	Organism		Accession	Position	Genes						
Bacillus/Clostridium											
Ban	an Bacillus anthracis		NC_003997.3	+ 1768115 1768228	BA1886						
	Bce Bacillus cereus		NC_004722.1	+ 1762546 1762659	BC1807	COG0531					
	Bha Bacillus halodurans		NC_002570.1	+ 632297 632415	BH0597	COG0569	BH0598	COG0168			
	Bacillus su		NC_000964.1	+ 485659 485769	yda0	COG0531					
	Bsu Bacillus subtilis		NC_000964.1	+ 3187277 3187391	yuaA	COG0569	yubG	COG0168			
	Cac Clostridum acetobutylicum		NC_003030.1	+ 1374250 1374352	CAC1232	COG0739					
	Cac Clostridum acetobutylicum		NC_003030.1	+ 3232101 3232194	CAC3081	COG3773					
	Cth Clostridium thermocellum		NZ_AABG02000023.1	- 19901 19999	Chte1033						
	Oih Oceanobacillus iheyensis		NC_004193.1	+ 1706113 1706226	OB1662	COG0569		COG0168 OB1664	COG0168		
	Tte Thermoanaerobacter tengcongensis		NC_003869.1	+ 927272 927372	TTE0923	COG0362	MetH	COG1410			
	Tte Thermoanaerobacter tengcongensis		NC_003869.1	+ 1020691 1020786	lytE	COG0739	_				
	Tte Thermoanaerobacter tengcongensis		NC_003869.1	- 1853287 1853392	OppA9	COG0747	DppB5	COG0601 DppC5	COG1173 DppD5	COG0444 OppF5	COG1124
Actinobacteria Cql Corynebacterium glutamicum NC 003450.2 - 2320625 2320754 NCgl2108 COG0791											
	Cgl Corynebacterium glutamicum		NC_003450.2	- 2320625 2320754							
	Sav Streptomyces avermitilis Sco Streptomyces coelicolor		NC_003155.2 NC 003888.3	- 5051496 5051620 + 4507179 4507303	SAV4118 SCD17.12	COG0739					
COG	Gene	Description	NC_003888.3	+ 450/1/9 450/303	SCD17.12	COG0739					
COG05		K+ transport systems,	NAD binding compone								
COG01		Trk-type K+ transport									
COG07											
COG05		Membrane proteins related to metalloendopeptidases Amino acid transporters									
COG07		Aminio acid transporters Cell wall-associated hydrolases (invasion-associated proteins)									
COG37		Cell wall hydrolyses involved in spore germination									
COG07		ABC-type dipeptide transport system, periplasmic component									
COG06		ABC-type dipeptide/oligopetide/nickel transport systems, permease components									
COG11		ABC-type dipeptide/oligopetide/nickel transport systems, permease components									
COG04		ABC-type dipeptide/lidopetide/lickel transport system, ATPase component									
COG11		ABC-type dipeptide/oligopeptide/nickel transport system, ATPase component									
COG02		Dihydrodipicolinate reductase									
COG03		6-phosphogluconate dehydrogenase									
COG14	10 metH_2	Methionine synthase I,	. cobalamin-binding	domain							

Structure Consensus Ban **BA1886** Bce BC1807 Bha **BH0597** Bsu vdaO Bsu yuaA Cac CAC1232 Cac CAC3081 Cth Chte1033 Oih 0B1662 Tte metH Tte lytE Tte OppA9 Cal Cal2188 CUGCGCG<mark>UGUGCCC</mark>G-AA-<mark>UCCU</mark>---GCAA--<mark>GGGAACCGCG</mark>GAA<mark>CCA</mark>------ACCUUCCUG---UCAACU------UCCGGUGGAAU<mark>CACCGGCGAUGCC-GCCGUG</mark>GCAA-<mark>CACGGCAGGUAUACGCGCG</mark>GAA<mark>GCA</mark>------ACCUUCCUG---Sav SAV4118 Sco SCD17.12 Structure Consensus CCGAAUCCGACAGCUAA<mark>CCUCGU</mark>-A<mark>AGCG-</mark>UU------AUAU<mark>UGAG</mark>AAGGAAGGUGGAGCUUGUGCGACAAAAAAAUAA------UGUCUACAAGUC------UGUCUACAAGUC------UAUUUCGUUAU-------GGCUUGUAGACAUUUUUUGUUUU Ban **BA1886** Bce BC1807 Bha BH0597 Bsu yda0 Bsu vuaA Cac CAC1232 Cac CAC3081 Cth Chte1033 Oih 0B1662 Tte metH Tte lytE Tte OppA9 Cgl **Cgl2188** GAACCCGACAGCUAA<mark>CUCGGUCAGCAA</mark>------ACA<mark>GGAAG</mark>AAUUUGGAGUUUCAUCAGAGCAAACAGGAAGAAUUUGGAGUUUCAUCAGUGGGUAAGCACCGUCGCAACAACUCGCAAGGCUGUAGCAGCAUCUGCAGUUGCG GAACCCGUCAGCUAA<mark>CCCGGU-AGGC-CA</mark>------GAAGGAAGGAAAGGAAGGCGCGCCCACGUGGCGUCCAACCGGCCUGCCCAGCAAACCUCGUUCGCACCGAGUGAGAAGUCGUACGAGUCGGAGACCUUCGGUUCCGGGGUGACGAGGGCCCCUG Sav SAV4118 Sco SCD17.12

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