Abb Organism	Accession	Position	Genes							
Bacillus/Clostridium										
# Bha <i>Bacillus halodurans</i>	NC 002570.1	- 2941523 2941593	BH2816	COG0404 E	3H2815	COG0403	BH2814	COG1003		
# Bsu <i>Bacillus subtilis</i>	NC 000964.1	- 2548793 2548870	yqhI	COG0404 y	7qhJ	COG0403	yqhK	COG1003		
# Lin <i>Listeria innocua</i>	NC 003212.1	+ 1379638 1379705	lin1385	COG0404 1	lin1386	COG0403	lin1387	COG1003		
<i>#</i> Lmo <i>Listeria monocytogenes</i>	NC 003210.1	+ 1372852 1372912	lmo1348	COG0404 1	lmo1349	COG0403	1mo1350	COG1003		
# Oih Oceanobacillus iheyensis	NC 004193.1	- 1936246 1936313	OB1904	COG0404 0	DB1903	COG0403	OB1902	COG1003		
# Sau Staphylococcus aureus	NC_002745.1	- 1576878 1576951	SA1367	COG0404 S	SA1366	COG0403	SA1365	COG1003		
* Cac Clostridium acetobutylicum	NC 003030.1	- 1621894 1621959	CAC1472	COG1113						
* Cte Clostridium tetani	NC 004557.1	- 2100508 2100583	CTC01975	COG1115						
* Smu Streptococcus mutans	NC_004350.1	+ 1115974 1116035	SMU.1175	COG1115						
* Spn Streptococcus pneumoniae	NC_003028.1	+ 387505 387569	SP0408	COG1115						
* Spy Streptococcus pyogenes	NC_002737.1	+ 1046454 1046516	<i>SPy1270</i>	COG1115						
Alpha Proteobacteria										
# Atu Agrobacterium tumefaciens	NC_003304.1	- 1462303 1462366	gcvT	COG0404 g	<i>JCVH</i>	COG0509	gcvP	COG1003		
# Bja Bradyrhizobium japonicum	NC_004463.1	+ 6318654 6318705	gcvT	COG0404 g	<i>JCVH</i>	COG0509	gcvP	COG1003		
# Bme Brucella melitensis chr II	NC_003318.1	+ 584402 584462	BMEI10559	COG0404 E	BMEII0560	COG0509	BMEII0561	COG1003		
# Brs <i>Brucella suis</i> chr II	NC_004311.1	- 713331 713391	gcvT	COG0404 g	<i>JCVH</i>	COG0509	gcvP	COG1003		
# Ccr Caulobacter crescentus	NC_002696.2	- 3606442 3603508	CC3355	COG0404 C	CC3354	COG0509	CC3353	COG0403	CC3352	COG100
# Mlo Mesorhizobium loti	NC_002678.1	+ 707702 707764	mlr0883	COG0404 n	nlr0884		mlr0885	COG1003		
# Mlo <i>Mesorhizobium loti</i> pMLa	NC_002679.1	+ 179384 179449	mlr9201	COG0665 n	nsr9402	COG3193				
<pre># Rpa Rhodopseudomonas palustris</pre>	NZ_AAAF01000001.	1 + 379419 379484	<i>Rpa10333</i>	COG0404 r			<i>Rpa10335</i>	COG1003		
# Sme Sinorhizobium meliloti	NC_003047.1	- 1674916 1674979	gcvT	COG0404 g	JCVH	COG0509	gcvP	COG1003		
Beta Proteobacteria										
# Rso Ralstonia solanacearum	NC_003295.1	+ 3545587 3545660	gcvT	COG0404 g	<i>JCVH</i>	COG0509	gcvP	COG1003		
Gamma Proteobacteria										
* Vch <i>Vibrio cholerae</i> chr I	NC_002505.1	- 1520438 1520513	VC1422	COG1115						
* Vvu Vibric vulnificus chr I	NC_004459.1	+ 2743961 2744036	VV12695	COG1115						
Actinobacteria										
# Mtu Mycobacterium tuberculosis	NC_000962.1	- 79214 79280	glyA2	COG0112 s	sdaA	COG1760				
# Mtu Mycobacterium tuberculosis	NC_000962.1	+ 2075623 2075696	gcvB	COG1003						
# Sco Streptomyces coelicolor	NC_003888.1	- 1457856 1457927	SC10A9.20c							
# Sco Streptomyces coelicolor	NC_003888.1	- 5959014 5959083	gcvI	COG0404 g	JCVH	COG0509	glyA2	COG0112	sdaA	COG176
Type I = $\#$, Type II = *										
COG Gene Description										
		pyridoxal-binding), N								
COG1003 gcvP_2 Glycine cleavage				omain						
		aminomethyltransferas	se)							
	e system H protein (lipoate-binding)								
COG1115 yaaJ Na+/alanine symp										
	nydroxymethyltransfe	erase								
COG1760 sdaA L-serine deamina										
	ate permease and re									
	acid oxidases (deam				_					
COG3193 glcG Uncharacterized	protein, possibly i	nvolved in utilizatio	on of glycol	ate and pr	copanediol	L				

n	Class I	*
В	Structure	······································
	Consensus	
		CAGAUUGAUAAAAAGCGGAUGAA <mark>AGCAAGGCGAGAGACACUGCA</mark> AGGAAUGAGCGCCCGAAGGAGCAAA <mark>GACA</mark> AUUAGGG
		GCAUGAAAAUAUGAGCGAAUGAC <mark>AGCAAGGGGAGAGACCUG</mark> A <mark>CCGA</mark> -AAACC <mark>UCGG</mark> GAUA <mark>CAGG</mark> CGCCGAAGGAGCAA- <mark>ACU</mark> GCGG <mark>ACU</mark> GAA <mark>UCUCUC</mark> AGGC-AAAAG-AA- <mark>CUCUUGCU</mark> CGACGCAA
		ACAUAAUAGAAUUAGCGGGUGAA <mark>UGUAAACAGAGAC</mark> A <mark>CUGU</mark> GAAAAGCAGCGCCGACGGGGAAAG <mark>CAUA</mark> AGUUA <mark>UCUCC</mark> AAGGC-AAAAG-GA- <mark>UGUUUACC</mark> GGACGCAA
		ACAUAAUAGAAUUAGCGGGUGAA <mark>UGUAAGCAGAGAC</mark> A <mark>CUGC</mark> GAAAAGCAGCGCCGACGGGGAAA-CCAUAUAUUAUGUGAAACUCUCAGGC-AAAAG-GA- <mark>UGUUUACC</mark> GGACGCAA
	Oih 0B1904	UACAUAUUUCAUCAUCAGCGGAAGAU <mark>UACAAGGGGAGAG</mark> U <mark>UUAC</mark> AACGAAUAG <mark>UDAA</mark> CGCCGAAGGAGCAA- <mark>CU</mark> GAAGA <mark>CC</mark> GAAU <mark>CUCUC</mark> AGGCCAAAAA-GA- <mark>CUCUUGUA</mark> UGACGCAA
	Sau SA1367	UAAAUUUAAUAAAAGCGAGUGAU <mark>CAGUAUUAGAGAC</mark> AAUAGAGCGUUAAGAC <mark>UUUAU</mark> CGCCGAAGGUGCAA- <mark>CUAH</mark> UUUAUUUACGAAA <mark>CUCUC</mark> AGGC-AAAAG-GA- <mark>UAAUACUC</mark> UAACGCGU
	Atu gcvI	UCGAAGAUAAUGAGCGUCGCA <mark>UCAUCGUUGGGAGA</mark> AA <mark>CCGC</mark> UUCAUUGCGGUGCCGAAGGAGCAA-CCG
	Bja gcvT	UGUACCCAUCUGUAUCGUACG <mark>CCCACCUCGGGAGAC</mark> A <mark>CCGGCU</mark> UUAGGC <mark>AGCCGG</mark> CGCCGAAGGAGCAA- <mark>CCC</mark> CCC <mark>CCC</mark> -AAA <mark>CUCUC</mark> AGGC-AAAAG-GA- <mark>CCG-</mark> QGUGGCUUUGACAGC
		CGUGUGGGGUGUUCUUGCACUG <mark>UCUGUGUGCGGGGGAGAGA<mark>GCC</mark>GUUAAG<mark>GGC</mark>CGCCGAAGGGGGAAAACGCCCGAAA<mark>UCUCUC</mark>AGGU-ACAAG-GAA<mark>CCGCAGGCGGGC</mark>UAAGACAA</mark>
	Brs gcvI	CGUGUGGGGUGUUUUUGCACUG <mark>UCUGUUUGCGGGAGAGAGCC</mark> GUUAAGGCCGCCGAAGGGGGAAAACGCCCGAAA <mark>UCUCUG</mark> AGGU-ACAAG-GAA <mark>CCGCAGGCCGC</mark> UAAGACAA
	Ccr CC3355	CUGUCCCUCAAAGAGCCCUC <mark>GACCCUCGCGGGAGACAUCGGGA</mark> UUCGA <mark>UCCCGA</mark> GGCCGAAGGCGCAA- <mark>CCG</mark> CCCCCG-AAACGCUCAGGC-AAAAG-GA-CCGCGCGGGUUUAGGAA
	Mlo mlr0883	
	Mlo mlr9201	GUAUAACUGCGGUGUUCAAAG <mark>CCUGGA-CGGGAGAGAUCGGC</mark> UACU
	Rpa Rpa10333	
	Sme gcvI	
	2	
	Mtu gcvB	ACGCUGGCAAACGCUGCUGACCCCCCCCGCGCGCGCGCAGACUCCCCGGCGACGCCCCCGAAGGACCCAAAGACCAACACCCCCC
	Sco gcvI	
	Class II	
	Consensus	gACuGyR.UgGA.GRA.YucUGGAGAga.YA.CGCCGAaGGCGCAA
	Cte CTC01975	UGGCGAGGACUGU-UAUUGGACGAAA <mark>CUCUGGAGAGA</mark> GACUUUUUUUAU <mark>AAAAGAG</mark> CACCGAAGGAGCAA- <mark>UUUG</mark> GUAAAA <mark>CCAAU</mark> GAAACUCUCAGGU-AAAAG-GA- <mark>CAGAG</mark> CGUAGAAGUGAAGUUUAAAUC
	Smu SMU.1175	UUAGGAUAACUGA-UAAUUGACGGAC <mark>UUCUGGAGAC</mark> A <mark>CCU</mark> ACUACU
	Spn SP0408	
	Spy SPy1270	UGAACGGGACUGUUUGAUGGACGGA <mark>CUUCUGGAGAGACCU</mark> UAUU <mark>AGG</mark> CGCCGAAGGGGCAA- <mark>GCCA</mark> UAC <mark>UGCU</mark> CAA <mark>UCUCUC</mark> AGGC-AAAAG-GA- <mark>CAGAAG</mark> GUAAAAUACAAAACACCAUUA
	Vch VC1422	AAGCGAGGACUGU-AGUUGGAGGAACCUCUGGAGAGACAACCGUUUAAUCCGGUCGCCGAAGGAGCAA-CCUCUCC-GCAUAUCCACACGUCAGAGCAAAGCCAAAGCGACCAAAGGCCAAUCUUUUA
	Vvu VV12695	AUGCGAGGACUGU-AGUUGGAGGAA <mark>CCUCUGGAGAG</mark> A <mark>ACCG</mark> UUAAAU <mark>CGGU</mark> CGCCGAAGGAGCAA- <mark>CUCUCG</mark> C-CCAUGU <mark>CCACGCU</mark> GAAA <mark>CUCUC</mark> AGGC-AAAAG-GA- <mark>CAGAGG</mark> AGUGGAAAGUUAUACCCCAA
	Lin 1in1385 Lmo 1mo1348 Oih OB1904 Sau SA1367 Atu gcvI Bja gcvT Bme BMEII0559 Brs gcvI Ccr CC3355 Mlo m1r0883 Mlo m1r9201 Rpa Rpa10333 Sme gcvI Rso gcvI Mtu glyA2 Mtu gcvB	
	Class II Consensus Cac CAC1472 Cte CTC01975 Smu SMU.1175 Spn SP0408 Spy SPy1270 Vch VC1422	AAGUAAUAUGAUAAAUUACUUCAAUUCAUAUCUUAUCCAUUGUGUCUCCAAUCAUAAAAUAUUUAUAGCGAAGAAGGCAUUUUUGAUACAUGCCUCUCGACUAAGAUGGAGGGAUAAAAUGGAUCAAACAAA

