|  |  |  |
| --- | --- | --- |
| **Lineage****(Schoch et al., 2020)** | **Organisms** | **Type of FAAL-like domain (domain organization)** |
| **Amoebozoa** | L8HIJ4|*Acanthamoeba castellanii* | Bacterial/Plant FAAL |
| **Ancyromonadida** | **-** | **-** |
| **Apusozoa** | **-** | **-** |
| **Breviatea** | **-** | **-** |
| **CRuMs** | **-** | **-** |
| **Cryptophyceae** | **-** | **-** |
| **Discoba** | **-** | **-** |
| **Glaucocystophyceae** | **-** | **-** |
| **Haptista** | R1DLD1|*Emiliania huxleyi* | Bacterial/Plant FAAL |
| **Hemimastigophora** | **-** | **-** |
| **Malawimonadida** | **-** | **-** |
| **Metamonada** | **-** | **-** |
| **Opisthokonta** |
| * Aphelida
 | **-** | **-** |
| * Choanoflagellata
 | A9UP98|*Monosiga brevicollis*;F2U8X9|*Salpingoeca rosetta* | Opisthokonta FAAL-like domains(two-domain) |
| * Filasterea
 | A0A0D2UCG9|*Capsaspora owczarzaki* | Opisthokonta FAAL-like domains(three-domain) |
| * Fungi
 | Many organisms (except Basidiomycetes) | Opisthokonta FAAL-like domains(three-domain) |
| * Ichthyosporea
 | **-** | **-** |
| * Metazoa
 |   | Opisthokonta FAAL-like domains(three-domain) |
| * Rotosphaerida
 | **-** | **-** |
| Rhodelphea | **-** | **-** |
| Rhodophyta | **-** | **-** |
| **SAR group** |  |  |
| * Stramenophiles
* Alveolata
* Rhizaria
 | A0A067C5L3|*Saprolegnia parasitica*;A0A1V9Z9Z4|*Achlya hypogyna* | Bacterial/Plant FAAL |
| V4ZF64|Toxoplasma gondii;U6GWK7|*Eimeria acervuline* | Bacterial/Plant FAAL |
| **-** | **-** |
| **Viridiplantae** | A0A445HLB4|*Glycine soja*; A0A3Q0EXH4|*Vigna radiata*Q01KB0 |*Oryza sativa*; UPI000CE285CA|*Quercus suber*; UPI0011E53342|*Rhodamnia argentea* | Bacterial/Plant Bacterial/Plant fused to HemY/CatalaseDi-domain form (tandem FAAL-like) |