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Abb	Organism	Accession	Position	Genes
<b>Bacillus/Clostridium</b>				
Bsu	<i>Bacillus subtilis</i>	NC_000964.1	+ 1375803 1375900	<i>ykkC</i> <a href="#">COG2076</a> <i>ykkD</i> <a href="#">COG2076</a>
Bsu	<i>Bacillus subtilis</i>	NC_000964.1	- 3987634 3987722	<i>yxD</i> <a href="#">COG1284</a>
Oih	<i>Oceanobacillus iheyensis</i>	NC_004193.1	- 3401641 3401723	<i>OB3264</i> <a href="#">COG2076</a> <i>OB3263</i> <a href="#">COG2076</a>
Bha	<i>Bacillus halodurans</i>	NC_002570.1	- 741877 741966	<i>BH0686</i> <a href="#">COG2076</a> <i>BH0685</i> <a href="#">COG2076</a>
Tte	<i>Thermoanaerobacter tengcongensis</i>	NC_003869.1	+ 586463 586553	<i>TTE0584</i> <a href="#">COG2252</a>
Gst	<i>Geobacillus stearothermophilus</i>	gnl OUACGT_1422 bstearo.fasta.screen.Contig257	+ 8552 8641	<i>NA</i>
<b>Cyanobacteria</b>				
Syn	<i>Synechocystis</i>	NC_000911.1	- 801282 801389	<i>speB</i> <a href="#">COG0010</a>
<b>Alpha Proteobacteria</b>				
Rpa	<i>Rhodopseudomonas palustris</i>	NZ_AAAF01000001.1	- 3051748 3051838	<i>Rpa12681</i> <a href="#">COG0715</a> <i>Rpa12680</i> <a href="#">COG0600</a> <i>Rpa12679</i> <a href="#">COG1116</a> <i>Rpa12678</i> <a href="#">COG3665</a> <i>Rpa12677</i> <a href="#">COG3665</a>
Rle	<i>Rhizobium leguminosarum</i>	gnl Sanger_216596 rhiz361f07.slk	+ 9906 10000	- <a href="#">COG0715</a> ... ?
<b>Beta Proteobacteria</b>				
Bfu	<i>Burkholderia fungorum</i>	NZ_AAAJ020000045	- 41546 41664	<i>Bcep4105</i> <a href="#">COG3665</a> <i>Bcep4104</i> <a href="#">COG3665</a> <i>Bcep4103</i> <a href="#">COG4770</a> <i>Bcep4102</i> <a href="#">COG0154</a> <i>Bcep4101</i> <a href="#">COG0600</a>
Bfu	<i>Burkholderia fungorum</i>	NZ_AAAJ020000045	+ 44724 44857	<i>Bcep4100</i> <a href="#">COG1116</a> <i>Bcep4109</i> <a href="#">COG0715</a>
Bce	<i>Burkholderia cenocepacia</i>	gnl Sanger_216591 Bcep1157h02.pic	- 576042 576159	- <a href="#">COG3665</a> ... ?
Neu	<i>Nitrosomonas europaea</i>	NC_004757.1	+ 2634433 2634522	<i>NE2420</i> <a href="#">COG4770</a>
Neu	<i>Nitrosomonas europaea</i>	NC_004757.1	- 2634103 2634191	<i>NE2419</i> <a href="#">COG0531</a> <i>NE2418</i> <a href="#">COG3665</a> <i>NE2417</i> <a href="#">COG3665</a> <i>NE2416</i> <a href="#">COG1984</a>
<b>Gamma Proteobacteria</b>				
Psy	<i>Pseudomonas syringae</i>	NC_004578.1	+ 4771381 4771469	<i>PSPTO4238</i> <a href="#">COG0715</a> <i>PSPTO4239</i> <a href="#">COG0600</a> <i>PSPTO4240</i> <a href="#">COG1116</a> <i>PSPTO4241</i> <a href="#">COG3665</a> <i>PSPTO4242</i> <a href="#">COG3665</a>
Pfl	<i>Pseudomonas fluorescens</i>	NZ_AAAT020000050.1	- 44662 44748	<i>Pflu2166</i> <a href="#">COG0715</a> <i>Pflu2165</i> <a href="#">COG0600</a> <i>Pflu2164</i> <a href="#">COG1116</a> <i>Pflu2163</i> <a href="#">COG3665</a> <i>Pflu2162</i> <a href="#">COG3665</a>
Ech	<i>Erwinia chrysanthemi</i>	gnl TIGR_198628 contig:223	+ 549581 549661	- <a href="#">COG0715</a> ... ?
Mde	<i>Microbulbifer degradans</i>	NZ_AABI02000012.1	+ 100719 100778	<i>Mdeg2136</i> <a href="#">COG0715</a> <i>Mdeg2137</i> <a href="#">COG0600</a> <i>Mdeg2138</i> <a href="#">COG1116</a> <i>Mdeg2139</i> <a href="#">COG3665</a> <i>Mdeg2140</i> <a href="#">COG3665</a>
<b>Epsilon Proteobacteria</b>				
Wsu	<i>Wolinella succinogenes</i>	NC_005090.1	+ 1067291 1067378	<i>WS1110</i> <a href="#">COG0715</a> <i>WS1111</i> <a href="#">COG0600</a> <i>WS1112</i> <a href="#">COG1116</a> <i>WS1113</i> <a href="#">COG3665</a> <i>WS1114</i> <a href="#">COG3665</a>
COG	Gene	Description		
<a href="#">COG3665</a>	<i>BS_ycgI</i>	Uncharacterized conserved protein		
<a href="#">COG2076</a>	<i>emrE</i>	Membrane transporters of cations and cationic drugs		
<a href="#">COG0715</a>	<i>ssuA</i>	ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components		
<a href="#">COG0600</a>	<i>ssuC</i>	ABC-type nitrate/sulfonate/bicarbonate transport systems, permease component		
<a href="#">COG1116</a>	<i>ssuB</i>	ABC-type nitrate/sulfonate/bicarbonate transport systems, ATPase component		
<a href="#">COG4770</a>	-	Acetyl/propionyl-CoA carboxylase, alpha subunit		
<a href="#">COG0010</a>	<i>speB</i>	Arginase/agmatinase/formiminoglutamate hydrolase, arginase family		
<a href="#">COG1984</a>	<i>ybgK</i>	Allophanate hydrolase subunit 2		
<a href="#">COG1284</a>	<i>BS_ydeO</i>	Uncharacterized conserved protein		
<a href="#">COG0154</a>	<i>BS_yerM</i>	Asp-tRNAAsn/Glu-tRNA <sub>Gln</sub> amidotransferase A subunit and related amidases		
<a href="#">COG2252</a>	<i>ygfQ</i>	Permeases		
<a href="#">COG0531</a>	<i>aniC</i>	Amino acid transporters		





