Oskar Protein
Bacteria
Non-Arthropod Eukaryota
Archea
A0A0G3CFD7_METBA | Methanosarcina barkeri CM1 | GDSL family lipase/acylhydrolase
R6T7B3_9BACE | Bacteroides sp. CAG:770 | GDSL-like protein
R5S0B3_9BACE | Bacteroides sp. CAG:545 | GDSL-like protein
A0A069S7Q5_9PORP | Parabacteroides distasonis str. 3776 Po2 i | Uncharacterized protein
A0A0J9FZD4_9PORP | Parabacteroides sp. D26 | Uncharacterized protein
A0A073IAZ3_9PORP | Porphyromonas sp. 31_2 | Uncharacterized protein
E1YW67_9PORP | Parabacteroides sp. 20_3 | GDSL-like protein
A0A0G1KN57_9BACT | candidate division WWE3 bacterium GW2011_GWC2_44_9 | Secreted protein
R5VMZ1_9FIRM | Firmicutes bacterium CAG:631 | GDSL-like protein
R2P1Z4_9ENTE | Enterococcus raffinosus ATCC 49464 | Uncharacterized protein
F2WJY6_9HYME | Messor pergandei | Oskar
F4WQN7_ACREC | Acromyrmex echinatior | Maternal effect protein oskar
A0A026WMY1_CERBI | Cerapachys biroi | Maternal effect protein oskar
E9IZ46_SOLIN | Solenopsis invicta | Putative uncharacterized protein
E2A7I8_CAMFO | Camponotus floridanus | Putative uncharacterized protein
A0A0J7KH44_LASNI | Lasius niger | Maternal effect protein oskar
E2BYH0_HARSA | Harpegnathos saltator | Putative uncharacterized protein
E1A883_NASVI | Nasonia vitripennis | Oskar
A0A0C9QHR7_9HYME | Fopius arisanus | Osk protein
K4MTL4_GRYBI | Gryllus bimaculatus | Oskar
E9I8K8_SOLIN | Solenopsis invicta | Putative uncharacterized protein
Q2PP79_AEDAE | Aedes aegypti | Oskar
B0WIV7_CULQU | Culex quinquefasciatus | Oskar
T1DTM7_ANOAQ | Anopheles aquasalis | Uncharacterized protein
W5JJ85_ANODA | Anopheles darlingi | Uncharacterized protein
A0A084WRU4_ANOSI | Anopheles sinensis | AGAP003545-PA-like protein
Q7PQJ3_ANOGA | Anopheles gambiae | AGAP003545-PA
U5EFJ8_9DIPT | Corethrella appendiculata | Putative oskar
W8CE30_CERCA | Ceratitis capitata | Maternal effect protein oskar
A0A0A1XRQ4_BACCU | Bactrocera cucurbitae | Maternal effect protein oskar
A0A034WRF5_BACDO | Bactrocera dorsalis | Maternal effect protein oskar
A0A0K8U7J3_BACLA | Bactrocera latifrons | Maternal effect protein oskar
A0A0L0CP24_LUCCU | Lucilia cuprina | Uncharacterized protein
T1PG45_MUSDO | Musca domestica | GDSL-like Lipase/Acylhydrolase
Q295Q4_DROPS | Drosophila pseudoobscura pseudoobscura | Uncharacterized protein, isoform A
A0A059PGF2_9MUSC | Drosophila pseudoobscura | GA10627
A0A059PF64_9MUSC | Drosophila pseudoobscura | GA10627
B4PTX6_DROYA | Drosophila yakuba | Uncharacterized protein
B4HKZ1_DROSE | Drosophila sechellia | GM23770
E8NH25_DROME | Drosophila melanogaster | RE24380p
A0A126GUR4_DROME | Drosophila melanogaster | Oskar, isoform D
B3P1W4_DROER | Drosophila erecta | GG13545
B3LZ06_DROAN | Drosophila ananassae | Uncharacterized protein
B4N815_DROWI | Drosophila willistoni | Uncharacterized protein
B4JTJ1_DROGR | Drosophila grimshawi | GH23955
B4K9E5_DROMO | Drosophila mojavensis | Uncharacterized protein
B4LXK5_DROVI | Drosophila virilis | Oskar
A1Y1T7_DROIM | Drosophila immigrans | Oskar
A0A0M4F3M8_DROBS | Drosophila busckii | Osk
A0A0J6BBM7_BREBE | Brevibacillus brevis | Lysophospholipase
A0A0H0SJ00_9BACL | Brevibacillus formosus | Lysophospholipase
J3A568_9BACL | Brevibacillus sp. BC25 | Lysophospholipase L1-like esterase
R5GT16_9FIRM | Eubacterium sp. CAG:786 | GDSL-like protein
R5LL12_9FIRM | Eubacterium sp. CAG:115 | GDSL-like protein
B7KKA6_CYAP7 | Cyanothece sp. (strain PCC 7424) | Lipolytic protein G-D-S-L family
F6DQC0_DESRL | Desulfotomaculum ruminis (strain ATCC 23193 / DSM 2154 / NCIB 8452 / DL) | Lipolytic protein G-D-S-L family
A0A078KJ49_9FIRM | [Clostridium] cellulosi | Uncharacterized protein
U6EVC2_CLOTA | Clostridium tetani 12124569 | Platelet activating factor acetylhydrolase-likeprotein
Q897X6_CLOTE | Clostridium tetani (strain Massachusetts / E88) | Platelet activating factor acetylhydrolase-like protein
R7ADB4_9BACE | Bacteroides pectinophilus CAG:437 | Uncharacterized protein
A0A095ZDI3_9FIRM | Tissierella bacterium S7-1-4 | Uncharacterized protein
A0A0L0WAR6_CLOPU | Clostridium purinilyticum | Lysophospholipase L1
A0A0C1UEU0_9CLOT | Clostridium argentinense CDC 2741 | GDSL-like Lipase/Acylhydrolase family protein
A0A072Y8N5_9CLOT | Clostridium sp. K25 | Acetylhydrolase
R4JC30_9BACT | uncultured bacterium BAC25G1 | Uncharacterized protein
K9WJ28_9CYAN | Microcoleus sp. PCC 7113 | Lysophospholipase L1-like esterase
A0A0M0WNM0_9BACI | Bacillus sp. FJAT-21351 | Lipase
D5DGY9_BACMD | Bacillus megaterium (strain DSM 319) | Lipase/Acylhydrolase (GDSL)
A5N8N5_CLOK5 | Clostridium kluyveri (strain ATCC 8527 / DSM 555 / NCIMB 10680) | Uncharacterized protein
W3AC50_9BACL | Planomicrobium glaciei CHR43 | Uncharacterized protein
A0A098EIL2_9BACL | Planomicrobium sp. ES2 | Multifunctional acyl-CoA thioesterase I and protease I and lysophospholipase L1
K8GFE2_9CYAN | Oscillatoriales cyanobacterium JSC-12 | Lysophospholipase L1-like esterase
G2HS43_9PROT | Arcobacter sp. L | Lipolytic protein
E6L4E3_9PROT | Arcobacter butzleri JV22 | Lipolytic protein
S5PEQ8_9PROT | Arcobacter butzleri 7h1h | Lipolytic enzyme, GDSL domain protein
A0A0G9K3L5_9PROT | Arcobacter butzleri L348 | Lipolytic protein
A0A0M1UPT0_9PROT | Arcobacter butzleri ED-1 | Lipolytic protein
A8EWS4_ARCB4 | Arcobacter butzleri (strain RM4018) | Lipolytic enzyme, GDSL domain
A0A0A6S1U2_STRUB | Streptococcus uberis | Acylneuraminate cytidylyltransferase
A0A0H1UPZ9_STRAG | Streptococcus agalactiae | Acylneuraminate cytidylyltransferase
E3RJZ5_PYRTT | Pyrenophora teres f. teres (strain 0-1) | Putative uncharacterized protein
A0A0L1HYX4_9PLEO | Stemphylium lycopersici | Carbohydrate esterase family 3 protein
G0S9F4_CHATD | Chaetomium thermophilum (strain DSM 1495 / CBS 144.50 / IMI 039719) | Putative uncharacterized protein
G2QVW9_THITE | Thielavia terrestris (strain ATCC 38088 / NRRL 8126) | Carbohydrate esterase family 3 protein
G2QGB0_MYCTT | Myceliophthora thermophila (strain ATCC 42464 / BCRC 31852 / DSM 1799) | Carbohydrate esterase family 3 protein
A0A094AE00_9PEZI | Pseudogymnoascus sp. VKM F-4281 (FW-2241) | Uncharacterized protein
A0A0E3QN36_METBA | Methanosarcina barkeri str. Wiesmoor | Putative tesA-like protease