Abb Orga	nism		Accession	Positi	on		Genes							
Bacillus/Clostridium														
Ban <i>Baci</i>	llus an	thracis	NC_003997.1	+ 1298	760	1298845	BA1359	COG0603	BA1360	COG0720	BA1361	COG0602	BA1362	COG0780
Bce Baci	llus ce	reus	NC 004722.1	+ 1318	948	1319033	BC1341	COG0603	BC1342	COG0720	BC1343	COG0602	BC1344	COG0780
Bha <i>Baci</i>	llus ha	lodurans	NC 002570.1	- 2373	266	2373355	BH2244	COG0603	BH2243	COG0720	BH2242	COG0602	BH2241	COG0780
Bsu <i>Baci</i>	llus sul	btilis	NC_000964.1	+ 1488	363	1488474	ykvJ	COG0603	ykvK	COG0720	ykvL	COG0602	ykvM	COG0780
Cpe Clos	tridium	perfringens	NC 003366.1	- 2295	254	2295337	CPE2003	COG1957	CPE2002	COG1268				
Oih Ocea	nobacil.	lus iheyensis	NC_004193.1	- 2245	729	2245818	OB2210	COG0780	<i>OB2209</i>	COG1738				
Oih Ocea	nobacil.	lus iheyensis	NC 004193.1	- 2885	800	2885886	OB2804	COG0720	OB2803	COG0602				
Sau Stap	hylococo	cus aureus	NC 002745.1	- 761	136	761234	SA0667	COG0603	SA0666	COG0720	SA0666	COG0602		
Sep Stap	hylococo	cus epidermis	NC_004461.1	- 477	721	477819	SE0487	COG0603	SE0486	COG0720	SE0485	COG0602		
COG G	ene	Description												
COG0603 y	baX	Predicted PP-loop	superfamily	ATPase										
COG0720 y	gcM	6-pyruvoyl-tetrahydropterin synthase												
COG0602 n	rdG	Organic radical activating enzymes												
COG0780 y	qcD_2	Enzyme related to GTP cyclohydrolase I												
COG1957 y	raaF	Inosine-uridine nucleoside N-ribohydrolase												
COG1268 B	S_yhfU	Uncharacterized conserved protein												
COG1738 y	hhg Uncharacterized conserved protein													

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Structure	······································	<<<<<<
Consensus	ry	
Bsu ykvJ	GAAGAAAAU <mark>CCGUG</mark> -CGAUA <mark>UGCGG</mark> -GAGAGGUUC-UAGCACAUCCCUCUAUA <mark>AAAAACUAAGGA</mark> CGA <mark>GCUGUAUC</mark>	CUUG <mark>GAUACGGC</mark> CU <mark>UUUUUA</mark> U <mark>GUUUUU</mark> CUAGAGCACCUUCCGAAAAAAGGUGUUUUUUUGCGUGA
Bha BH2244	UGAAGAAUU <mark>UCACAG</mark> GUUUUC <mark>UGUGA</mark> -GAGAGGUUCGCGAACUCCCUCUAUAAA <mark>AAAC</mark> U <mark>AAGGCAAGGCUGUAUC</mark>	AAGC <mark>GGUACAGUUUUCUUU</mark> UC <mark>GUUU</mark> GCCGCUAGCCGGCGAGGGUUUUUCGAGCUCGUUCUUCA
Ban BA1359	GAAGGAAUUCCGUGCAAUGCACGG-GAGAGGUUCGCGAACUCCCUCUAUAAAAAACUAUGGAAACAAUAUC-	UUUA <mark>GGUAUUGUUUUGUUUUU</mark> UAUUGUGACAGUUCAAGAACGUUCUUCUUCUUCUUAUUCG
Bce BC1341	GAAGAAAUUCCGUGCACCCCCCCCCG-GAGAGGUUCGCGAACUCCCUCUAUAAAAAACUAUGGAAACAACAAUAUC-	CUUA <mark>GGUAUUGUUUUGUUUUU</mark> UAUUGUGACAGUUCAAGAACGUUCUUCUUCUUAUUUA
Oih 0B2210	UGAUUGUAC <mark>AACAAA</mark> CAUAAU <mark>UUUGUU</mark> AGAGGUUCUUAGCUUCA-ACCCUCUAUAAAAAA <mark>CUAAGGA</mark> CAA <mark>AC</mark> AAUGAUUU	AUUC <mark>AAGUCAUGUUCCUUAG</mark> GGGACAUGACUUUUUUUAUGGAAAAGGAGGUAAUAAGU
Oih 0B2804	CAUAGAAUUCUGCA-CUAC <mark>UGCAG</mark> -GAGAGGUUCGCGAUUUAAAUCCCUCUAU <mark>AAAAAAC</mark> UAAGGAGAUAAAC <mark>AACACG</mark>	CUUCUU <mark>UGUGUUGUUUUUU</mark> UGAUUGGAUGAACUGUGAAAAAAACAGUCGAUCCAUCAU
Sep SE0487	UUAUUCUAU <mark>GUU</mark> CCGUGCAAAAUAAUAACAGAGGUUCCUAGCGAAA-CCCCUCUAUAAAAAACUA <mark>GACAU</mark> GAAAAUUUCAAC	A <mark>AUGAA</mark> UUUC <mark>UUCAU</mark> AUUUAUA <mark>AUGUU</mark> AAGACUAUAUAUGUCUUUAAUAUUUCUGUCUAUCUUUU
Sau SA0667	GGUAUAUUC <mark>UAUUCAU</mark> CGUACAUAA <mark>AUGAAUA</mark> UCAGAGGUUUCUAGCUGAA-ACCCUCUAUAAAAAACUAGAC <mark>AUUGAA</mark> A <mark>UUUCAA</mark> -	ACAUUCG <mark>UUGG</mark> U <mark>AA</mark> ACC <mark>UUUAAU</mark> AUAUAUUAUAGGAGCAACCCAUUUCUUUCGUCUAUCUU
Cpe CPE2003	UAAAAAAAU <mark>CCAA</mark> UGUAAU <mark>UUGG</mark> -UAGAGGUUCGUAAC-CAUCCCUCUAUAAAAAACU <mark>AAGGG</mark> C <mark>UGUAACUGU</mark>	AUUAUAGG <mark>AUAGUUAUACUCUU</mark> UAGUAUGCCUGUAAUAUAGUUUUUAUUAUUUUUAGGCU

Note: The aligned Bsu sequence from Genbank (CUAGC-ACAUCCCUC) differs from the experimentally probed sequence from Subtilist (CUAGCUACA-CCCUC).

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