1; Terrabacter; counts= 1; multicellularity status: NA**
  - EAD1+Trypsin*->EAD1+STAND_NTPase->STAND_NTPase+wHTH+TPRs->
- **GCA_001401405.1; Pseudomonas syringae group genomosp. 3; counts= 1; multicellularity status: FALSE**
  - ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->
- **GCA_001485435.1; Deinococcus grandis; counts= 1; multicellularity status: NA**
  - EAD1*->
- **GCA_001509775.1; Streptomyces violaceusniger; counts= 1; multicellularity status: TRUE**
  - EAD1+CASPASE*->
- **GCA_001533325.1; Burkholderia ubonensis; counts= 1; multicellularity status: FALSE**
  - ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->
- **GCF_001547895.1; Pseudomonas sp. Os17; counts= 1; multicellularity status: NA**
  - GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->
- **GCA_001547895.1; Pseudomonas sp. Os17; counts= 1; multicellularity status: NA**
  - GAP1-N1+GAP1-M+GAP1-C+EAD1->CASPASE+EAD1*->
- **GCF_001586755.1; Cylindrospermopsis raciborskii; counts= 1; multicellularity status: NA**

  - RHH->EAD1+Trypsin*->

- **GCA_001548455.1; Fischerella sp. NIES-3754; counts= 1; multicellularity status: NA**
  - EAD1+CASPASE->EAD1+TPRs*->
- **GCA_001625455.1; Pseudomonas fluorescens; counts= 1; multicellularity status: FALSE**
  - PNP_UDP_1+EAD1*->GAP2->ZnR+DO-GTPase2->
- **GCA_001636575.1; Frankia casuarinae; counts= 1; multicellularity status: TRUE**
  - EAD1+cNMP_cyclase+TIR*->
- **GCF_001641335.1; Bradyrhizobium stylosanthis; counts= 1; multicellularity status: TRUE**
  - Trypsin+EAD1+helical_region*->
- **GCF_001650215.1; Streptomyces sp. RTd22; counts= 1; multicellularity status: TRUE**
  - EAD1+Trypsin*->VMAP-M0+VMAP-C->MoxR->
- **GCA_001693485.1; Bradyrhizobium sp. LMTR 3; counts= 1; multicellularity status: TRUE**
  - Trypsin+EAD1+helical_region*->
- **GCF_001636565.1; Frankia sp. EI5c; counts= 1; multicellularity status: TRUE**
  - pntlT4_fusion_domain+EAD1*->
- **GCA_001651875.1; Sinorhizobium saheli; counts= 1; multicellularity status: TRUE**
  - GAP1-N1+GAP1-M+GAP1-C+EAD1->CASPASE+EAD1*->
- **GCA_001672445.1; Mesorhizobium sp. WSM3873; counts= 1; multicellularity status: TRUE**
  - EAD1+Trypsin*->?->STAND_NTPase+wHTH+TPRs->
- **GCA_001514035.1; Streptomyces yokosukanensis; counts= 1; multicellularity status: TRUE**
  - EAD1+CASPASE->ZnF->E1(active)+E1_C_unk->EAD1+YukDl-Nterm+UB+E2*->JAB-N+JAB->?->CDC48-like->
- **GCA_001676615.1; Labrys sp. WJW; counts= 1; multicellularity status: NA**
  - EAD1+Trypsin*->
- **GCF_001624695.1; Labrenzia sp. OB1; counts= 1; multicellularity status: FALSE**
  - EAD1+Trypsin*->
- **GCA_001650175.1; Opitutaceae bacterium TSB47; counts= 1; multicellularity status: NA**
  - CASPASE+EAD1*->
- **GCF_001718095.1; Vibrio cholerae; counts= 1; multicellularity status: FALSE**
  - PNP_UDP_1+EAD1*->GAP2->ZnR+DO-GTPase2->DO-GTPase1->
- **GCA_001727475.1; Vibrio parahaemolyticus; counts= 1; multicellularity status: FALSE**

  - GAP2->ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->

- **GCA_001735805.1; Streptomyces puniciscabiei; counts= 1; multicellularity status: TRUE**
  - *
- **GCF_001748165.1; Streptomyces sp. SPMA113; counts= 1; multicellularity status: TRUE**
  - EAD1+CASPASE*->
- **GCA_001756285.1; Frankia sp. CgIM4; counts= 1; multicellularity status: NA**
  - EAD1+cNMP_cyclase+TIR*->
- **GCA_001758345.1; Acinetobacter towneri; counts= 1; multicellularity status: NA**
  - EAD1+??*->?->ZnR+DO-GTPase2->DO-GTPase1->
- **GCA_001866675.1; Streptomyces sp. MUSC 14; counts= 1; multicellularity status: TRUE**
  - ZnF->E1(active)+E1_C_unk->EAD1+YukDl-Nterm+UB+E2*->JAB-N+JAB->?->CDC48-like->
- **GCA_001866665.1; Streptomyces sp. MUSC 1; counts= 1; multicellularity status: TRUE**
  - EAD1+CASPASE->ZnF->E1(active)+E1_C_unk->EAD1+YukDl-Nterm+UB+E2*->JAB-N+JAB->?->CDC48-like->
- **GCA_001904645.1; Fischerella major; counts= 1; multicellularity status: NA**
  - EAD1+CASPASE->EAD1+TPRs*->
- **GCA_001904675.1; Scytonema sp. HK-05; counts= 1; multicellularity status: TRUE**
  - TCAD3+TCAD4+CASPASE+EAD1*->EAD1+VMAP-M1+VMAP-C->MoxR->vWA+Beta-rich+HTH+FGS-fold_domain->
- **GCA_900111765.1; Myxococcus fulvus; counts= 1; multicellularity status: TRUE**
  - EAD1+Trypsin*->
- **GCA_001942465.1; Actinomadura sp. CNU-125; counts= 1; multicellularity status: TRUE**
  - ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->
- **GCF_001942465.1; Actinomadura sp. CNU-125; counts= 1; multicellularity status: TRUE**
  - ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1->CASPASE+EAD1*->
- **GCA_001983015.1; Frankia sp. CcI156; counts= 1; multicellularity status: NA**
  - EAD1+cNMP_cyclase+TIR*->
- **GCA_002007105.1; Hymenobacter sp. CRA2; counts= 1; multicellularity status: FALSE**
  - ZnR+DO-GTPase2->?->?->GAP1-N1+GAP1-M+GAP1-C+PNP_UDP_1+EAD1*->
- **GCA_002021875.1; Streptomyces hygroscopicus; counts= 1; multicellularity status: TRUE**
  - EAD1+CASPASE*->
- **GCF_000725495.1; Streptomyces aureus; counts= 1; multicellularity status: TRUE**

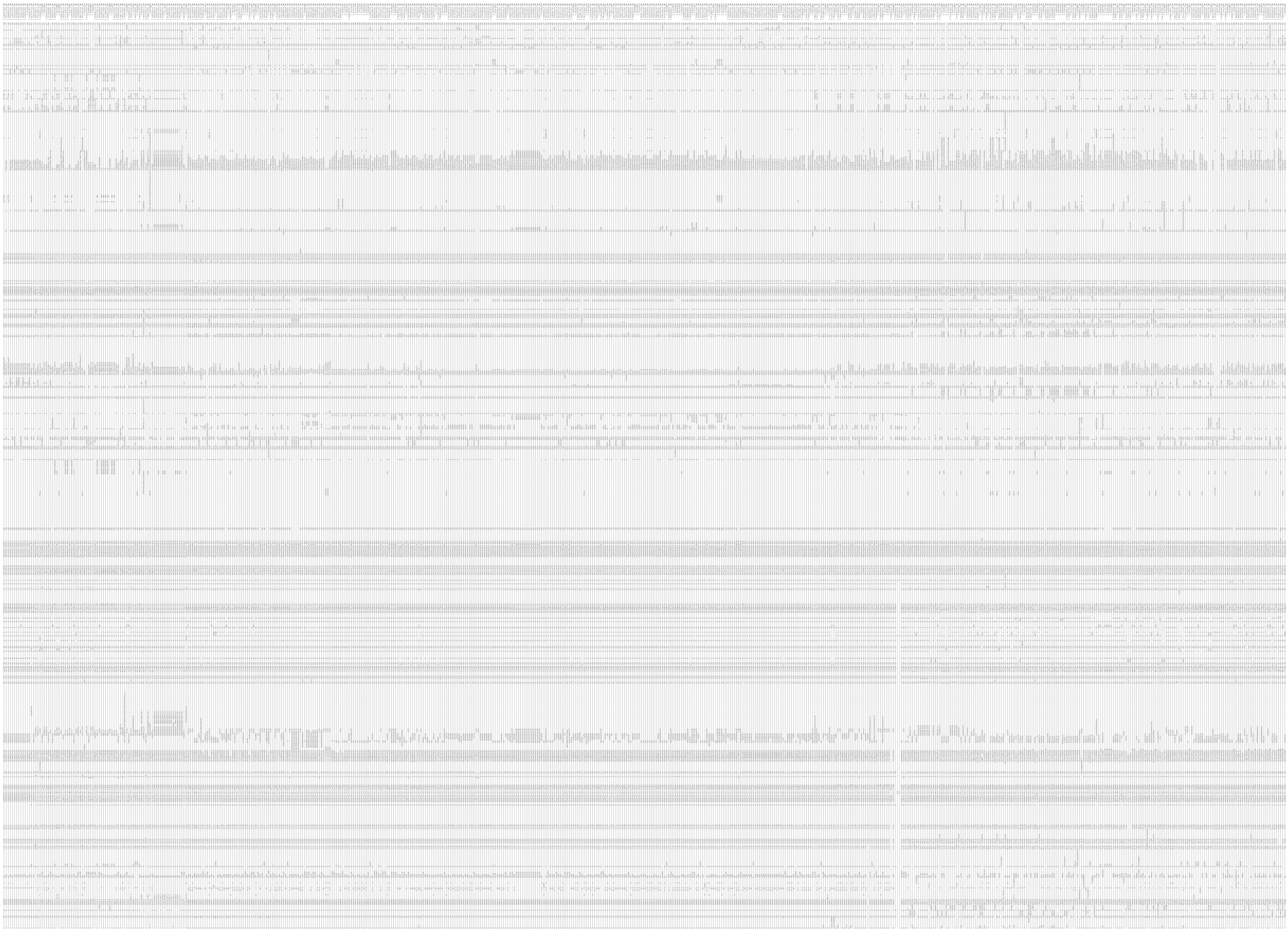
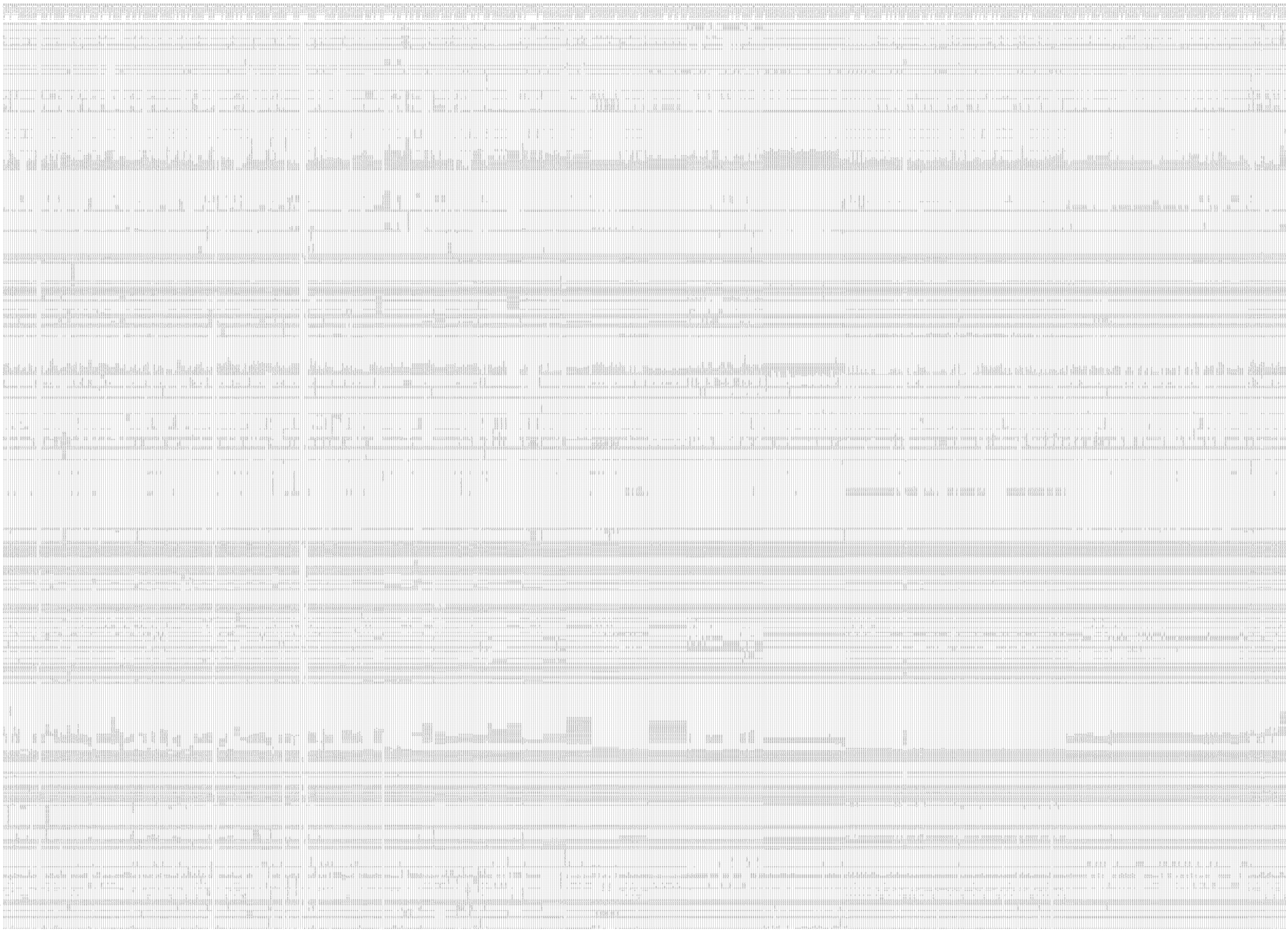
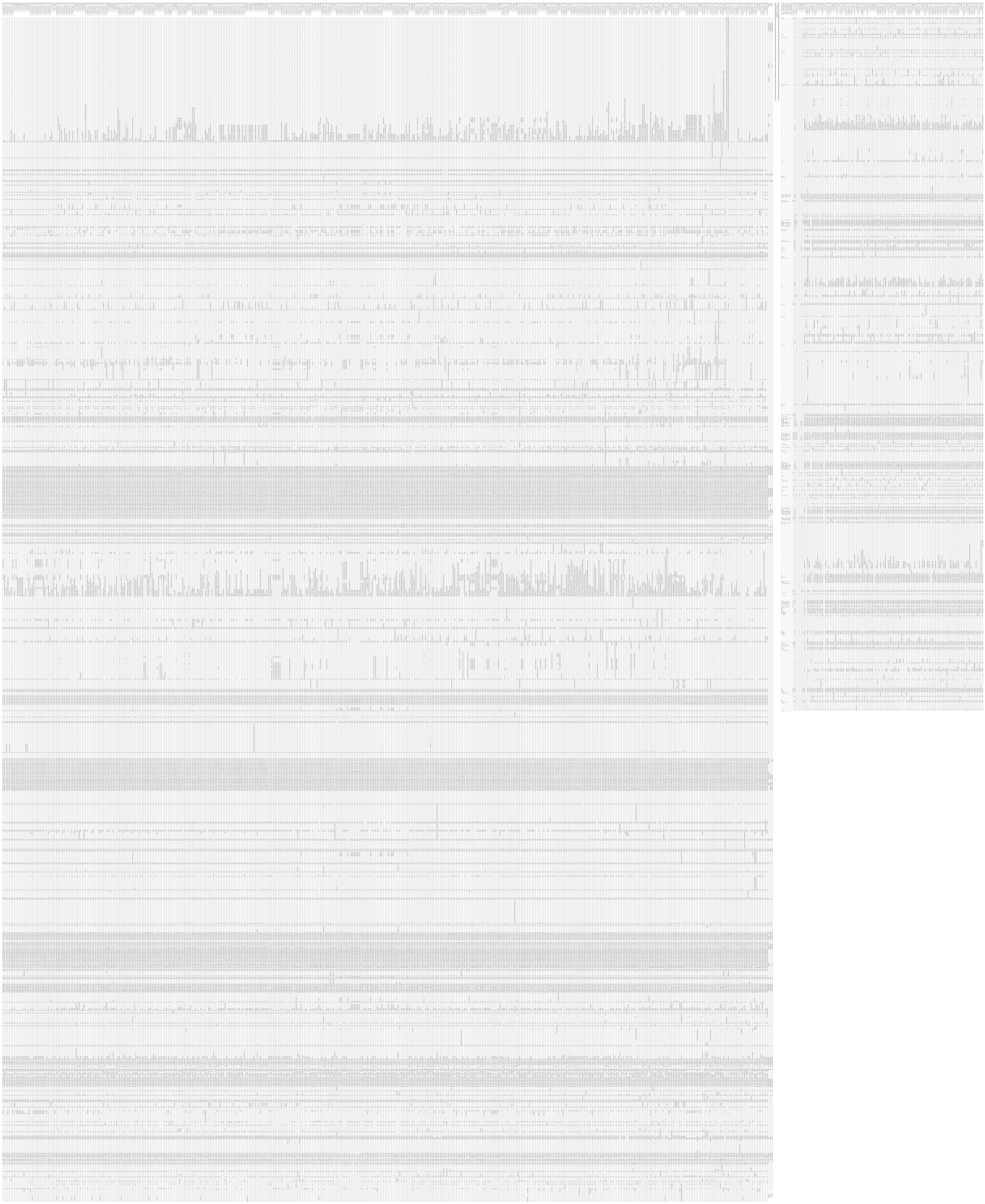
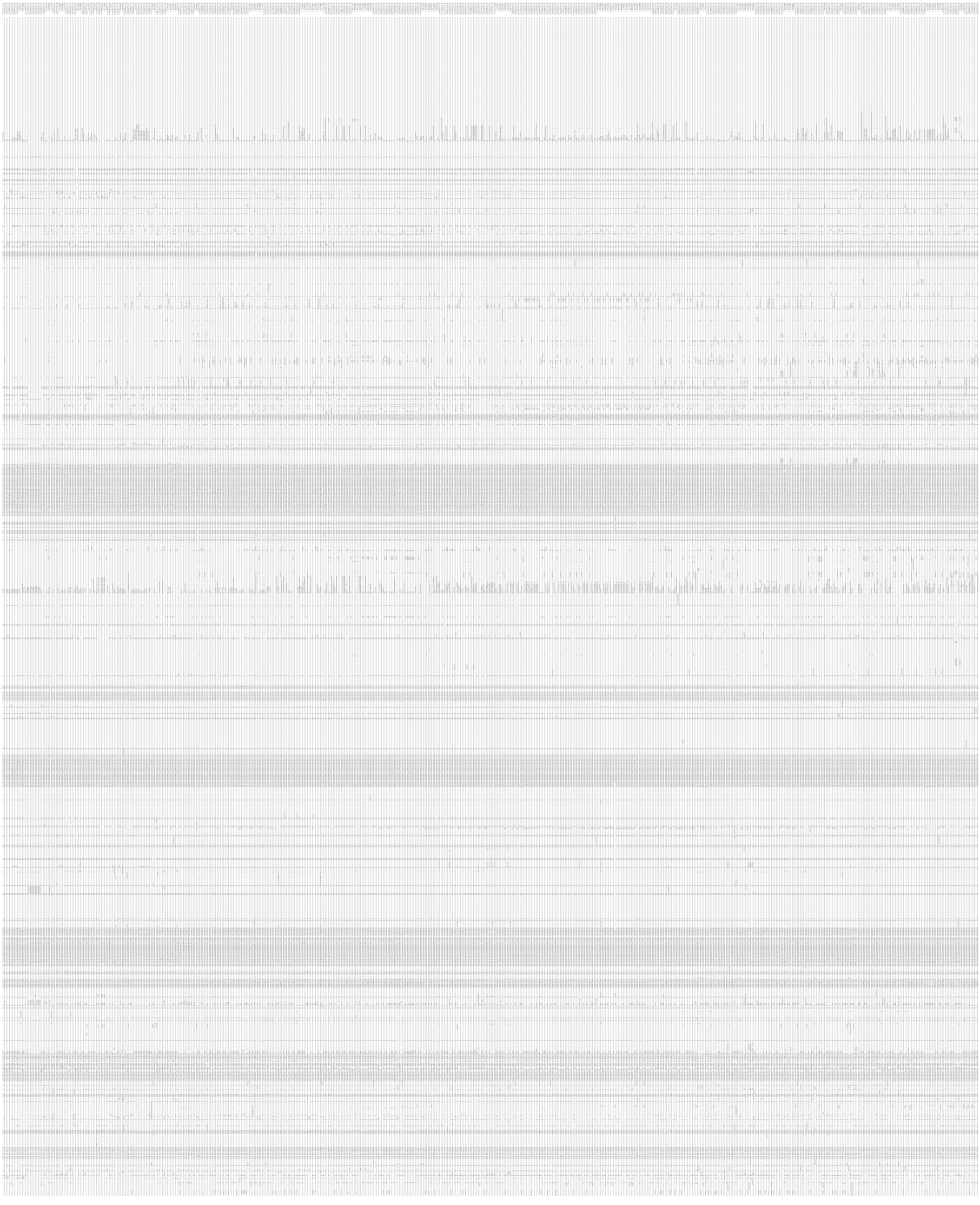
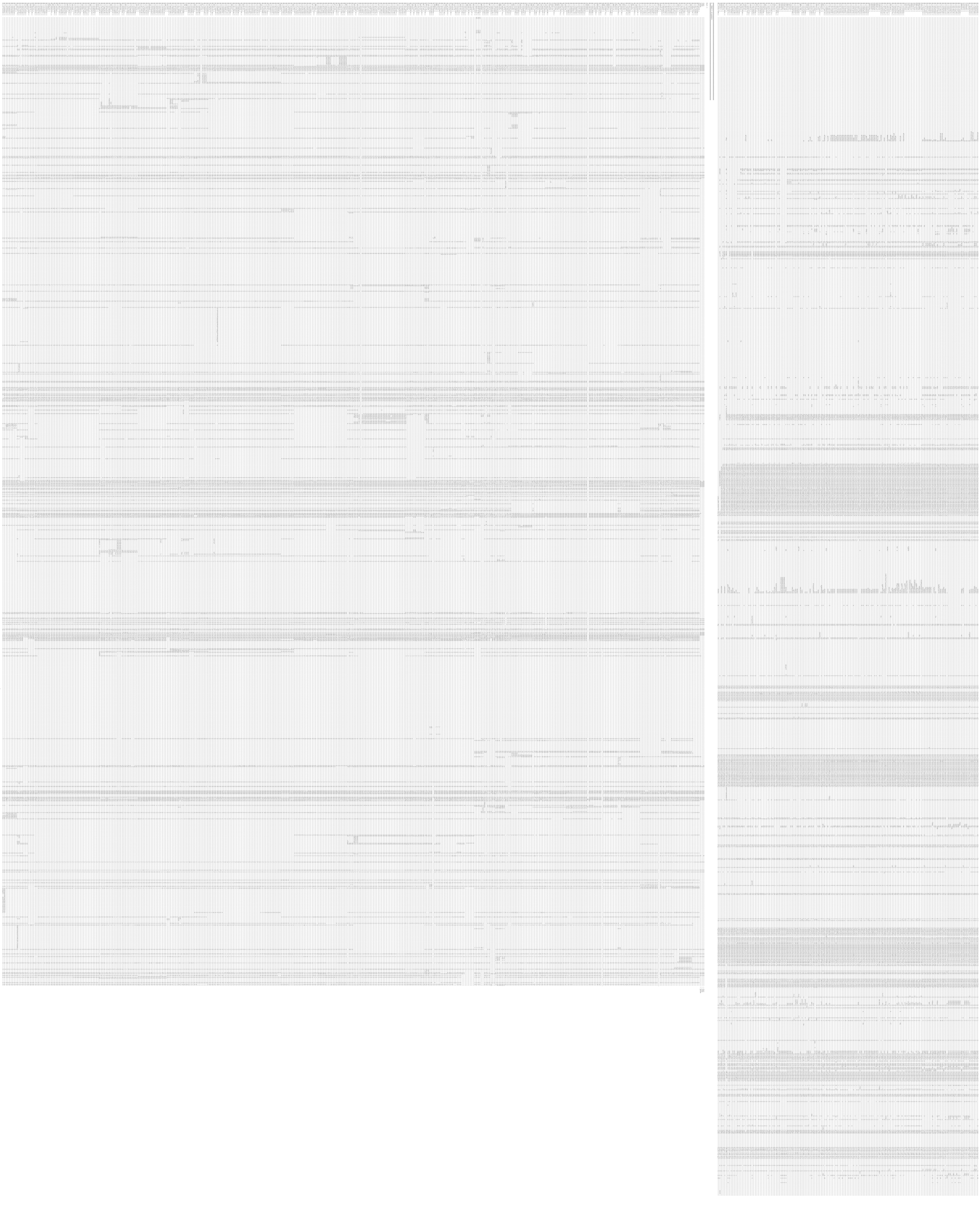
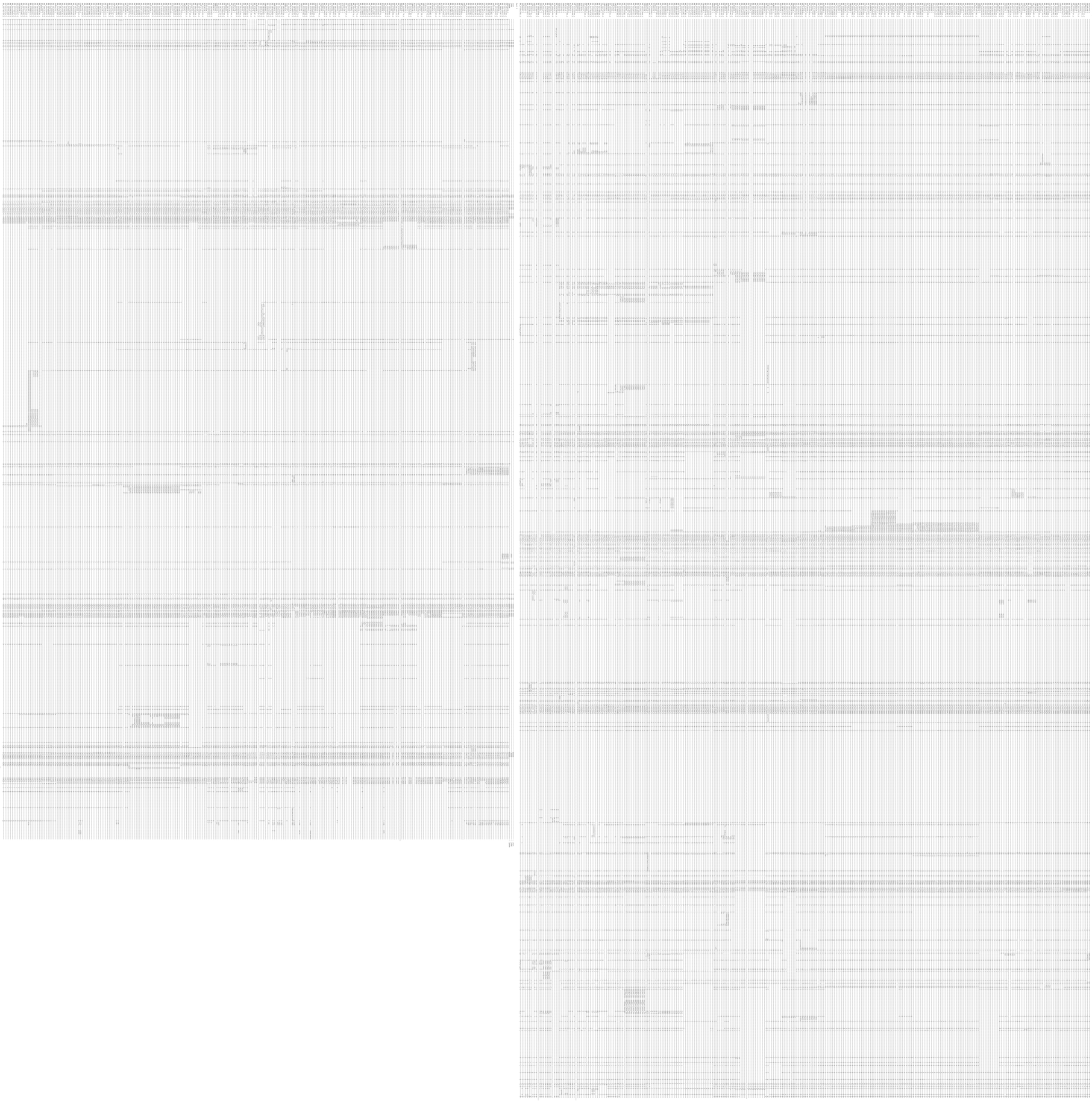
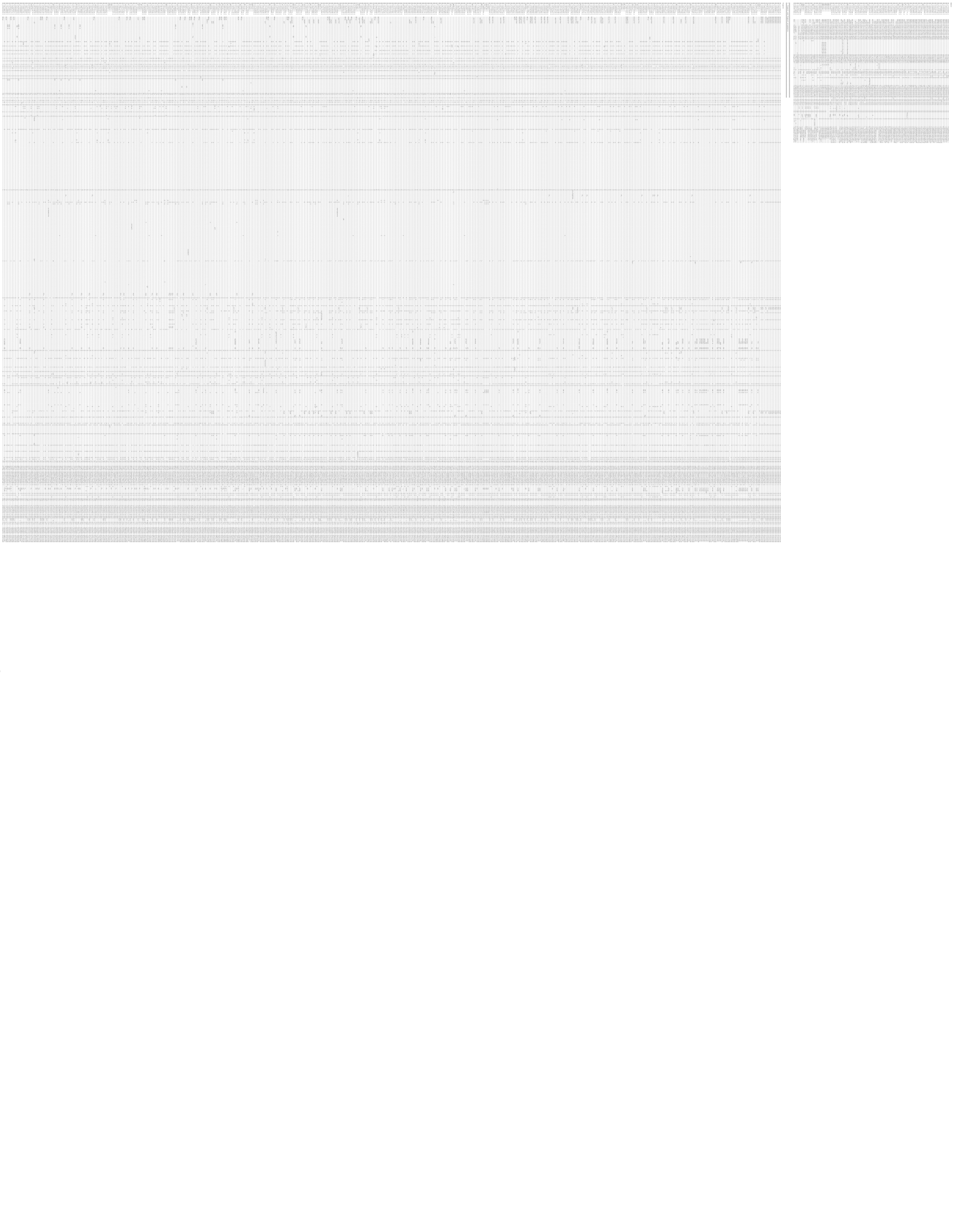
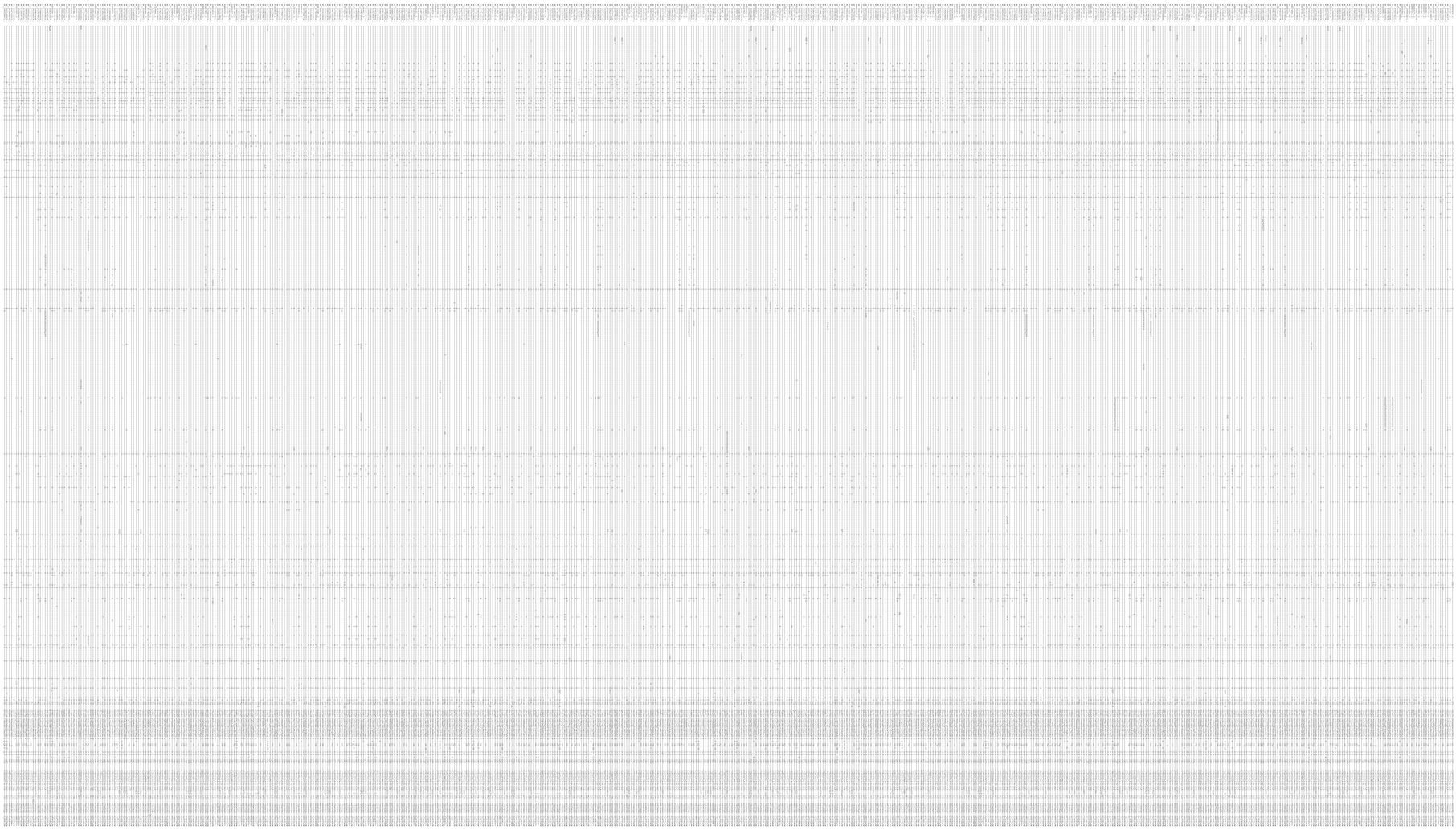
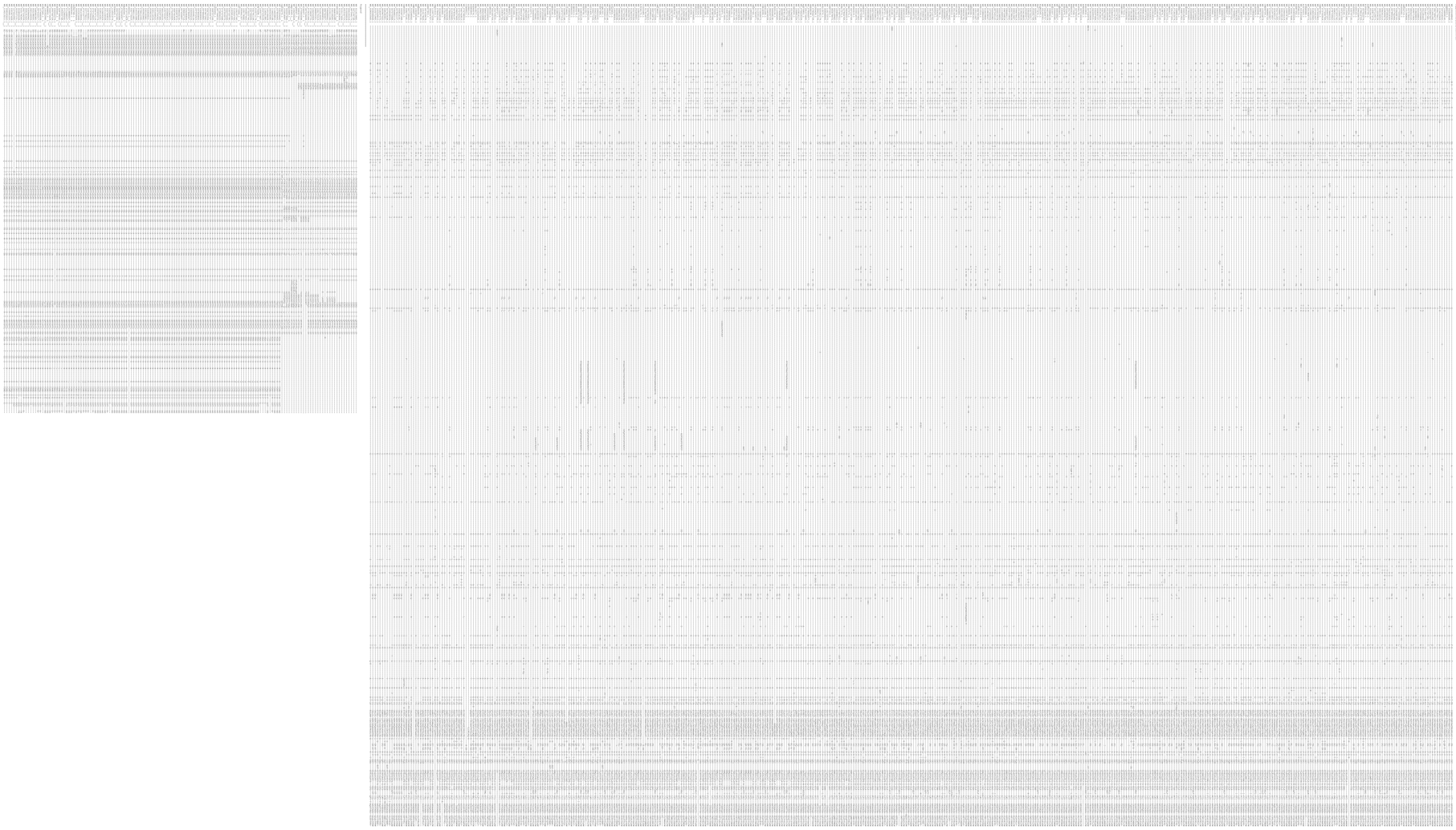
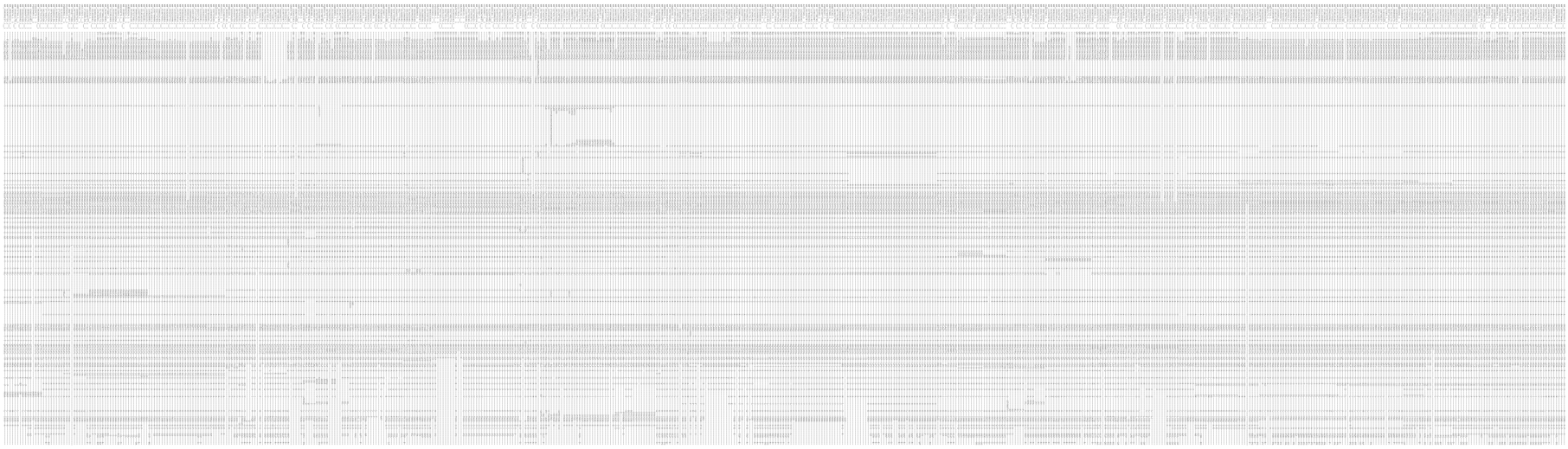
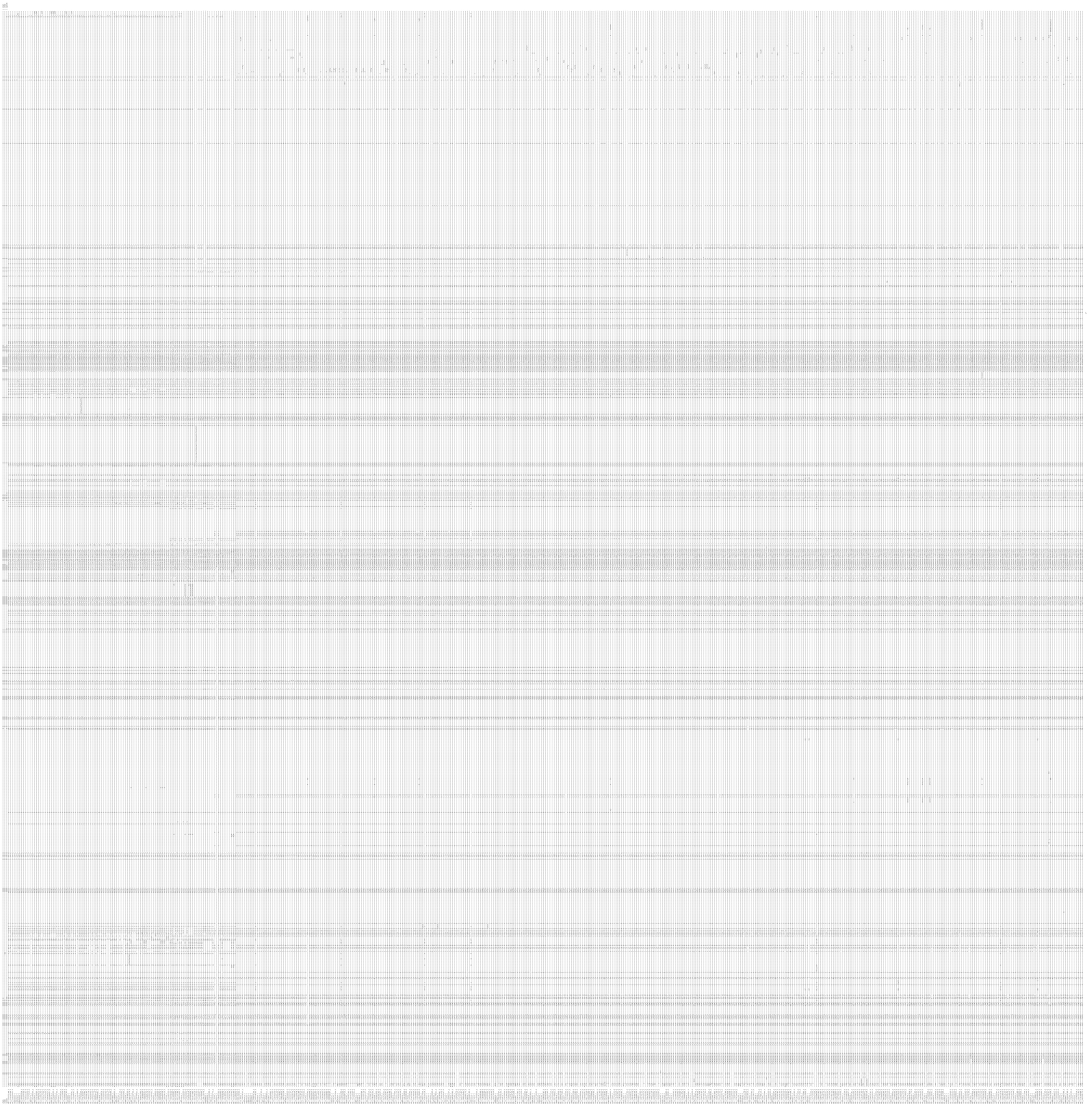
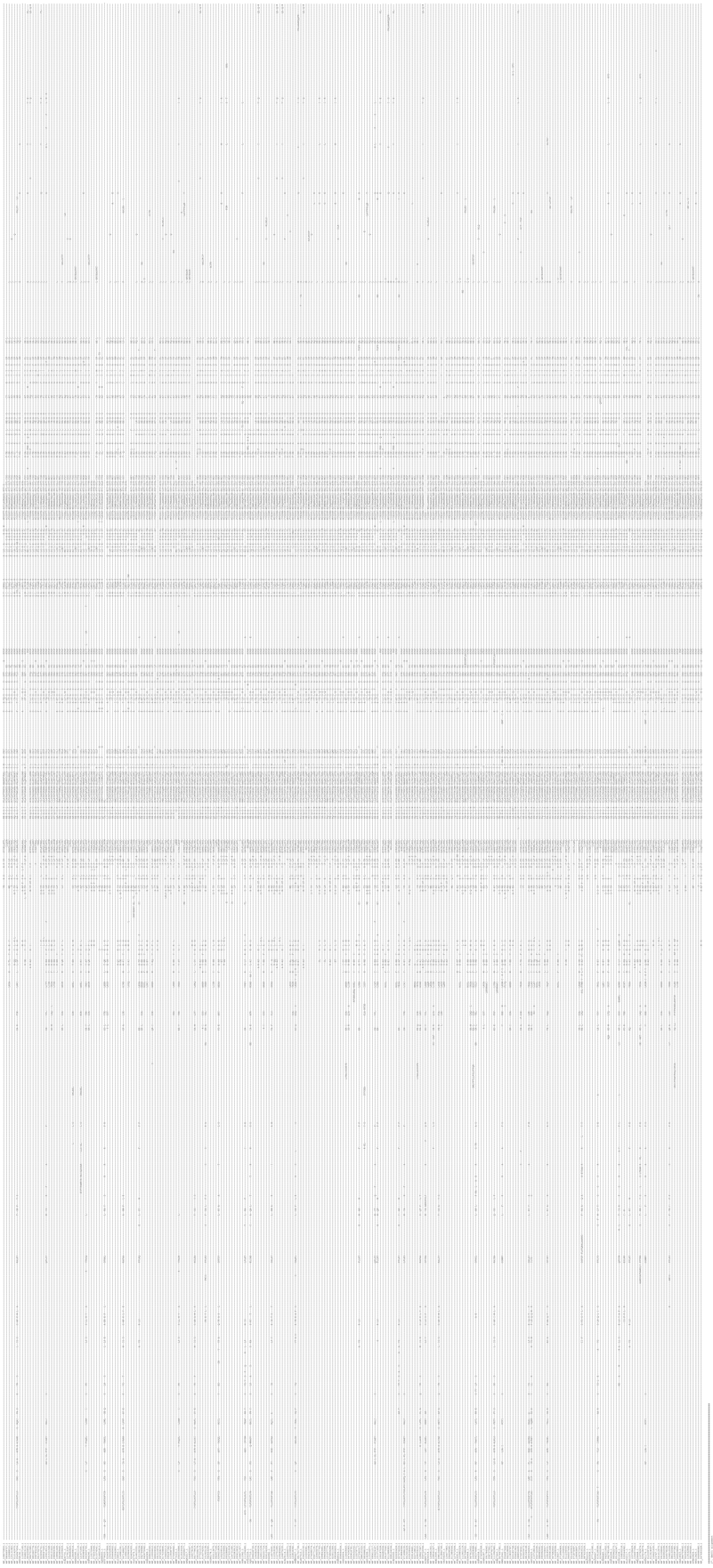
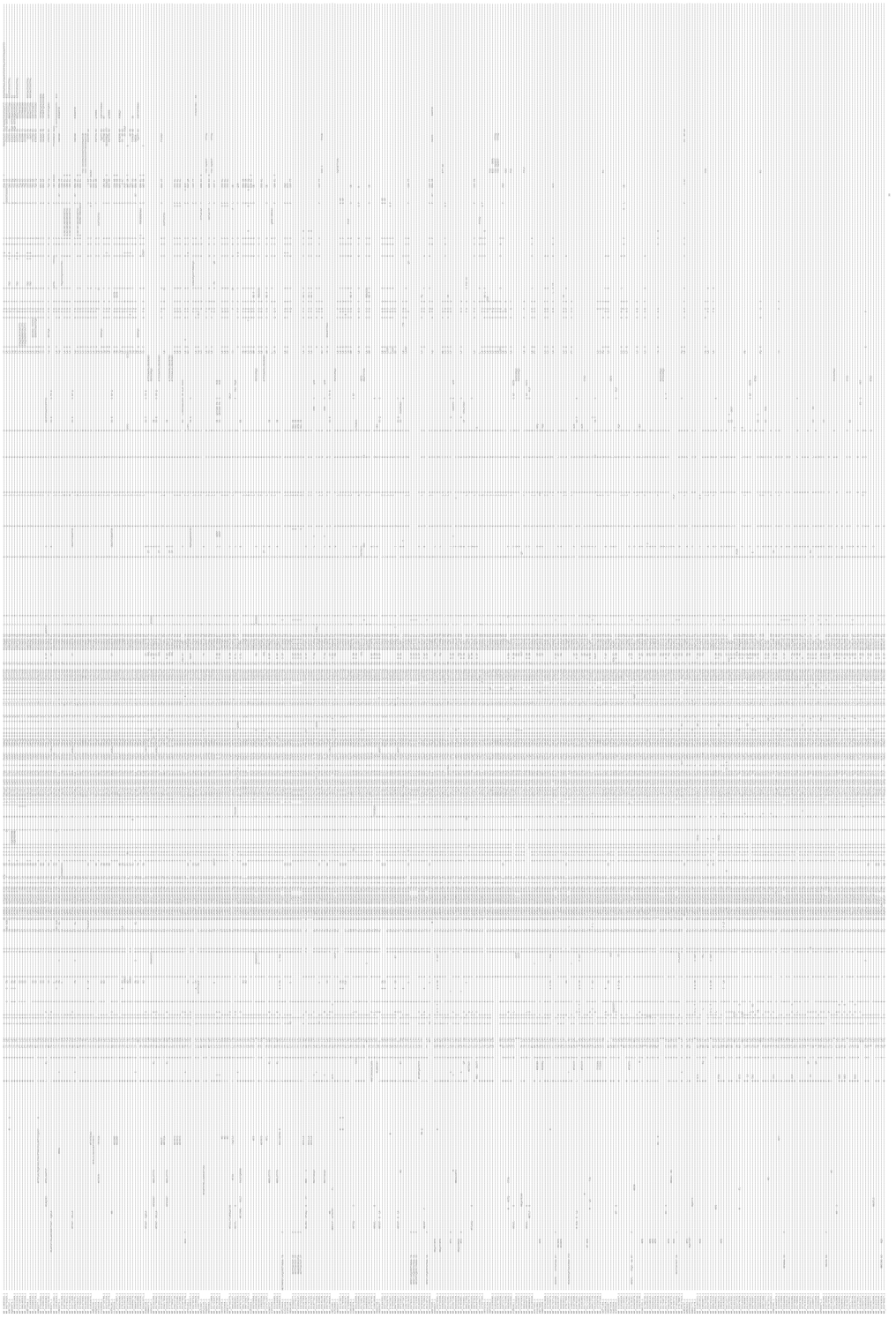
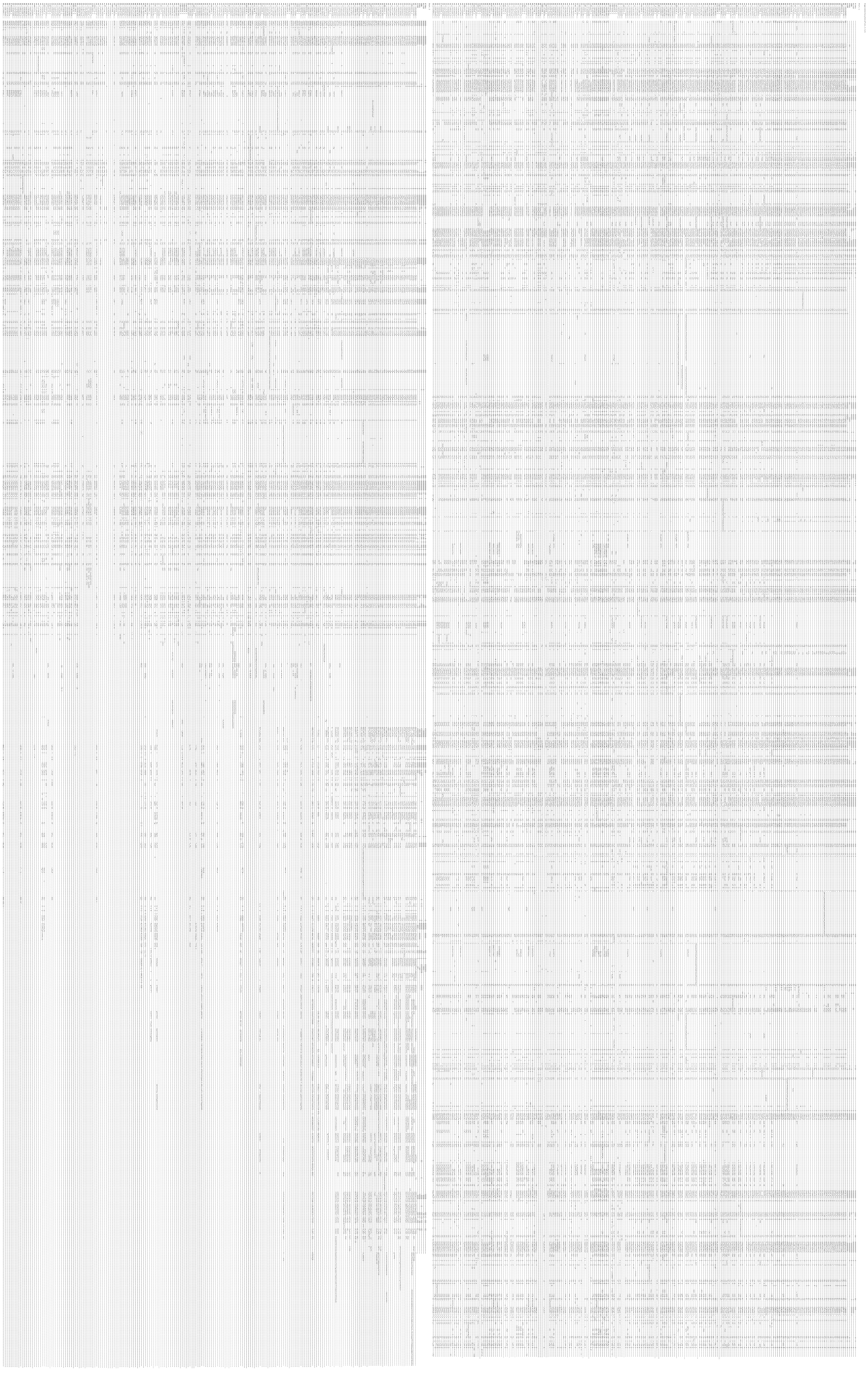
  - EAD1+Trypsin*->

- **GCA_001983975.1; Streptomyces autolyticus; counts= 1; multicellularity status: TRUE**
  - EAD1+CASPASE*->
- **GCA_002326205.1; Pseudomonas; counts= 1; multicellularity status: FALSE**
  - ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->
- **GCF_002071875.1; Burkholderia cenocepacia; counts= 1; multicellularity status: FALSE**
  - ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1->CASPASE+EAD1*->
- **GCA_002071905.1; Burkholderia cenocepacia; counts= 1; multicellularity status: FALSE**
  - ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->
- **GCF_001533325.1; Burkholderia ubonensis; counts= 1; multicellularity status: FALSE**
  - ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1->CASPASE+EAD1*->
- **GCF_000067165.1; Sorangium cellulosum; counts= 1; multicellularity status: TRUE**
  - STAND_NTPase+wHTH+TPRs+BetaPropeller+EAD1->EAD1+Trypsin*->
- **GCF_000834545.1; Pseudomonas fluorescens; counts= 1; multicellularity status: FALSE**
  - ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->
- **GCF_001655155.1; Mycobacteroides immunogenum; counts= 1; multicellularity status: NA**
  - PNP_UDP_1+EAD1*->
- **GCF_001277295.1; Anabaena sp. WA102; counts= 1; multicellularity status: TRUE**
  - EAD1+Trypsin*->TM+TM+TM->EAD1+TPRs->
- **GCF_001589285.1; Sorangium cellulosum; counts= 1; multicellularity status: TRUE**
  - EAD1+APATPase+wHTH+TPRs+BetaPropeller+EAD7*->||<-EAD7+CASPASE
- **GCF_000789435.1; Aphanizomenon flos-aquae; counts= 1; multicellularity status: NA**
  - EAD1+Trypsin->TM+TM+TM->EAD1+BetaPropeller*->
- **GCF_000935305.1; Pseudomonas oryzihabitans; counts= 1; multicellularity status: FALSE**
  - ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1->CASPASE+EAD1*->
- **GCA_001296055.1; Novosphingobium sp. AAP93; counts= 1; multicellularity status: FALSE**
  - EAD1+Trypsin*->
- **GCF_001422775.1; Methylobacterium sp. Leaf87; counts= 1; multicellularity status: TRUE**
  - GAP1-N1+GAP1-M+GAP1-C+EAD1->CASPASE+EAD1*->
- **GCF_001424165.1; Massilia sp. Leaf139; counts= 1; multicellularity status: NA**

  - EAD1+Trypsin*->EAD1+P-loop_NTPase->STAND_NTPase+wHTH+TPRs->
- **GCF_001428505.1; Terrabacter sp. Root181; counts= 1; multicellularity status: TRUE**
  - EAD1+Trypsin*->EAD1+STAND_NTPase->STAND_NTPase+wHTH+TPRs->
- **GCF_001429645.1; Terrabacter sp. Soil810; counts= 1; multicellularity status: NA**
  - EAD1+Trypsin*->EAD1+STAND_NTPase->STAND_NTPase+wHTH+TPRs->
- **GCF_001469165.1; Thiohalocapsa sp. ML1; counts= 1; multicellularity status: TRUE**
  - ZnF->E1(active)+E1_C_unk->TIR->EAD1+YukDl-Nterm+UB+E2*->
- **GCF_001548455.1; Fischerella sp. NIES-3754; counts= 1; multicellularity status: NA**
  - EAD1+CASPASE*->EAD1+TPRs->
- **GCF_001655615.1; Pseudomonas sp. GR 6-02; counts= 1; multicellularity status: NA**
  - EAD1+Trypsin*->?->STAND_NTPase+wHTH+TPRs->
- **GCF_001767235.1; Moorea producens; counts= 1; multicellularity status: TRUE**
  - EAD1+VMAP-M1+FGS-fold_domain->EAD1->VMAP-M1+FGS-fold_domain->EAD1+VMAP-M1+FGS-fold_domain*->
- **GCF_001854205.1; Moorea producens; counts= 1; multicellularity status: TRUE**
  - EAD1+CASPASE+FGS-fold_domain*->
- **GCF_001854805.1; Frankia sp. BMG5.36; counts= 1; multicellularity status: NA**
  - EAD1+APATPase+wHTH+TPRs*->
- **GCF_900117425.1; Novosphingobium sp. NDB2Meth1; counts= 1; multicellularity status: FALSE**
  - EAD1+Trypsin*->
- **GCF_001904745.1; Calothrix sp. HK-06; counts= 1; multicellularity status: NA**
  - CASPASE+EAD1*->EAD1->
- **GCF_000022085.1; Methylobacterium nodulans; counts= 1; multicellularity status: TRUE**
  - <-Trypsin+Endonuclease_NS(HNH)||EAD1+Trypsin*->
- **GCF_000379525.1; Lamprocystis purpurea; counts= 1; multicellularity status: TRUE**
  - EAD1+Trypsin*->EAD1+STAND_NTPase->STAND_NTPase+wHTH+TPRs->
- **GCF_001050195.2; Anaerolinea thermolimosa; counts= 1; multicellularity status: NA**
  - EAD1+Trypsin*->
- **GCF_001651875.1; Sinorhizobium saheli; counts= 1; multicellularity status: TRUE**
  - GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->
- **GCF_001904645.1; Fischerella major; counts= 1; multicellularity status: NA**

  - EAD1+CASPASE*->EAD1+TPRs->

- **GCF_002091475.1; Sphingomonas azotifigens; counts= 1; multicellularity status: FALSE**
  - EAD1+Trypsin*->
- **GCF_000503075.1; Mesorhizobium sp. LSHC422A00; counts= 1; multicellularity status: TRUE**
  - EAD1+Trypsin+??+TM+TM+TM+low_complexity*->
- **GCF_000503035.1; Mesorhizobium sp. LSHC412B00; counts= 1; multicellularity status: TRUE**
  - EAD1+Trypsin+??+CarboxypepD-reg-IG+papain-like_peptidoglycan_hydrolase*->
- **GCA_002099355.1; Frankia casuarinae; counts= 1; multicellularity status: TRUE**
  - EAD1+cNMP_cyclase+TIR*->
- **GCA_002099325.1; Frankia sp. KB5; counts= 1; multicellularity status: NA**
  - EAD1+cNMP_cyclase+TIR*->
- **GCF_001017755.1; Frankia coriariae; counts= 1; multicellularity status: TRUE**
  - TIR+EAD1*->
- **GCA_002143185.1; Acinetobacter baumannii; counts= 1; multicellularity status: FALSE**
  - ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->
- **GCF_002154275.1; Streptomyces castelarensis; counts= 1; multicellularity status: TRUE**
  - EAD1+CASPASE*->
- **GCF_002155885.1; Streptomyces rhizosphaericus; counts= 1; multicellularity status: TRUE**
  - EAD1+CASPASE*->
- **GCF_002157355.1; Variovorax sp. JS1663; counts= 1; multicellularity status: NA**
  - EAD1+Trypsin*->EAD1+STAND_NTPase->STAND_NTPase+wHTH+TPRs->
- **GCA_002163975.1; Nostocales cyanobacterium HT-58-2; counts= 1; multicellularity status: NA**
  - MoxR->helical_region+vWA->?->TIR+EAD1*->
- **GCF_002163975.1; Nostocales cyanobacterium HT-58-2; counts= 1; multicellularity status: NA**
  - EAD1+P-loop_NTPase(i)*->MoxR->helical_region+vWA->
- **GCA_002212765.2; Haliangium sp. UPWRP_2; counts= 1; multicellularity status: TRUE**
  - EAD7+EAD1+Trypsin*->
- **GCA_900188005.1; Actinoplanes regularis; counts= 1; multicellularity status: TRUE**
  - vWA->?->?->EAD1+Trypsin*->
- **GCA_900188295.1; Paracoccus sediminis; counts= 1; multicellularity status: NA**

  - EAD1+Trypsin->EAD1+STAND_NTPase*->STAND_NTPase+wHTH+TM+TM->
- **GCA_004310385.1; Paracoccus sediminis; counts= 1; multicellularity status: NA**
  - EAD1+Trypsin*->EAD1+STAND_NTPase->STAND_NTPase+wHTH+TM+TM->
- **GCA_900101905.1; Myxococcus virescens; counts= 1; multicellularity status: TRUE**
  - EAD1+Trypsin*->
- **GCF_900111115.1; Giesbergeria anulus; counts= 1; multicellularity status: FALSE**
  - ZnR+DO-GTPase2->DO-GTPase1->GAP1-N1+GAP1-M+GAP1-C+EAD1*->CASPASE+EAD1->
- **GCA_900104165.1; Phyllobacterium sp. YR620; counts= 1; multicellularity status: TRUE**
  - EAD1+Trypsin*->
- **GCF_900112185.1; Bosea sp. DSM 18164; counts= 1; multicellularity status: TRUE**
  - EAD1+Trypsin*->
- **GCA_900095025.1; Acinetobacter albensis; counts= 1; multicellularity status: NA**
  - EAD1+??*->?->ZnR+DO-GTPase2->DO-GTPase1->
- **GCA_900102195.1; Pseudonocardia oroxyli; counts= 1; multicellularity status: NA**
  - pntlT4_fusion_domain+EAD1+Trypsin*->
- **GCF_900100605.1; Sinosporangium album; counts= 1; multicellularity status: TRUE**
  - EAD1+CASPASE*->E1(active)+E1_C_unk->EAD1+YukDl-Nterm+UB+E2->JAB-N+JAB->
- **GCA_900100605.1; Sinosporangium album; counts= 1; multicellularity status: TRUE**
  - EAD1+CASPASE->E1(active)+E1_C_unk->EAD1+YukDl-Nterm+UB+E2*->JAB-N+JAB->?->CDC48-like->
- **GCA_900099985.1; Thermostaphylospora chromogena; counts= 1; multicellularity status: TRUE**
  - EAD1+CASPASE*->
- **GCA_900105695.1; Streptomyces melanosporofaciens; counts= 1; multicellularity status: TRUE**
  - *
- **GCF_900187555.1; Pseudomonas sp. Irchel s3f19; counts= 1; multicellularity status: NA**
  - PNP_UDP_1+EAD1*->GAP2->
- **GCA_002283555.1; Rubrivirga sp. SAORIC476; counts= 1; multicellularity status: NA**
  - EAD1+Trypsin(frag)*->
- **GCA_002300355.1; Streptomyces sp. TLI_235; counts= 1; multicellularity status: NA**
  - EAD1+Trypsin->EAD1+STAND_NTPase*->STAND_NTPase+wHTH+TPRs->
- **GCF_002300355.1; Streptomyces sp. TLI_235; counts= 1; multicellularity status: NA**

  - EAD1+Trypsin*->EAD1+STAND_NTPase->STAND_NTPase+wHTH+TPRs->
- **GCA_002303785.1; Rahnella victoriana; counts= 1; multicellularity status: NA**
  - EAD1+??*->
- **GCA_002305895.1; Myxococcus macrosporus; counts= 1; multicellularity status: TRUE**
  - EAD1+Trypsin*->
- **GCF_900112715.1; Nannocystis exedens; counts= 1; multicellularity status: TRUE**
  - EAD1+??*->
- **GCA_002368415.1; Calothrix sp. NIES-4105; counts= 1; multicellularity status: NA**
  - LRR_region+sGTP_APGTPase+COR+??+EAD1*->
- **GCF_002368455.1; Calothrix sp. NIES-4071; counts= 1; multicellularity status: TRUE**
  - LRR_region+sGTP_APGTPase+COR+??+EAD1*->
- **GCF_002407205.1; Rhodobacter sp. CZR27; counts= 1; multicellularity status: FALSE**
  - Trypsin->EAD1+Trypsin*->EAD1+HExxH+helical_region->TM+Endonuclease_NS(HNH)+LytR_C/SPOR->
- **GCA_900215205.1; Actinoplanes atraurantiacus; counts= 1; multicellularity status: TRUE**
  - Trypsin->EAD1+Trypsin+STAND_NTPase->EAD1+STAND_NTPase+TPRs*->
- **GCA_002591335.1; Streptomyces malaysiensis; counts= 1; multicellularity status: TRUE**
  - EAD1+CASPASE*->
- **GCA_002631205.1; Lewinella marina; counts= 1; multicellularity status: NA**
  - EAD1+Trypsin*->
- **GCA_002812405.1; Streptomyces sp. M56; counts= 1; multicellularity status: TRUE**
  - EAD1+CASPASE*->
- **GCA_002831565.1; Spirosoma sp. HA7; counts= 1; multicellularity status: NA**
  - EAD1+Trypsin*->EAD1+SIR2->STAND_NTPase+wHTH+TM+BetaPropeller->
- **GCF_002844445.1; Rhodobacter azotoformans; counts= 1; multicellularity status: FALSE**
  - Trypsin->EAD1+Trypsin*->EAD1+HExxH+helical_region->TM+Endonuclease_NS(HNH)+LytR_C/SPOR->