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Abb	Organism	Accession	Position	Genes
Bacillus/Clostridium				
# Bha	<i>Bacillus halodurans</i>	NC_002570.1	- 2941523 2941593	<i>BH2816</i> COG0404 <i>BH2815</i> COG0403 <i>BH2814</i> COG1003
# Bsu	<i>Bacillus subtilis</i>	NC_000964.1	- 2548793 2548870	<i>yqhI</i> COG0404 <i>yqhJ</i> COG0403 <i>yqhK</i> COG1003
# Lin	<i>Listeria innocua</i>	NC_003212.1	+ 1379638 1379705	<i>lin1385</i> COG0404 <i>lin1386</i> COG0403 <i>lin1387</i> COG1003
# Lmo	<i>Listeria monocytogenes</i>	NC_003210.1	+ 1936246 1936313	<i>lmo1348</i> COG0404 <i>lmo1349</i> COG0403 <i>lmo1350</i> COG1003
# Oih	<i>Oceanobacillus iheyensis</i>	NC_004193.1	- 1936246 1936313	<i>OB1904</i> COG0404 <i>OB1903</i> COG0403 <i>OB1902</i> COG1003
# Sau	<i>Staphylococcus aureus</i>	NC_002745.1	- 1576878 1576951	<i>SA1367</i> COG0404 <i>SA1366</i> COG0403 <i>SA1365</i> COG1003
* Cac	<i>Clostridium acetobutylicum</i>	NC_003030.1	- 1621894 1621959	<i>CAC1472</i> COG1115
* Cte	<i>Clostridium tetani</i>	NC_004557.1	- 2100508 2100583	<i>CTC01975</i> COG1115
* Smu	<i>Streptococcus mutans</i>	NC_004350.1	+ 1115974 1116035	<i>SMU.1175</i> COG1115
* Spn	<i>Streptococcus pneumoniae</i>	NC_003028.1	+ 387505 387569	<i>SP0408</i> COG1115
* Spy	<i>Streptococcus pyogenes</i>	NC_002737.1	+ 1046454 1046516	<i>SPy1270</i> COG1115
Alpha Proteobacteria				
# Atu	<i>Agrobacterium tumefaciens</i>	NC_003304.1	- 1462303 1462366	<i>gcvT</i> COG0404 <i>gcvH</i> COG0509 <i>gcvP</i> COG1003
# Bja	<i>Bradyrhizobium japonicum</i>	NC_004463.1	+ 6318654 6318705	<i>gcvT</i> COG0404 <i>gcvH</i> COG0509 <i>gcvP</i> COG1003
# Bme	<i>Brucella melitensis</i> chr II	NC_003318.1	+ 584402 584462	<i>BMEII0559</i> COG0404 <i>BMEII0560</i> COG0509 <i>BMEII0561</i> COG1003
# Brs	<i>Brucella suis</i> chr II	NC_004311.1	- 713331 713391	<i>gcvT</i> COG0404 <i>gcvH</i> COG0509 <i>gcvP</i> COG1003
# Ccr	<i>Caulobacter crescentus</i>	NC_002696.2	- 3606442 3603508	<i>CC3355</i> COG0404 <i>CC3354</i> COG0509 <i>CC3353</i> COG0403 CC3352 COG1003
# Mlo	<i>Mesorhizobium loti</i>	NC_002678.1	+ 707702 707764	<i>mlr0883</i> COG0404 <i>mlr0884</i> COG0509 <i>mlr0885</i> COG1003
# Mlo	<i>Mesorhizobium loti</i> pMLa	NC_002679.1	+ 179384 179449	<i>mlr9201</i> COG0665 <i>msr9402</i> COG3193
# Rpa	<i>Rhodopseudomonas palustris</i>	NZ_AAAF01000001.1	+ 379419 379484	<i>Rpa10333</i> COG0404 <i>rpa10334</i> COG0509 <i>Rpa10335</i> COG1003
# Sme	<i>Sinorhizobium meliloti</i>	NC_003047.1	- 1674916 1674979	<i>gcvT</i> COG0404 <i>gcvH</i> COG0509 <i>gcvP</i> COG1003
Beta Proteobacteria				
# Rso	<i>Ralstonia solanacearum</i>	NC_003295.1	+ 3545587 3545660	<i>gcvT</i> COG0404 <i>gcvH</i> COG0509 <i>gcvP</i> COG1003
Gamma Proteobacteria				
* Vch	<i>Vibrio cholerae</i> chr I	NC_002505.1	- 1520438 1520513	<i>VC1422</i> COG1115
* Vvu	<i>Vibrio vulnificus</i> chr I	NC_004459.1	+ 2743961 2744036	<i>VV12695</i> COG1115
Actinobacteria				
# Mtu	<i>Mycobacterium tuberculosis</i>	NC_000962.1	- 79214 79280	<i>glyA2</i> COG0112 <i>sdaA</i> COG1760
# Mtu	<i>Mycobacterium tuberculosis</i>	NC_000962.1	+ 2075623 2075696	<i>gcvB</i> COG1003
# Sco	<i>Streptomyces coelicolor</i>	NC_003888.1	- 1457856 1457927	<i>SC10A9.20c</i> COG1003
# Sco	<i>Streptomyces coelicolor</i>	NC_003888.1	- 5959014 5959083	<i>gcvI</i> COG0404 <i>gcvH</i> COG0509 <i>glyA2</i> COG0112 <i>sdaA</i> COG1760

Type I = #, Type II = *

COG	Gene	Description
COG0403	<i>gcvP_1</i>	Glycine cleavage system protein P (pyridoxal-binding), N-terminal domain
COG1003	<i>gcvP_2</i>	Glycine cleavage system protein P (pyridoxal-binding), C-terminal domain
COG0404	<i>gcvI</i>	Glycine cleavage system T protein (aminomethyltransferase)
COG0509	<i>gcvH</i>	Glycine cleavage system H protein (lipoate-binding)
COG1115	<i>yaaJ</i>	Na ⁺ /alanine symporter
COG0112	<i>glyA</i>	Glycine/serine hydroxymethyltransferase
COG1760	<i>sdaA</i>	L-serine deaminase
COG1113	<i>ansP</i>	Gamma-aminobutyrate permease and related permeases
COG0665	<i>dadA</i>	Glycine/D-amino acid oxidases (deaminating)
COG3193	<i>glcG</i>	Uncharacterized protein, possibly involved in utilization of glycolate and propanediol

