Each tree is a Bayesian consensus tree, based on an alignment of homologues from one or more of the target taxa studied in this survey, where LGT from prokaryotes to eukaryotes is the most parsimonious explanation for the resulting tree topology. The key for the symbols used to indicate the taxonomy of the analyses sequences and provide taxonomic contextualization for the candidate LGT is indicated just after the list of trees. A parallel phylogenetic analysis was performed with pairwise maximum likelihood distances calculated with the same models used for the Bayesian analysis with trees rooted at the target taxa as the root. This analysis allowed the identification of putative LGT events. In this approach, LGT events are identified first as branches with a high posterior probability (support) and then as branches with the remaining branches being collapsed into polytomies. The LGTs supported by at least one node (trees numbered ONXXX) or at least two nodes (trees numbered TNXXX) separating the trees from other outgroups. Details where the trees are the only eukaryote (or taxa from related taxa), the latter support by deep LGT prior specialization events) among prokaryotic sequences are also labeled as TNXX. The accession number and annotations of the sequences from the target taxa (boxed in the trees) are indicated. A PROBUS analysis investigated the potential presence of a signal peptide (SP) and transmembrane domains (TMD).

Entries in the table of contents below are clickable hyperlinks to the tree figures.
<table>
<thead>
<tr>
<th>Bacteria</th>
<th>Archaea</th>
<th>Eukaryotes</th>
<th>Viruses</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Actinobacteria</td>
<td>Crenarchaeota</td>
<td>Amoebozoa</td>
<td>Bacteria</td>
</tr>
<tr>
<td>Aquificae</td>
<td>Euryarchaeota</td>
<td>Opihitokonta</td>
<td></td>
</tr>
<tr>
<td>Bacteroidetes/Chlorobi group</td>
<td>Korarchaeota</td>
<td>Nucleariidae</td>
<td></td>
</tr>
<tr>
<td>Caldivirga</td>
<td>Nanoarchaeota</td>
<td>Centroheliozoa</td>
<td></td>
</tr>
<tr>
<td>Chitinophagaceae</td>
<td>Thaumarchaeota</td>
<td>Apusozoa</td>
<td></td>
</tr>
<tr>
<td>Chloroflexi</td>
<td></td>
<td>Katablepharidophyta</td>
<td></td>
</tr>
<tr>
<td>Cyanobacteria</td>
<td></td>
<td>Rhizaria</td>
<td></td>
</tr>
<tr>
<td>Deferribacteres</td>
<td></td>
<td>Heterolobosea</td>
<td></td>
</tr>
<tr>
<td>Deinococcus-Thermus</td>
<td></td>
<td>Fornicata</td>
<td></td>
</tr>
<tr>
<td>Dictyoglomi</td>
<td></td>
<td>Malawimonadidae</td>
<td></td>
</tr>
<tr>
<td>Elusimicrobia</td>
<td></td>
<td>Euglenozoa</td>
<td></td>
</tr>
<tr>
<td>Fibrobacteres/Acidobacteria group</td>
<td></td>
<td>Jakobida</td>
<td></td>
</tr>
<tr>
<td>Firmicutes</td>
<td></td>
<td>Oxymonadida</td>
<td></td>
</tr>
<tr>
<td>Fusobacteria</td>
<td></td>
<td>Parabasalia</td>
<td></td>
</tr>
<tr>
<td>Gemmatimonadetes</td>
<td></td>
<td>Haptophyceae</td>
<td></td>
</tr>
<tr>
<td>Nitrospirae</td>
<td></td>
<td>Cryptophyta</td>
<td></td>
</tr>
<tr>
<td>Planctomycetes</td>
<td></td>
<td>Alveolata</td>
<td></td>
</tr>
<tr>
<td>Proteobacteria</td>
<td></td>
<td>Rhodophyta</td>
<td></td>
</tr>
<tr>
<td>Spirochaetes</td>
<td></td>
<td>Glaucocystophyceae</td>
<td></td>
</tr>
<tr>
<td>Synergistetes</td>
<td></td>
<td>Viridiplantae</td>
<td></td>
</tr>
<tr>
<td>Terriceae</td>
<td></td>
<td>unclassified Eukaryota</td>
<td></td>
</tr>
<tr>
<td>Thermotogae</td>
<td></td>
<td>unclassified environmental samples</td>
<td></td>
</tr>
<tr>
<td>Thermococcales</td>
<td></td>
<td>environmental samples</td>
<td></td>
</tr>
<tr>
<td>Thermodesulfobacteria</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Thermotogae</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>unclassified Archaea</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>environmental samples</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Bacteria</td>
<td>Archaea</td>
<td>Eukaryotes</td>
<td>Viruses</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
Candy accession: Q51F93_ENTHI
RefSeq accession: XP_656980.1
Uniprot accession: C4LSR8_ENTHI
Comments: LGT - EH ONE NODE - LGT INTO PLASMODIUM?

KEGG PATHWAY - level 2: Valine, leucine and isoleucine degradation, Valine, leucine and isoleucine biosynthesis, Pantothenate and CoA biosynthesis

Adjacent taxa in tree: Firmicutes
Candy accession: Q51GY0_ENTHI
RefSeq accession: XP_657511.1
Uniprot accession: C4LSZ9_ENTHI
Comments: LGT - EH ONE NODE
Species affected: EH
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:2.7.6.2
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: thiamine pyrophosphokinase
Name of enzyme/protein: Thiamine pyrophosphokinase
KEGG PATHWAY - level 1: Metabolism of Cofactors and Vitamins
KEGG PATHWAY - level 2: Thiamine metabolism

Arabidopsis thaliana
VIR
Oryza sativa
VIR
Xenopus (Silurana) tropicalis
OPI
Bos taurus
OPI
Dictyostelium discoideum
AMO
Caenorhabditis elegans
OPI
Caenorhabditis briggsae
OPI
Trichomonas vaginalis
PAR
Schizosaccharomyces pombe
OPI
Tetrahymena thermophila
ALV
Rhodobacter sphaeroides
PRO
Bartonella quintana
PRO
Bartonella henselae
PRO
Brucella melitensis
PRO
Brucella abortus
PRO
Rhizobium etli
PRO
Agrobacterium tumefaciens
PRO
Chelativorans sp. BNC1
PRO
Deinococcus geothermalis
D-T
Symbiobacterium thermophilum
FIR
Bacillus cereus
FIR
Bacillus anthracis
FIR
Staphylococcus epidermidis
FIR
Exiguobacterium sibiricum
FIR
Oceanobacillus iheyensis
FIR
Listeria monocytogenes
FIR
Caldanaerobacter subterraneus
FIR
Caldicellulosiruptor saccharolyticus
FIR
Chloroflexus aurantiacus
CHL
Desulfitobacterium hafniense
FIR
Desulfotomaculum reducens
FIR
Syntrophus aciditrophicus
PRO
Tropheryma whipplei
ACT
Alkaliphilus metalliredigens
FIR
Clostridium thermocellum
FIR
Syntrophomonas wolfei
FIR
Halothermothrix orenii
FIR
Thermotoga maritima
THET
Fusobacterium nucleatum
FUS
Clostridium beijerinckii
FIR
Carboxydothermus hydrogenoformans
FIR
Q51GY0
ENTHI Entamoeba histolytica
AMO
Bacteroides thetaiotaomicron
BC
Bacteroides fragilis
BC
1.00/100
0.99/85
1.00/81
1.00/96
1.00/80
1.00/100
0.99/77
1.00/100
0.97/75
1.00/100
1.00/100
1.00/100
1.00/98
1.00/98
1.00/100
1.00/96
1.00/70
0.95/73
0.5
Candy accession: TV89808120
RefSeq accession: XP_001313482.1
Uniprot accession: A2F3H3_TRIVA
Comments: LGT - TV ONE NODE
Species affected: TV
Adjacent taxa in tree: Protobacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: CutC family protein
Name of enzyme/protein: Predicted CutC Uncharacterized protein
involved in copper resistance
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na
<table>
<thead>
<tr>
<th>Accession</th>
<th>Species Affected</th>
<th>Name of Enzyme/Protein</th>
<th>EC Annotation</th>
<th>RefSeq Annotation</th>
<th>KEGG Pathway - Level 1</th>
<th>KEGG Pathway - Level 2</th>
</tr>
</thead>
<tbody>
<tr>
<td>PV091555</td>
<td>PF, PV, PY</td>
<td>Predicted flavin mononucleotide phosphatase, haloacid dehalogenase</td>
<td>EC: 3.8.1.2</td>
<td>hypothetical protein</td>
<td>Xenobiotics Biodegradation and Metabolism</td>
<td>Chlorocyclohexane and chlorobenzene degradation, Chloroalkane and chloroalkene degradation</td>
</tr>
<tr>
<td>Q7RGW5</td>
<td>PF, PV, PY</td>
<td>(S)-2-haloacid dehalogenase</td>
<td></td>
<td>haloacid dehalogenase-like hydrolase</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

**Diagram:**
- **Methanosarcina barkeri** EURL
- **Clostridium beijerinckii** FIRG
- **Bacillus clausii** FIRG
- **Halothermothrix orenii** FIRG
- **Bacillus cereus** FIRG
- **Clostridium beijerinckii** FIRG
- **Staphylococcus epidermidis** FIRG
- **Xenopus (Silurana) tropicalis** OPI
- **Drosophila melanogaster** OPI
- **Photobacterium sp. SKA34** PRO
- **Vibrio parahaemolyticus** PRO
- **Methanococcus maripaludis** EUR
- **Pyrococcus abyssi** EUR
- **Streptococcus suis** FIRG
- **Enterococcus faecalis** FIRG
- **Chlorobium phaeobacteroides** BC
- **Flavobacteria bacterium BBFL7** BC
- **Bacillus licheniformis** FIRG
- **Bacillus cereus** FIRG
- **Drosophila melanogaster** OPI
- **Sulfolobus tokodaii** CRE
- **Sulfolobus tokodaii** CRE
- **Escherichia coli** PRO
- **Shigella sonnei** PRO
- **Shigella boydii** PRO
- **Escherichia coli** PRO
- **Shigella flexneri** PRO
- **Escherichia coli** PRO
- **Salmonella enterica** PRO
- **Pectobacterium atrosepticum** PRO
- **Yersinia pestis** PRO
- **Serratia marcescens** PRO
- **Sodalis glossinidius** PRO
- **Wigglesworthia glossinidia** PRO
- **Candidatus Blochmannia floridanus** PRO
- **Actinobacillus succinogenes** PRO
- **Pasteurella multocida** PRO
- **Vibrio parahaemolyticus** PRO
- **Photobacterium sp. SKA34** PRO
- **Pseudoalteromonas haloplanktis** PRO
- **Shewanella sp. MR-7** PRO
- **Polaromonas sp. JS666** PRO
- **Burkholderia cenocepacia** PRO
- **Xanthomonas axonopodis** PRO
- **Azotobacter vinelandii** PRO
- **Pseudomonas aeruginosa** PRO
- **uncultured marine bacterium Ant4D3** EB
- **Neptuniibacter caesariensis** PRO
- **Halorhodospira halophila** PRO
- **Nitrosococcus oceani** PRO
- **Alkalilimnicola ehrlichii** PRO
Candy accession: Q54LR7_DICDI
RefSeq accession: XP_637763.1
Uniprot accession: Q54LR7_DICDI
Comments: LGT - DD ONE NODE
Species affected: DD
Adjacent taxa in tree: Tenericute
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein DDB_G0286443
Name of enzyme/protein: Protein containing Type 1 glutamine amidotransferase (GATase1)-like domain
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na

Mycoplasma mycoides
Mycoplasma capricolum
Q54LR7 DICDI Dictyostelium discoideum
Mesoplasma florum
Thiobacillus denitrificans
Alkalilimnicola ehrlichii
Halorhodospira halophila
Thiomicrospira crunogena
Oryza sativa
Arabidopsis thaliana
Entamoeba histolytica
Borrelia garinii
Borrelia burgdorfi
Giardia intestinalis
Streptococcus pneumoniae
Streptococcus thermophilus
Bacteroides fragilis
Bacteroides thetaiotaomicron
Clostridium perfringens
Clostridium tetani
Clostridium acetobutylicum
Halothermothrix orenii
Gloeobacter violaceus
Helicobacter hepaticus
Trichomonas vaginalis
Clostridium beijerinckii
Treponema denticola
Bacillus licheniformis
Methanosaeta thermophila
Dehalococcoides ethenogenes
Dehalococcoides sp. BAV1

1.00/100
1.00/94
1.00/99
1.00/100
1.00/97
0.99/77
1.00/100
1.00/100
1.00/80
1.00/97
1.00/100
0.5
Candy accession: Q86HZ8_DICDI
RefSeq accession: XP_644821.1
Uniprot accession: Q557D9_DICDI
Comments: LGT - DD ONE NODE
Species affected: DD
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:2.1.1.34
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein DDB_G0273135
Name of enzyme/protein: tRNA (guanosine18-2'-O)-methyltransferase
KEGG PATHWAY - level 1: Translation - Genetic Information Processing
KEGG PATHWAY - level 2: Transfer RNA biogenesis

Staphylococcus aureus FIRG
Francisella tularensis PROG
Schistosoma japonicum OPII
Plasmodium falciparum ALV
Clostridium perfringens FIRG
Bacteroides thetaiotaomicron BC
Bacteroides fragilis BC
Q86HZ8 DICDI Dictyostelium discoideum
Flavobacteria bacterium BBFL7 BC
Candidatus Solibacter usitatus F-A
Candidatus Protochlamydia amoebophila C-V
Bdellovibrio bacteriovorus PRO
Salinibacter ruber BC
Chlorobium phaeobacteroides BC
Prosthecochloris aestuarii BC
Pelodictyon phaeoclathratiforme BC
Pelodictyon luteolum BC
Chlorobium tepidum BC
Chlorobium chlorochromatii BC
Chlorobium limicola BC
Chlorobium chlorochromatii BC

1.00/97
1.00/91
0.95/78
1.00/81
1.00/99
1.00/100
0.5
Candy accession: TV122580003
RefSeq accession: XP_001285086.1
Uniprot accession: A2HEL1_TRIVA
Comments: LGT - TV ONLY
Species affected: TV
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Predicted D12 class N6 adenine-specific DNA methyltransferase
KEGG PATHWAY - level 1: Other function - Genetic Information Processing
KEGG PATHWAY - level 2: na
Candy accession: Q4GY96_9TRYP
RefSeq accession: XP_001219175.1
Uniprot accession: Q4GY96_9TRYP
Comments: LGT - TB ONLY
Species affected: TB
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:3.1.1.32
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: phospholipase A1
Name of enzyme/protein: phospholipase A1
KEGG PATHWAY - level 1: Lipid Metabolism
KEGG PATHWAY - level 2: Glycerophospholipid metabolism, alpha-Linolenic acid metabolism

<table>
<thead>
<tr>
<th>Yersinia pestis</th>
</tr>
</thead>
<tbody>
<tr>
<td>PROG</td>
</tr>
<tr>
<td>Yersinia pseudotuberculosis</td>
</tr>
<tr>
<td>PROG</td>
</tr>
<tr>
<td>Yersinia enterocolitica</td>
</tr>
<tr>
<td>PROG</td>
</tr>
<tr>
<td>Clostridium thermocellum</td>
</tr>
<tr>
<td>FIRG</td>
</tr>
<tr>
<td>Q4GY96 9TRYP</td>
</tr>
<tr>
<td>Trypanosoma brucei</td>
</tr>
<tr>
<td>EUGI</td>
</tr>
<tr>
<td>Photorhabdus luminescens</td>
</tr>
<tr>
<td>PROG</td>
</tr>
</tbody>
</table>

1.00/99
1.00/100
1.00/91
0.5
Candy accession: Q4Q0L8_LEIMA
RefSeq accession: XP_001687130.1
Uniprot accession: Q4Q0L8_LEIMA
Comments: LGT - KINETOPLASTIDS ONLY
Species affected: LM, TB, TC
Adjacent taxa in tree: Proteobacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Macrocin-O-methyltransferase
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na
Candy accession: Q4Q5Y1_LEIMA
RefSeq accession: XP_001685267.1
Uniprot accession: Q4Q5Y1_LEIMA
Comments: LGT - KINETOPLASTIDS ONLY
Species affected: LM, TC
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:3.5.1.16
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: acetylornithine deacetylase
KEGG PATHWAY - level 1: Amino Acid Metabolism
KEGG PATHWAY - level 2: Arginine and proline metabolism
uncultured bacterium
Trypanosoma cruzi
Agrobacterium tumefaciens
Mesorhizobium loti
Rhizobium etli
Sinorhizobium fredii
0.99/99
0.98/85
1.00/100
0.5
Candy accession: Q4Q6Z3_LEIMA
RefSeq accession: XP_001684905.1
Uniprot accession: Q4Q6Z3_LEIMA
Comments: LGT - KINETOPLASTIDS ONLY
Species affected: LM, TB, TC
Adjacent taxa in tree: Cyanobacteria - Trichodesmium
EC annotation - (Blast/Profile): na
PHOBIUS SP: Y
PHOBIUS TMD: 1
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Protein containing peptidase M14-like domain
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na

Bordetella pertussis
Bordetella bronchiseptica
Bordetella parapertussis
Rhodopseudomonas palustris
Bordetella avium
Pseudomonas fluorescens
Magnetococcus sp. MC-1
Trypanosoma cruzi
Trypanosoma brucei
Cupriavidus pinatubonensis
Cupriavidus metallidurans
Polaromonas sp. JS666
Ralstonia solanacearum
Cupriavidus metallidurans
Bordetella avium
1.00/87
1.00/100
1.00/100
1.00/100
1.00/99
1.00/100
0.2
Candy accession: Q4QBB1_LEIMA
RefSeq accession: XP_001683387.1
Uniprot accession: Q4QBB1_LEIMA
Comments: LGT - LM ONLY
Species affected: LM
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:6.1.1.20
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: phenylalanyl-tRNA synthetase beta chain
KEGG PATHWAY - level 1: Translation - Genetic Information
Processing
KEGG PATHWAY - level 2: Aminoacyl-tRNA biosynthesis

Lactobacillus johnsonii
Lactobacillus acidophilus
Desulfotomaculum reducens
Lactococcus lactis
Mycoplasma penetrans
Shewanella baltica
Oceanobacillus iheyensis
Staphylococcus epidermidis

1.00/100
0.2
<table>
<thead>
<tr>
<th>Species</th>
<th>Accession</th>
<th>Coverage</th>
<th>Identity</th>
<th>Query Coverage</th>
<th>Identity</th>
</tr>
</thead>
<tbody>
<tr>
<td>Burkholderia cenocepacia</td>
<td>Burkholderia ambifaria</td>
<td>1.00/100</td>
<td>1.00/99</td>
<td>1.00/87</td>
<td>1.00/99</td>
</tr>
<tr>
<td>Burkholderia vietnamiensis</td>
<td>Burkholderia thailandensis</td>
<td>1.00/100</td>
<td>1.00/99</td>
<td>1.00/87</td>
<td>1.00/99</td>
</tr>
<tr>
<td>Burkholderia mallei</td>
<td>Burkholderia cenocepacia</td>
<td>1.00/100</td>
<td>1.00/99</td>
<td>1.00/87</td>
<td>1.00/99</td>
</tr>
<tr>
<td>Burkholderia ambifaria</td>
<td>Burkholderia vietnamiensis</td>
<td>1.00/100</td>
<td>1.00/99</td>
<td>1.00/87</td>
<td>1.00/99</td>
</tr>
<tr>
<td>Burkholderia thailandensis</td>
<td>Burkholderia mallei</td>
<td>1.00/100</td>
<td>1.00/99</td>
<td>1.00/87</td>
<td>1.00/99</td>
</tr>
<tr>
<td>Burkholderia cenocepacia</td>
<td>Burkholderia thailandensis</td>
<td>1.00/100</td>
<td>1.00/99</td>
<td>1.00/87</td>
<td>1.00/99</td>
</tr>
<tr>
<td>Burkholderia vietnamiensis</td>
<td>Burkholderia mallei</td>
<td>1.00/100</td>
<td>1.00/99</td>
<td>1.00/87</td>
<td>1.00/99</td>
</tr>
<tr>
<td>Burkholderia ambifaria</td>
<td>Burkholderia cenocepacia</td>
<td>1.00/100</td>
<td>1.00/99</td>
<td>1.00/87</td>
<td>1.00/99</td>
</tr>
<tr>
<td>Burkholderia thailandensis</td>
<td>Burkholderia mallei</td>
<td>1.00/100</td>
<td>1.00/99</td>
<td>1.00/87</td>
<td>1.00/99</td>
</tr>
<tr>
<td>Burkholderia cenocepacia</td>
<td>Burkholderia ambifaria</td>
<td>1.00/100</td>
<td>1.00/99</td>
<td>1.00/87</td>
<td>1.00/99</td>
</tr>
<tr>
<td>Burkholderia vietnamiensis</td>
<td>Burkholderia thailandensis</td>
<td>1.00/100</td>
<td>1.00/99</td>
<td>1.00/87</td>
<td>1.00/99</td>
</tr>
<tr>
<td>Burkholderia ambifaria</td>
<td>Burkholderia cenocepacia</td>
<td>1.00/100</td>
<td>1.00/99</td>
<td>1.00/87</td>
<td>1.00/99</td>
</tr>
<tr>
<td>Burkholderia thailandensis</td>
<td>Burkholderia mallei</td>
<td>1.00/100</td>
<td>1.00/99</td>
<td>1.00/87</td>
<td>1.00/99</td>
</tr>
<tr>
<td>Burkholderia cenocepacia</td>
<td>Burkholderia ambifaria</td>
<td>1.00/100</td>
<td>1.00/99</td>
<td>1.00/87</td>
<td>1.00/99</td>
</tr>
<tr>
<td>Burkholderia vietnamiensis</td>
<td>Burkholderia thailandensis</td>
<td>1.00/100</td>
<td>1.00/99</td>
<td>1.00/87</td>
<td>1.00/99</td>
</tr>
<tr>
<td>Burkholderia ambifaria</td>
<td>Burkholderia cenocepacia</td>
<td>1.00/100</td>
<td>1.00/99</td>
<td>1.00/87</td>
<td>1.00/99</td>
</tr>
<tr>
<td>Burkholderia thailandensis</td>
<td>Burkholderia mallei</td>
<td>1.00/100</td>
<td>1.00/99</td>
<td>1.00/87</td>
<td>1.00/99</td>
</tr>
</tbody>
</table>
Candy accession: Q4QH87_LEIMA
RefSeq accession: XP_001681461.1
Uniprot accession: Q4QH87_LEIMA
Comments: LGT - LM ONLY
Species affected: LM
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Protein containing DUF1861
KEGG PATHWAY - level 1: Function unknown
KEGG PATHWAY - level 2: na
Candy accession: Q4QIU1_LEIMA
RefSeq accession: XP_001680907.1
Uniprot accession: Q4QIU1_LEIMA
Comments: LGT - KINETOPLASTIDS ONLY
Species affected: LM,TB,TC
Adjacent taxa in tree: Proteobacteria
EC annotation - (Blast/Profile): EC:3.5.1.16
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: acetylornithine deacetylase
KEGG PATHWAY - level 1: Amino Acid Metabolism
KEGG PATHWAY - level 2: Arginine and proline metabolism
Candy accession: Q7R5L6_GIALA
RefSeq accession: XP_001707536.1
Uniprot accession: A8BDW4_GIALA
Comments: LGT - GI ONLY
Species affected: GI
Adjacent taxa in tree: Firmicutes
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: Transglutaminase/protease, putative
Name of enzyme/protein: Transglutaminase/protease, putative
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na
Species affected: PY
Adjacent taxa in tree: Bacteria

Name of enzyme/protein: Putative ribosomal subunit interface protein; sigma-54 modulation protein

KEGG PATHWAY - level 1: Other function - Genetic Information Processing
KEGG PATHWAY - level 2: na
Candy accession: Q7R799_PLAYO
RefSeq accession: XP_728635.1
Uniprot accession: Q7R799_PLAYO
Comments: LGT - PY ONLY
Species affected: PY
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Protein containing DUF2699
KEGG PATHWAY - level 1: Function unknown
KEGG PATHWAY - level 2: na
Comments: LGT - KINETOPLASTIDS ONLY - THE PROTEINS POSSESS THE BACTERIAL CEST DOMAIN HENCE IT IS CONSIDERED AS A CANDIDATE B->E LGT
Candy accession: Q9NKQ8_LEIMA
RefSeq accession: XP_001687362.1
Uniprot accession: Q9NKQ8_LEIMA
Comments: LGT - LM ONLY
Species affected: LM
Adjacent taxa in tree: Bacteria

EC annotation - (Blast/Profile): EC:4.2.1.75
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: uroporphyrinogen-III synthase
KEGG PATHWAY - level 1: Metabolism of Cofactors and Vitamins
KEGG PATHWAY - level 2: Porphyrin and chlorophyll metabolism
Candy accession: Q38CZ3_9TRYP
RefSeq accession: XP_827657.1
Uniprot accession: Q38CZ3_9TRYP
Comments: LGT - KINETOPLASTIDS ONLY - ADDITIONAL BACTERIA TAXA ARE RECOVERED BUT COREPSOND TO MUCH WEAKER HITS HENCE IT IS CONSIDERED AS A CANDIDATE B->E LGT
Species affected: LM, TB, TC
Adjacent taxa in tree: Chlamydiae/Verrucomicrobia
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Predicted Rossmann fold nucleotide-binding protein
KEGG PATHWAY - level 1: Other function - Genetic Information Processing
KEGG PATHWAY - level 2: na
1.00/87
1.00/100
1.00/100
1.00/100
1.00/100
0.2
**Comments:** LGT - EH ONLY

**Species affected:** EH

**Adjacent taxa in tree:** Bacteroides

**RefSeq annotation:** hypothetical protein

**Name of enzyme/protein:** Protein containing DUF1810

**KEGG PATHWAY - level 1:** Function unknown

**KEGG PATHWAY - level 2:** na

**EC annotation - (Blast/Profile): na**

**PHOBIUS SP:** 0

**PHOBIUS TMD:** 0

**Candy accession:** Q50VJ7

**RefSeq accession:** XP_651004.1

**Uniprot accession:** C4MBP5

**Entamoeba histolytica**

Bacteroides thetaiotaomicron

Bradyrhizobium sp. BTAi1

Bradyrhizobium japonicum

Albidiferax ferrireducens

Polaromonas sp. JS666

Mycobacterium vanbaalenii

Mycobacterium gilvum

Rhodospirillum rubrum

Rhodobacter sphaeroides

Ruegeria pomeroyi

Ruegeria sp. TM1040

Arthrobacter sp. FB24

Mesorhizobium loti

Polaromonas sp. JS666

Chlorobium phaeobacteroides

Sinorhizobium meliloti

Rhizobium etli

Nitrobacter hamburgensis

Pseudomonas fluorescens

Oceanicola granulosus

Legionella pneumophila

Acidiphilium cryptum

Pseudomonas syringae

Psychrobacter arcticus

Mycobacterium avium

Mycobacterium tuberculosis

Mycobacterium bovis

1.00/100

1.00/99

0.96/94

1.00/96

1.00/82

1.00/85

1.00/85

1.00/98

0.2
Candy accession: Q50XL0_ENTHI
RefSeq accession: XP_651699.1
Uniprot accession: C4M0V4_ENTHI
Comments: LGT - EH ONLY
Species affected: EH
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Protein containing cupin-like fold and unknown function
KEGG PATHWAY - level 1: Function unknown
KEGG PATHWAY - level 2: na

Geobacter uraniumreducens
Pelobacter propionicus
Pelodictyon phaeoclathratiform
Chlorobium limicola
Synechocystis sp.
Photobacterium profundum
Prosthecochloris aestuarii
Chlorobium phaeobacteroides
Entamoeba histolytica
Prochlorococcus marinus
Synechococcus sp.
Gluconobacter oxydans
Pseudomonas aeruginosa
Burkholderia sp.
Chromobacterium violaceum
Pseudomonas syringae
Methylobacillus flagellatus
Photorhabdus luminescens
Shewanella baltica

1.00/100
1.00/88
1.00/92
1.00/100
1.00/82
1.00/91
0.5
Candy accession: Q51DS8_ENTHI
RefSeq accession: XP_656375.1
Uniprot accession: C4LSD2_ENTHI
Comments: LGT - EH ONLY
Species affected: EH
Adjacent taxa in tree: Prokaryotes
EC annotation - (Blast/Profile): EC:1.-.-.-
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: nitroreductase family protein
Name of enzyme/protein: nitroreductase family protein
KEGG PATHWAY - level 1: Reaction
KEGG PATHWAY - level 2: Reaction
Candy accession: Q54I75_DICDI
RefSeq accession: XP_636504.1
Uniprot accession: Q54I75_DICDI
Comments: LGT - DD ONLY
Species affected: DD
Adjacent taxa in tree: Protobacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein DDB_G0288943
Name of enzyme/protein: Protein containing DUF796
KEGG PATHWAY - level 1: Function unknown
KEGG PATHWAY - level 2: na

Pseudomonas fluorescens
Pseudomonas aeruginosa
Dictyostelium discoideum
Dictyostelium discoideum
Azotobacter vinelandii
Salmonella choleraesuis
Salmonella typhimurium
Salmonella typhi
Salmonella paratyphi

1.00/100
0.99/85
1.00/100
0.5
Dictyostelium discoideum

AMO

Protein containing peptidase M66 domain

KEGG PATHWAY - level 1: Function unknown

KEGG PATHWAY - level 2: na
Candy accession: Q54L61_DICDI
RefSeq accession: XP_637502.1
Uniprot accession: Q54L61_DICDI
Comments: LGT - DD ONLY
Species affected: DD
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein DDB_G0286879
Name of enzyme/protein: Hypothetical protein
KEGG PATHWAY - level 1: Function unknown
KEGG PATHWAY - level 2: na

Bdellovibrio bacteriovorus
Idiomarina loihiensis
Synechocystis sp. PCC 6803
Oceanobacillus iheyensis
Bacillus clausii
Symbiobacterium thermophilum
Bacillus cereus
Bacillus thuringiensis
Bacillus anthracis
Bacillus thuringiensis
Bacillus weihenstephanensis
Bacillus cereus
1.00/100
0.99/80
0.2
<table>
<thead>
<tr>
<th>Species</th>
<th>NCBI Taxonomy</th>
<th>Comments</th>
<th>Accessions</th>
<th>EC Annotation</th>
<th>KEGG Pathway level 1</th>
<th>KEGG Pathway level 2</th>
</tr>
</thead>
<tbody>
<tr>
<td>Candidatus Solibacter usitatus</td>
<td>215303516</td>
<td>DD ONLY</td>
<td>Q54YR0_DICDI</td>
<td>EC:2.3.1.128</td>
<td>Reaction</td>
<td>Reaction</td>
</tr>
<tr>
<td>Chloroflexus aurantiacus</td>
<td>215303516</td>
<td></td>
<td>XP_002649169.1</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Dictyostelium discoideum</td>
<td>215303516</td>
<td></td>
<td>C7G007_DICDI</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ruminococcus flavefaciens</td>
<td>215303516</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Caldicellulosiruptor saccharolyticus</td>
<td>215303516</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Caldanaerobacter subterraneus</td>
<td>215303516</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Thermoanaerobacter pseudethanolicus</td>
<td>215303516</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
Burkholderia vietnamiensis
Burkholderia ambifaria
Burkholderia cenocepacia
Burkholderia sp. 383
Burkholderia pseudomallei
Burkholderia mallei
Burkholderia thailandensis
Nitrobacter hamburgensis
Mesorhizobium loti
Bradyrhizobium sp. BTAi1
Rhodopseudomonas palustris
Ralstonia solanacearum
Cupriavidus metallidurans
Cupriavidus pinatubonensis
Xanthobacter autotrophicus
Zymomonas mobilis
Agrobacterium tumefaciens
Pseudomonas aeruginosa
Synechococcus sp. WH 8102
Prochlorococcus marinus
Synechococcus sp. CC9902
Synechococcus sp. CC9605

1.00/100
1.00/85
1.00/100
0.96/70
0.98/100
0.99/74
1.00/100
1.00/100
1.00/93
0.5
Candy accession: Q513M6
RefSeq accession: XP_653421.1
Uniprot accession: C4M2N2
Comments: LGT - EH ONLY
Species affected: EH
Adjacent taxa in tree: Proteobacteria - Pelobacter
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Putative redox-active protein (C_GCAxxG_C_C)
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na
Candy accession: Q516Y7_ENTHI
RefSeq accession: XP_654288.1
Uniprot accession: C4M6B4_ENTHI

Comments: LGT - EH ONLY with 4 Archaea

Species affected: EH

Adjacent taxa in tree: Archaea

EC annotation - (Blast/Profile): na

PHOBIUS SP: 0
PHOBIUS TMD: 0

RefSeq annotation: hypothetical protein

Name of enzyme/protein: Predicted phosphohydrolase

KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na
Candy accession: T52_01632
RefSeq accession: XP_002369463.1
Uniprot accession: B6KNP0_TOXGO
Comments: LGT - TG ONLY
Species affected: TG
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 7
RefSeq annotation: zinc transporter ZIP domain-containing protein
Name of enzyme/protein: zinc transporter ZIP domain-containing protein
KEGG PATHWAY - level 1: Other function - Membrane transport
KEGG PATHWAY - level 2: na
Candy accession: TV83237063
RefSeq accession: XP_001309866.1
Uniprot accession: A2FDT7_TRIVA
Comments: LGT - TV ONLY
Species affected: TV
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Protein containing DUF3111
KEGG PATHWAY - level 1: Function unknown
KEGG PATHWAY - level 2: na

FIRG

- Bacillus cereus
- Bacillus weihenstephanensis
- Bacillus anthracis
- Bacillus thuringiensis
- Bacillus cereus

TV83237063 Trichomonas vaginalis

PARI

- Candidatus Solibacter usitatus

1.00/100
0.2
Candy accession: TV83928086
RefSeq accession: XP_001309751.1
Uniprot accession: A2FE49_TRIVA
Comments: LGT - TV ONLY
Species affected: TV
Adjacent taxa in tree: Actinobacteria - Bifidobacterium
EC annotation - (Blast/Profile): EC:4.1.1.44
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: 4-carboxymuconolactone decarboxylase
Name of enzyme/protein: 4-carboxymuconolactone decarboxylase
KEGG PATHWAY - level 1: Xenobiotics Biodegradation and Metabolism
KEGG PATHWAY - level 2: Benzoate degradation

1.00/99
1.00/97
0.96/89
1.00/96
1.00/100
1.00/100
0.2
Candy accession: TV84285194
RefSeq accession: XP_001323014.1
Uniprot accession: A2E9A6_TRIVA
Comments: LGT - TV ONLY
Species affected: TV
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: NDP-hexose 3,4-dehydratase
Name of enzyme/protein: Predicted 3-amino-5-hydroxybenzoic acid synthase family
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na
Candy accession: TV85862250
RefSeq accession: XP_001325565.1
Uniprot accession: A2E1Z3_TRIVA
Comments: LGT - TV ONLY
Species affected: TV
Adjacent taxa in tree: Prokaryotes
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Predicted selenium-dependent hydroxylase accessory protein YqeC
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na

Enterococcus faecalis
Desulfotalea psychrophila
Rubrobacter xylanophilus
Geobacter metallireducens
Carboxydothermus hydrogenoformans
Desulfitobacterium hafniense
Moorella thermoacetica
TV85862250 Trichomonas vaginalis
Haloarcula marismortui
Candy accession: TV86997188
RefSeq accession: XP_001327447.1
Uniprot accession: A2DWN9_TRIVA
Comments: LGT - TV ONLY
Species affected: TV
Adjacent taxa in tree: Firmicutes
EC annotation - (Blast/Profile): EC:3.2.1.4
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: xylanase
Name of enzyme/protein: endo-1,4-beta-D-glucanase
KEGG PATHWAY - level 1: Carbohydrate Metabolism
KEGG PATHWAY - level 2: Starch and sucrose metabolism

Trichomonas vaginalis
Clostridium thermocellum
Bacteroides fragilis
Bacteroides thetaiotaomicron
1.00/90
0.5
Candy accession: TV87363164
RefSeq accession: XP_001325291.1
Uniprot accession: A2E2P0_TRIVA
Comments: LGT - TV ONLY
Species affected: TV
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: ATP-dependent Zn protease
Name of enzyme/protein: Protein containing DUF1846
KEGG PATHWAY - level 1: Function unknown
KEGG PATHWAY - level 2: na
Candy accession: TV87719223
RefSeq accession: XP_001325053.1
Uniprot accession: A2E3D9_TRIVA
Comments: LGT - TV ONLY
Species affected: TV
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:4.4.1.5
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: Lactoylglutathione lyase
Name of enzyme/protein: lactoylglutathione lyase
KEGG PATHWAY - level 1: Carbohydrate Metabolism
KEGG PATHWAY - level 2: Pyruvate metabolism
Candy accession: TV87835279
RefSeq accession: XP_001327568.1
Uniprot accession: A2DW44_TRIVA
Comments: LGT - TV ONLY
Species affected: TV
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Hypothetical protein
KEGG PATHWAY - level 1: Function unknown
KEGG PATHWAY - level 2: na
**Candy accession:** TV87854275  
**RefSeq accession:** XP_001578953.1  
**Uniprot accession:** A2DNX2_TRIVA  
**Comments:** LGT - TV ONLY  
**Species affected:** TV  
**Adjacent taxa in tree:** Archaea - Pyrobaculum  
**EC annotation - (Blast/Profile):** na  
**PHOBIUS SP:** 0  
**PHOBIUS TMD:** 0  
**RefSeq annotation:** hypothetical protein  
**Name of enzyme/protein:** Predicted L-ara-isomerases L-fucose isomerase (FucIase) and L-arabinose isomerase (AI) family  
**KEGG PATHWAY - level 1:** Other function  
**KEGG PATHWAY - level 2:** na
Candy accession: TV88428086
RefSeq accession: XP_001307935.1
Uniprot accession: A2FJ91_TRIVA
Comments: LGT - TV ONLY
Species affected: TV
Adjacent taxa in tree: Firmicutes
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: Transposase IS116/IS110/IS902 family
protein
Name of enzyme/protein: Transposase IS116/IS110/IS902 family
protein
KEGG PATHWAY - level 1: Other function - Genetic Information
Processing
KEGG PATHWAY - level 2: na
Candy accession: TV90417119
RefSeq accession: XP_001320377.1
Uniprot accession: A2EGR6_TRIVA
Comments: LGT - TV ONLY
Species affected: TV
Adjacent taxa in tree: Prokaryotes
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Protein containing carbohydrate kinase domain
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na
Candy accession: TV90492230
RefSeq accession: XP_001579117.1
Uniprot accession: A2DNE3_TRIVA
Comments: LGT - TV ONLY
Species affected: TV
Adjacent taxa in tree: Archaea
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Protein containing DUF3737
KEGG PATHWAY - level 1: Function unknown
KEGG PATHWAY - level 2: na

Methanococcus maripaludis EUR
Methanosarcina barkeri EUR
Methanosarcina acetivorans EUR
Trichomonas vaginalis PAR
Trichomonas vaginalis PAR
TV90492230 Trichomonas vaginalis PAR
Lactobacillus johnsonii FIR
Lactobacillus acidophilus FIR
Lactobacillus reuteri FIR
Lactobacillus plantarum FIR
Bacteroides fragilis BC
Bacteroides thetaiotaomicron BC

1.00/100
1.00/98
1.00/100
1.00/100
1.00/100
0.98/83
1.00/99
0.2
Candy accession: TV94782134
RefSeq accession: XP_001321629.1
Uniprot accession: A2ED51_TRIVA
Comments: LGT - TV ONLY
Species affected: TV
Adjacent taxa in tree: Proteobacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 1
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Predicted disintegrin and metalloprotease-like protein
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na
<table>
<thead>
<tr>
<th>Species</th>
<th>Accession</th>
<th>Comments</th>
<th>Adjacent taxa in tree</th>
<th>EC annotation - (Blast/Profile)</th>
<th>PHOBIUS SP</th>
<th>PHOBIUS TMD</th>
<th>RefSeq annotation</th>
<th>Name of enzyme/protein</th>
<th>KEGG PATHWAY - level 1</th>
<th>KEGG PATHWAY - level 2</th>
</tr>
</thead>
<tbody>
<tr>
<td>Desulfitobacterium hafniense</td>
<td>FIRG</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Mycoplasma penetrans</td>
<td>TENG</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Trichomonas vaginalis</td>
<td>PARI</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Treponema denticola</td>
<td>SPIG</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>TV96281253 Trichomonas vaginalis</td>
<td>PARI</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Lactobacillus acidophilus</td>
<td>FIRG</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Treponema denticola</td>
<td>SPIG</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

1.00/100 0.2
Candy accession: TV97114181
RefSeq accession: XP_001326490.1
Uniprot accession: A2DZD8_TRIVA
Comments: LGT - TV ONLY
Species affected: TV
Adjacent taxa in tree: Prokaryotes
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Predicted adenosine specific kinase
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na
<table>
<thead>
<tr>
<th>Species</th>
<th>Accession</th>
<th>Comments</th>
<th>Adjacent taxa in tree</th>
<th>EC annotation (Blast/Profile)</th>
<th>PHOBIUS SP</th>
<th>PHOBIUS TMD</th>
<th>RefSeq annotation</th>
<th>Name of enzyme/protein</th>
<th>KEGG PATHWAY - level 1</th>
<th>KEGG PATHWAY - level 2</th>
</tr>
</thead>
<tbody>
<tr>
<td>Leishmania major</td>
<td>Q4Q2V9_LEIMA</td>
<td>LGT - KINETOPLASTIDS ONLY</td>
<td>Firmicutes</td>
<td>EC:2.6.1.42</td>
<td>0</td>
<td>0</td>
<td>hypothetical protein</td>
<td>branched-chain amino acid aminotransferase</td>
<td>Amino Acid Metabolism, Metabolism of Cofactors and Vitamins</td>
<td>Valine, leucine and isoleucine degradation and biosynthesis, Pantothenate and CoA biosynthesis</td>
</tr>
<tr>
<td>Alkaliphilus metalliredigens</td>
<td>FIRG</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Clostridium beijerinckii</td>
<td>FIRG</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Q4Q2V9 LEIMA</td>
<td>Trypanosoma brucei</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Trypanosoma cruzi</td>
<td>Trypanosoma cruzi</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Trypanosoma cruzi</td>
<td>Trypanosoma cruzi</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

1.00/100
1.00/99
1.00/100
0.5
Candy accession: Q4Q8S0_LEIMA
RefSeq accession: XP_001684278.1
Uniprot accession: Q4Q8S0_LEIMA
Comments: LGT - LM TWO NODES
Species affected: LM
Adjacent taxa in tree: Proteobacteria
EC annotation - (Blast/Profile): EC:2.7.2.11
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: glutamate 5-kinase
Name of enzyme/protein: Glutamate 5-kinase
KEGG PATHWAY - level 1: Amino Acid Metabolism
KEGG PATHWAY - level 2: Arginine and proline metabolism
Candy accession: Q7R5Z7_GIALA
RefSeq accession: XP_001706848.1
Uniprot accession: A8BII9_GIALA
Comments: LGT - GI ONLY
Species affected: GI
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:3.1.3.15
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: Histidinol-phosphatase, putative
Name of enzyme/protein: Histidinol-phosphatase
KEGG PATHWAY - level 1: Amino Acid Metabolism
KEGG PATHWAY - level 2: Histidine metabolism

Oceanobacillus iheyensis FIR G
Caldicellulosiruptor saccharolyticus FIR G
Clostridium acetobutylicum FIR G
Oceanobacillus ... FIR G
Carboxydothermus hydrogenoformans FIR G
1.00/100
0.99/96
1.00/96
1.00/100
1.00/100
1.00/99
0.2

Syntrophomonas wolfei FIR G
Symbiobacterium thermophilum FIR G
Halothermothrix orenii FIR G
Caldanaerobacter subterraneus FIR G
Carboxydothermus hydrogenoformans FIR G
Moorella thermoacetica FIR G
Q7R5Z7 GIALA Giardia intestinalis FOR G
Syntrophomonas wolfei FIR G
Symbiobacterium thermophilum FIR G
Halothermothrix orenii FIR G
Caldanaerobacter subterraneus FIR G
Carboxydothermus hydrogenoformans FIR G
Moorella thermoacetica FIR G
Q7R5Z7 GIALA Giardia intestinalis FOR G
Syntrophomonas wolfei FIR G
Symbiobacterium thermophilum FIR G
Halothermothrix orenii FIR G
Caldanaerobacter subterraneus FIR G
Carboxydothermus hydrogenoformans FIR G
Moorella thermoacetica FIR G
Q7R5Z7 GIALA Giardia intestinalis FOR G
Syntrophomonas wolfei FIR G
Symbiobacterium thermophilum FIR G
Halothermothrix orenii FIR G
Caldanaerobacter subterraneus FIR G
Carboxydothermus hydrogenoformans FIR G
Moorella thermoacetica FIR G
Q7R5Z7 GIALA Giardia intestinalis FOR G
Syntrophomonas wolfei FIR G
Symbiobacterium thermophilum FIR G
Halothermothrix orenii FIR G
Caldanaerobacter subterraneus FIR G
Carboxydothermus hydrogenoformans FIR G
Moorella thermoacetica FIR G
Q7R5Z7
Candy accession: Q7R406_GIALA
RefSeq accession: XP_001709106.1
Uniprot accession: A8B707_GIALA
Comments: LGT - GI + ONE CANDIDA AND PHAGE
Species affected: GI
Adjacent taxa in tree: Bacteroidetes/Chlorobi - Chlorobium
EC annotation - (Blast/Profile): EC:3.6.1.-
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: Helicase-related protein
Name of enzyme/protein: DNA/RNA helicase
KEGG PATHWAY - level 1: Reaction
KEGG PATHWAY - level 2: Reaction
Species affected: EH
Adjacent taxa in tree: Proteobacteria
EC annotation - (Blast/Profile): EC:1.7.1.4
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: Fe-S cluster assembly protein NifU
Name of enzyme/protein: nitrite reductase [NAD(P)H]
KEGG PATHWAY - level 1: Energy Metabolism
KEGG PATHWAY - level 2: Nitrogen metabolism
Candy accession: Q54B13_DICDI
RefSeq accession: XP_628903.1
Uniprot accession: Q54B13_DICDI
Comments: LGT - DD ONLY
Species affected: DD
Adjacent taxa in tree: Bacteroidetes/Chlorobi - Flavobacterium
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein DDB_G0293956
Name of enzyme/protein: Predicted tRNA-binding protein
KEGG PATHWAY - level 1: Other function - Genetic Information
Processing
KEGG PATHWAY - level 2: na
Candy accession: Q54BY6_DICDI
RefSeq accession: XP_629205.1
Uniprot accession: Q54BY6_DICDI
Comments: LGT - DD ONLY
Species affected: DD
Adjacent taxa in tree: Proteobacteria
EC annotation - (Blast/Profile): EC:3.4.21.26
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein DDB_G0293330
Name of enzyme/protein: Hypothetical protein
KEGG PATHWAY - level 1: Reaction
KEGG PATHWAY - level 2: Reaction

Bacillus weihenstephanensis
FIR
G

Bacillus cereus
FIR
G

Bacillus thuringiensis
FIR
G

Bacillus anthracis
FIR
G

Bacillus cytotoxicus
FIR
G

Bacillus cereus
FIR
G

Bacillus thuringiensis
FIR
G

Bacillus cereus
FIR
G

Bacillus licheniformis
FIR
G

Mycobacterium avium
ACT
G

Bacillus subtilis
FIR
G

Burkholderia pseudomallei
PRO
G

Burkholderia mallei
PRO
G

Burkholderia sp. 383
PRO
G

Burkholderia cenocepacia
PRO
G

Chromobacterium violaceum
PRO
G

Photorhabdus luminescens
PRO
G

Photorhabdus luminescens
PRO
G

Photobacterium profundum
PRO
G

Aliivibrio fischeri
PRO
G

Dictyostelium discoideum
AMO
I

0.98/95
1.00/99
0.97/78
0.98/75
1.00/100
0.98/100
1.00/100
1.00/100
1.00/100
0.2
<table>
<thead>
<tr>
<th>Accession</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Q54LW1_DICDI</td>
<td>Candy accession</td>
</tr>
<tr>
<td>XP_637719.1</td>
<td>RefSeq accession</td>
</tr>
<tr>
<td>Q54LW1_DICDI</td>
<td>Uniprot accession</td>
</tr>
<tr>
<td>LGT - DD ONLY + 2 BACT + ONE ARCHAEA</td>
<td>Comments</td>
</tr>
<tr>
<td>DD</td>
<td>Species affected</td>
</tr>
<tr>
<td>Prokaryotes</td>
<td>Adjacent taxa in tree</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Annotation</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>EC annotation</td>
<td>(Blast/Profile): na</td>
</tr>
<tr>
<td>PHOBIUS SP</td>
<td>0</td>
</tr>
<tr>
<td>PHOBIUS TMD</td>
<td>0</td>
</tr>
<tr>
<td>RefSeq annotation</td>
<td>hypothetical protein DDB_G0286383</td>
</tr>
</tbody>
</table>

**KEGG PATHWAY - level 1:** Other function - Signal Transduction

**KEGG PATHWAY - level 2:** na

**Name of enzyme/protein:** Protein containing GAF domain

**Pseudoalteromonas haloplanktis**

**Chromobacterium violaceum**

**Halobacterium salinarum**

<table>
<thead>
<tr>
<th>Value</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>0.2</td>
<td></td>
</tr>
</tbody>
</table>
Candy accession: Q54TU4_DICDI
RefSeq accession: XP_640717.1
Uniprot accession: Q54TU4_DICDI
Comments: LGT - DD
Species affected: DD
Adjacent taxa in tree: Prokaryotes
EC annotation - (Blast/Profile): na
PHOBIUS SP: Y
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein DDB_G0281495
Name of enzyme/protein: Protein containing DUF377
KEGG PATHWAY - level 1: Function unknown
KEGG PATHWAY - level 2: na

Thermoanaerobacter pseudethanolicus
Caldanaerobacter subterraneus
Symbiobacterium thermophilum
Thermoanaerobacter pseudethanolicus
Bacteroides thetaiotaomicron
Pyrococcus furiosus
Thermococcus litoralis

1.00/99
1.00/100
1.00/100
0.98/78
0.5
Candy accession: Q55G42_DICDI
RefSeq accession: XP_647341.1
Uniprot accession: Q55G42_DICDI
Comments: LGT - DD ONLY
Species affected: DD
Adjacent taxa in tree: Prokaryotes
EC annotation - (Blast/Profile): EC:2.1.1.14
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein DDB_G0267834
Name of enzyme/protein: 5-methyltetrahydropteroyltriglutamate---homocysteine S-methyltransferase
KEGG PATHWAY - level 1: Amino Acid Metabolism
KEGG PATHWAY - level 2: Cysteine and methionine metabolism
Candy accession: Q57XJ4_9TRYP
RefSeq accession: XP_843936.1
Uniprot accession: Q57XJ4_9TRYP
Comments: LGT - KINETOPLASTIDS ONLY
Species affected: LM, LD, TB, TC
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Protein containing phytanoyl-COA dioxygenase domain
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na

Synechococcus sp. JA-2-3Ba(2-13)
Novosphingobium aromaticivorans
Streptomyces kanamyceticus
Rhodopseudomonas palustris
Leishmania major
Leishmania donovani
Trypanosoma brucei
Trypanosoma cruzi

1.00/100
1.00/100
1.00/100
0.5
Candy accession: T57_01777
RefSeq accession: XP_002368713.1
Uniprot accession: B6KLW3_TOXGO
Comments: LGT - APICOMPLEXA ONLY
Species affected: TG, PF, PV, PY
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:3.4.24.-
PHOBIUS SP: 0
PHOBIUS TMD: 6
RefSeq annotation: sterol-regulatory element binding protein site 2 protease, putative
Name of enzyme/protein: Predicted sterol regulatory element-binding protein/peptidase M50 family
protein
KEGG PATHWAY - level 1: Reaction
KEGG PATHWAY - level 2: Reaction
Burkholderia vietnamiensis
Burkholderia ambifaria
Ralstonia solanacearum
Polaromonas sp. JS666
Albidiferax ferrireducens
Geobacillus kaustophilus
Bacillus licheniformis
Bacillus subtilis
Pelobacter propionicus
Pelobacter carbinolicus
Francisella tularensis
Neisseria gonorrhoeae
Neisseria meningitidis
Dechloromonas aromatica
Nitrosomonas eutropha
Syntrophobacter fumaroxidans
Aromatoleum aromaticum
Methylococcus capsulatus
Nitrosococcus oceani
Legionella pneumophila
Rubrobacter xylanophilus
Thermoplasma volcanium
Rhodospirillum rubrum
Magnetococcus sp. MC-1
Listeria innocua
Moorella thermoacetica
Thermoanaerobacter pseudethanolicus
Aquifex aeolicus
Clostridium acetobutylicum
Anaeromyxobacter dehalogenans
Bdellovibrio bacteriovorus
Thiomicrospira crunogena
Coxiella burnetii
Chromobacterium violaceum
Thiobacillus denitrificans
Caldicellulosiruptor saccharolyticus
Mycobacterium bovis
Mycobacterium tuberculosis
Mycobacterium avium
Mycobacterium gilvum
Mycobacterium vanbaalenii
Streptomyces coelicolor
Streptomyces avermitilis
Nocardia farcinica
Thermobifida fusca
Toxoplasma gondii
Caulobacter vibrioides
Plasmodium chabaudi
Plasmodium yoelii
Plasmodium berghei
Plasmodium vivax
Plasmodium falciparum
Candy accession: TV81617225
RefSeq accession: XP_001324287.1
Uniprot accession: A2E5M3_TRIVA
Comments: LGT - TV ONLY
Species affected: TV
Adjacent taxa in tree: Bacteria

EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Predicted D12 class N6 adenine-specific DNA methyltransferase

KEGG PATHWAY - level 1: Other function - Genetic Information Processing
KEGG PATHWAY - level 2: na
Candy accession: TV87640196
RefSeq accession: XP_001327002.1
Uniprot accession: A2DXR9_TRIVA
Comments: LGT - TV TWO NODES + LGT INTO FUNGI
Species affected: TV, FUNGI
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: opdE downstream ORF 2
Name of enzyme/protein: Predicted hydrolases of the alpha/beta superfamily
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na

Shewanella amazonensis
Shewanella sp. ANA-3
Shewanella loihica
Pseudomonas syringae group genomosp. 3
Pseudomonas syringae
Xylella fastidiosa
Aspergillus oryzae
Ralstonia solanacearum
Shewanella baltica
Bdellovibrio bacteriovorus
Pelobacter carbinolicus
Bacteroides thetaiotaomicron
Escherichia coli
Mannheimia succiniciproducens
Helicobacter hepaticus
Enterococcus faecium
Bacteroides fragilis
TV87640196 Trichomonas vaginalis
Methanosarcina acetivorans
Methanosarcina barkeri
Methanococcus maripaludis
Desulfovibrio alaskensis
Escherichia coli
Shigella sonnei
Shigella boydii
Shigella flexneri
Escherichia coli
Vibrio parahaemolyticus
Shewanella loihica
Burkholderia sp. 383
Yarrowia lipolytica
Burkholderia sp. 383
Bacillus cereus
Bacillus cereus
Bacillus thuringiensis
Escherichia coli
Bacillus weihenstephanensis
Clostridium beijerinckii
Pectobacterium atrosepticum
Aspergillus oryzae
Chromobacterium violaceum
Vibrio sp. DAT722
Yersinia pestis
Yersinia pseudotuberculosis
Geobacter uraniireducens
Paracoccus denitrificans
Chelativorans sp. BNC1
Anaeromyxobacter dehalogenans
Candidatus Solibacter usitatus

0.95/97
1.00/100
1.00/100
1.00/99
1.00/100
0.99/99
1.00/99
1.00/74
1.00/78
1.00/100
0.98/100
1.00/87
1.00/82
0.96/81
1.00/82
1.00/100
1.00/87
1.00/100
1.00/92
1.00/100
0.98/85
0.2
Candy accession: TV87759087
RefSeq accession: XP_001312818.1
Uniprot accession: A2F5C5_TRIVA
Comments: LGT - TV TWO NODES + LGT INTO FUNGI

Species affected: TV

Adjacent taxa in tree: Bacteroidetes/Chlorobi - Bacteroides

EC annotation - (Blast/Profile): EC:2.1.1.-

PHOBIUS SP: 0
PHOBIUS TMD: 0

RefSeq annotation: O-methyltransferase N-terminus family

Name of enzyme/protein: transferase

KEGG PATHWAY - level 1: Reaction
KEGG PATHWAY - level 2: Reaction
Candy accession: TV88428064
RefSeq accession: XP_001307952.1
Uniprot accession: A2FJA8_TRIVA
Comments: LGT - TV ONLY
Species affected: TV
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:2.7.7.8
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: S1 RNA binding domain containing protein
Name of enzyme/protein: polyribonucleotide nucleotidyltransferase
KEGG PATHWAY - level 1: Nucleotide Metabolism
KEGG PATHWAY - level 2: Purine metabolism, Pyrimidine metabolism
Candy accession: TV89272063
RefSeq accession: XP_001308218.1
Uniprot accession: A2FIH1_TRIVA
Comments: LGT - TV TWO NODES + ANIMALS
Species affected: TV
Adjacent taxa in tree: Bacteroidetes/Chlorobi - Bacteroides
EC annotation - (Blast/Profile): EC:5.1.3.8
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: renin binding protein
Name of enzyme/protein: N-acylglucosamine 2-epimerase
KEGG PATHWAY - level 1: Carbohydrate Metabolism
KEGG PATHWAY - level 2: Amino sugar and nucleotide sugar metabolism
KINASE domain-containing protein A2DHK4_TRIVA

Comments: LGT - TV TWO NODES + FUNGI

KEGG PATHWAY - level 2: Galactose metabolism, Other glycan degradation, Glycosaminoglycan degradation, Sphingolipid metabolism

EC annotation - (Blast/Profile): EC:3.2.1.23

Adjacent taxa in tree: Bacteroidetes/Chlorobi - Bacteroides

Species affected: TV, FUNGI

RefSeq accession: XP_001581038.1

Candy accession: TV92921294

Uniprot accession: A2DHK4_TRIVA
Candy accession: TV90013073
RefSeq accession: XP_001313313.1
Uniprot accession: A2F3W8_TRIVA
Comments: LGT - TV TWO NODES + FUNGI
Species affected: TV, FUNGI
Adjacent taxa in tree: Proteobacteria - Francisella
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: beta lactamase
Name of enzyme/protein: Predicted Zn-dependent hydrolases of the beta-lactamase
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na

Pseudomonas syringae group genomosp. 3
PRO

Bordetella pertussis
PRO

Shewanella sp. ANA-3
PRO

Actinobacillus succinogenes
PRO

Pseudomonas aeruginosa
PRO

Pseudomonas fluorescens
PRO

Bacillus subtilis
FIR

Bacillus sp. NRRL B-14911
FIR

Bacillus licheniformis
FIR

Synechococcus elongatus
CYA

Trichomonas vaginalis
PAR

Hahella chejuensis
PRO

Nitrobacter hamburgensis
PRO

Trichomonas vaginalis
PAR

Exiguobacterium sibiricum
FIR

Pectobacterium atrosepticum
PRO

Xanthomonas euvesicatoria
PRO

Debaryomyces hansenii
OPI

Escherichia coli
PRO

Shewanella loihica
PRO

Staphylococcus aureus
FIR

TV90013073 Trichomonas vaginalis
PAR

Francisella tularensis
PRO

Flavobacteria bacterium BBFL7
BC

Bdellovibrio bacteriovorus
PRO

Streptomyces coelicolor
ACT

Streptomyces avermitilis
ACT

1.00/100
1.00/100
1.00/73
1.00/95
0.99/80
0.99/81
0.5
Candy accession: TV96353085
RefSeq accession: XP_001307242.1
Uniprot accession: A2FL96_TRIVA
Comments: LGT - TV TWO NODES
Species affected: TV
Adjacent taxa in tree: Bacteroidetes/Chlorobi - Chlorobium
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Protein containing cysteine synthase domain
KEGG PATHWAY - level 1: Function unknown
KEGG PATHWAY - level 2: na
Candy accession: Q7RD47_PLAYO
RefSeq accession: XP_726051.1
Uniprot accession: Q7RD47_PLAYO
Comments: LGT - APICOMPLEXA TWO NODES (+CYANOBACTERIA EGT INTO PLANTS)
Species affected: PF,PV,PY,PB,PC,TA,TG
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:1.1.1.267
PHOBIUS SP: Y
PHOBIUS TMD: 0
RefSeq annotation: 1-deoxy-D-xylulose 5-phosphate reductoisomerase
Name of enzyme/protein: 1-deoxy-D-xylulose 5-phosphate reductoisomerase
KEGG PATHWAY - level 1: Metabolism of Terpenoids and Polyketides
KEGG PATHWAY - level 2: Terpenoid backbone biosynthesis
Candy accession: Q5CYQ7_CRYPV
RefSeq accession: XP_628323.1
Uniprot accession: Q5CYQ7_CRYPV
Comments: LGT - CRYPTOSPORIDIUM ONLY - 3 PAIRS OF CP+CH PARALOGUES
Species affected: CP, CH
Adjacent taxa in tree: Proteobacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 6
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Putative ABC-type long-chain fatty acid transport system
KEGG PATHWAY - level 1: Other function - Membrane transport
KEGG PATHWAY - level 2: na
Candy accession: Q7R1P4_GIALA
RefSeq accession: XP_001706109.1
Uniprot accession: A8BMJ3_GIALA
Comments: LGT - GI TWO NODES - PHAGES - DEAP LGT INTO FUNGI
Species affected: GI, FUNGI
Adjacent taxa in tree: Proteobacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: Phosphatase similar to the C-terminal domain of histone macroH2A1
Name of enzyme/protein: Predicted Macro domain, Poa1p-like family
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na
Candy accession: Q7R6G7_GIALA
RefSeq accession: XP_001707931.1
Uniprot accession: A8BCL1_GIALA
Comments: LGT - GI ONLY
Species affected: GI
Adjacent taxa in tree: Prokaryotes
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: Nitroreductase Fd-NR2
Name of enzyme/protein: Predicted oxidoreductase
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na

Methanosarcina acetivorans EUR
Methanosarcina mazei EUR
Methanosarcina barkeri EUR
Desulfovibrio vulgaris PRO
Syntrophus aciditrophicus PRO
Desulfotomaculum reducens FIR
Clostridium acetobutylicum FIR
Clostridium beijerinckii FIR
Methanococcoides burtonii EUR
Geobacter sulfurreducens PRO
Methanosphaera stadtmanae EUR
Methanospirillum hungatei EUR
Methanospirillum hungatei EUR
Q7R6G7 GIALA Giardia intestinalis FOR
Desulfovibrio alaskensis PRO
Pelobacter carbinolicus PRO
Desulfotalea psychrophila PRO
Pelobacter propionicus PRO
Chlorobaculum tepidum BC

1.00/72
1.00/100
1.00/95
1.00/100
1.00/98
1.00/97
1.00/100
0.5
Species affected: DD

Adjacent taxa in tree: Firmicutes - Bacillus

Comments: LGT - DD TWO NODES

RefSeq annotation: arylamine N-acetyltransferase family protein

RefSeq annotation: arylamine N-acetyltransferase family protein

KEGG PATHWAY - level 1: Biosynthesis of Other Secondary Metabolites, Xenobiotics Biodegradation and Metabolism,

KEGG PATHWAY - level 2: Caffeine metabolism, Nitrotoluene degradation, Drug metabolism - other enzymes
Candy accession: Q55DP5_DICDI
RefSeq accession: XP_646086.1
Uniprot accession: Q55DP5_DICDI
Comments: LGT - DD ONLY
Species affected: DD
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 1
RefSeq annotation: hypothetical protein DDB_G0270564
Name of enzyme/protein: Predicted RNA methyltransferase
KEGG PATHWAY - level 1: Other function - Genetic Information Processing
KEGG PATHWAY - level 2: na

Gloeobacter violaceus
Nitrosococcus oceani
Bacillus halodurans
Q55DP5 DICDI Dictyostelium discoideum
Rhodopseudomonas palustris
Burkholderia thailandensis
Burkholderia pseudomallei
Burkholderia mallei

1.00/100
0.97/82
0.5
Candy accession: TV80444129
RefSeq accession: XP_001317907.1
Uniprot accession: A2ENQ8_TRIVA
Comments: LGT - TV TWO NODES + LGT INTO FUNGI
Species affected: TV, FUNGI
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:4.2.1.1
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: Carbonic anhydrase family protein
Name of enzyme/protein: Carbonic anhydrase
KEGG PATHWAY - level 1: Energy Metabolism
KEGG PATHWAY - level 2: Nitrogen metabolism
Candy accession: TV80724024
RefSeq accession: XP_001300299.1
Uniprot accession: A2G653_TRIVA
Comments: LGT - TV TWO NODES + LGT INTO FUNGI
Species affected: TV, FUNGI
Adjacent taxa in tree: Firmicutes - Clostridium
EC annotation - (Blast/Profile): EC:3.2.1.17
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: glycosyl hydrolase
Name of enzyme/protein: lysozyme
KEGG PATHWAY - level 1: Reaction
KEGG PATHWAY - level 2: Reaction
Candy accession: TV80792013
RefSeq accession: XP_001579050.1
Uniprot accession: A2DN76_TRIVA
Comments: LGT - TV ONLY
Species affected: TV
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: hypothetical protein
Name of enzyme/protein: Predicted DNA polymerase
KEGG PATHWAY - level 1: Other function - Genetic Information
Processing
KEGG PATHWAY - level 2: na
Candy accession: TV90013073
RefSeq accession: XP_001313313.1
Uniprot accession: A2F3W8_TRIVA
Comments: LGT - TV TWO NODES + ONE FUNGI
Species affected: TV
Adjacent taxa in tree: Proteobacteria - Francisella
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: Zn-dependent hydrolase of beta-lactamase
Name of enzyme/protein: Zn-dependent hydrolase of beta-lactamase
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na

PRO
G
Bordetella pertussis

PRO
G
Shewanella sp. ANA-3

PRO
G
Actinobacillus succinogenes

PRO
G
Pseudomonas aeruginosa

PRO
G
Pseudomonas fluorescens

PRO
G
Nitrobacter hamburgensis

PRO
G
Trichomonas vaginalis

PAR
I
Shewanella loihica

PRO
G
Escherichia coli

PAR
I
Trichomonas vaginalis

OPI
I
Debaryomyces hansenii

CYA
G
Hahella chejuensis

PRO
G
Xanthomonas euvesicatoria

PRO
G
Bacillus subtilis

FIR
G
Bacillus sp. NRRL B-14911

FIR
G
Bacillus licheniformis

FIR
G
Staphylococcus aureus

FIR
G
Pectobacterium atrosepticum

PRO
G
Exiguobacterium sibiricum

PRO
G
TV90013073 Trichomonas vaginalis

PRO
G
Francisella tularensis

Flavobacteria bacterium BBFL7

Bdellovibrio bacteriovorus

Streptomyces coelicolor

Streptomyces avermitilis

1.00/100

1.00/100

1.00/73

1.00/95

0.99/80

0.99/81

0.5
Candy accession: TV87998038
RefSeq accession: XP_001302090.1
Uniprot accession: A2G102_TRIVA
Comments: LGT - TV TWO NODES
Species affected: TV
Adjacent taxa in tree: Prokaryotes
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 11
RefSeq annotation: major facilitator superfamily transporter
Name of enzyme/protein: major facilitator superfamily transporter
KEGG PATHWAY - level 1: Other function - Membrane transport
KEGG PATHWAY - level 2: na

Azotobacter vinelandii
Bacillus licheniformis
Pseudomonas fluorescens
Candidatus Solibacter usitatus
Burkholderia thailandensis
Xenopus (Silurana) tropicalis
Macaca fascicularis
Tetraodon nigroviridis
Danio rerio
Photobacterium sp. SKA34
Sulfolobus tokodaii
Thermoplasma volcanium
Sulfolobus solfataricus
Ferroplasma acidarmanus
Arabidopsis thaliana
Nocardia farcinica
Arthrobacter sp. FB24
Burkholderia mallei
Magnetospirillum magneticum
Streptomyces avermitilis
Burkholderia cenocepacia
Burkholderia sp. 383
Leptospira interrogans
Candy accession: TV92683026
RefSeq accession: XP_001302496.1
Uniprot accession: A2FZU4_TRIVA
Comments: LGT - TV TWO NODES
Species affected: TV
Adjacent taxa in tree: Prokaryotes
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: nitroimidazole resistance protein
Name of enzyme/protein: Predicted flavin-nucleotide-binding protein/5-nitroimidazole antibiotic
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na
Candy accession: Q516J9_ENTHI
RefSeq accession: XP_654156.2
Uniprot accession: C4LU35_ENTHI
Comments: LGT - EH TWO NODES
Species affected: EH
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): na
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: 5-nitroimidazole antibiotic resistance protein
Name of enzyme/protein: Predicted flavin-nucleotide-binding protein/5-nitroimidazole antibiotic
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na
Candy accession: TV94275097
RefSeq accession: XP_001313279.1
Uniprot accession: A2F3Z6_TRIVA
Comments: LGT - TV TWO NODES + LGT INTO FUNGI
Species affected: TV, FUNGI
Adjacent taxa in tree: Bacteroidetes/Chlorobi - Bacteroides
EC annotation - (Blast/Profile): EC:5.1.3.3
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: Aldose 1-epimerase family protein
Name of enzyme/protein: Aldose 1-epimerase
KEGG PATHWAY - level 1: Carbohydrate Metabolism
KEGG PATHWAY - level 2: Glycolysis / Gluconeogenesis
Species affected: TV

Adjacent taxa in tree: Bacteria

EC annotation - (Blast/Profile): EC: 5.1.3.2

PHOBIUS SP: 0

PHOBIUS TMD: 1

RefSeq annotation: hypothetical protein

Name of enzyme/protein: UDP-glucose 4-epimerase

KEGG PATHWAY - level 1: Carbohydrate Metabolism

KEGG PATHWAY - level 2: Galactose metabolism, Amino sugar and nucleotide sugar metabolism
Candy accession: EAL47525
RefSeq accession: XP_652912.1
Uniprot accession: C4M4C4_ENTHI
Comments: LGT - EH ONLY
Species affected: EH
Adjacent taxa in tree: Prokaryotes
EC annotation - (Blast/Profile): na
PHOBIUS SP: Y
PHOBIUS TMD: 0
RefSeq annotation: competence protein ComEC
Name of enzyme/protein: Predicted lactamase B superafamily
KEGG PATHWAY - level 1: Other function
KEGG PATHWAY - level 2: na
Candy accession: TV143798005
RefSeq accession: XP_001294330.1
Uniprot accession: A2GN67_TRIVA
Comments: LGT - TV ONLY
Species affected: TV
Adjacent taxa in tree: Bacteria
EC annotation - (Blast/Profile): EC:2.4.1.58
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: glycosyl transferase
Name of enzyme/protein: lipopolysaccharide glucosyltransferase I
KEGG PATHWAY - level 1: Glycan Biosynthesis and Metabolism
KEGG PATHWAY - level 2: Lipopolysaccharide biosynthesis

Brachyspira murdochii
Ralstonia eutropha
Salmonella enterica
Bacteroides fragilis
Actinobacillus minor
Trichomonas vaginalis
Enterococcus faecium
Lactobacillus johnsonii
Streptococcus mitis
Clostridium leptum
Haemophilus ducreyi
Neisseria gonorrhoeae

1.00/100
0.5
Candy accession: EAL49869
RefSeq accession: XP_655257.1
Uniprot accession: Q769I7_ENTHI
Comments: LGT - EH TWO NODES
Species affected: EH
Adjacent taxa in tree: Proteobacteria
EC annotation - (Blast/Profile): EC:2.8.1.7
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: cysteine desulfurase
Name of enzyme/protein: Cysteine desulfurase
KEGG PATHWAY - level 1: Metabolism of Cofactors and Vitamins
KEGG PATHWAY - level 2: Thiamine metabolism
Candy accession: TC0085
RefSeq accession: XP_803162.1
Uniprot accession: PRCMB_TRYCR
Comments: LGT - TC TWO NODES
Species affected: TC
Adjacent taxa in tree: Firmicutes - Clostridium
EC annotation - (Blast/Profile): EC:5.1.1.4
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: proline racemase
Name of enzyme/protein: Proline racemase
KEGG PATHWAY - level 1: Amino Acid Metabolism
KEGG PATHWAY - level 2: Arginine and proline metabolism
Candy accession: XP 001330346
RefSeq accession: XP_001330346
Uniprot accession: A2F0H0_TRIVA
Comments: LGT - TV TWO NODES
Species affected: TV
Adjacent taxa in tree: Protobacteria
EC annotation - (Blast/Profile): EC:2.2.1.2
PHOBIUS SP: 0
PHOBIUS TMD: 0
RefSeq annotation: Transaldolase A
Name of enzyme/protein: Transaldolase
KEGG PATHWAY - level 1: Carbohydrate Metabolism
KEGG PATHWAY - level 2: Pentose phosphate pathway