Abb	Organism	Accession	Position			Genes							

Bacillus/Clostridium

Ban	*Bacillus anthracis*	NC_003997.3	+	824029	824109	*BA0809*	COG3339	*dedA*	COG0586				
Ban	*Bacillus anthracis*	NC_003997.3	−	1269052	1269154	*BA1322*	COG0861						
Bha	*Bacillus halodurans*	NC_002570.1	−	2677841	2677933	*BH2553*	COG0861						
Bsu	*Bacillus subtilis*	NC_000964.1	+	1410104	1410202	*ykoY*	COG0861						
Bsu	*Bacillus subtilis*	NC_000964.1	−	4169043	4169122	*yybP*	-------						
Cpe	*Clostridium perfringens*	NC_003366.1	−	421415	421495	*CPE0333*	COG0474						
Cpe	*Clostridium perfringens*	NC_003366.1	−	665199	665285	*CPE0535*	COG1971						
Dha	*Desulfitobacterium hafniense*	NZ_AAAW02000220.1	−	1350	1427	*Desu0831*	COG0861						
Lla	*Lactococcus lactis*	NC_002662.1	−	1405837	1405926	*yoaB*	COG0474						
Lpl	*Lactobacillus plantarum*	NC_004567.1	+	523159	523235	*pacL2*	COG0474						
Lin	*Listeria innocua*	NC_003212.1	+	1013076	1013174	*lin0990*	COG0861	*lin0991*	COG0861	*lin0992*	COG0168		
Lmo	*Listeria monocytogenes*	NC_003210.1	+	1021476	1021575	*lmo0991*	COG0861	*lmo0992*	COG0861	*lmo0993*	COG0168		
Oih	*Oceanobacillus iheyensis*	NC_004193.1	−	1328491	1328574	*OB1286*	-------	*OB1285*	COG0515				
Oih	*Oceanobacillus iheyensis*	NC_004193.1	−	3147546	3147625	*OB3036*	COG0861						
Sau	*Staphylococcus aureus*	NC_002745.1	+	995888	995990	*SA0878*	COG0861						
Sep	*Staphylococcus epidermidis*	NC_004461.1	+	711305	711434	*SE0721*	COG0861						
Sag	*Streptococcus agalactiae*	NC_004116.1	+	526370	526445	*SAG0514*	COG0474						
Smu	*Streptococcus mutans*	NC_004350.1	+	681851	681927	*SMU.723*	COG0474						
Spn	*Streptococcus pneumoniae*	NC_003028.1	−	1461088	1461178	*SP1551*	COG0474						
Spy	*Streptococcus pyogenes*	NC_002737.1	+	500062	500139	*pacL*	COG0474						
Tte	*Thermoanaerobacter tengcongensis*	NC_003869.1	+	36548	36622	*MgtA4*	COG0474						
Tte	*Thermoanaerobacter tengcongensis*	NC_003869.1	+	255482	255587	*OadB*	COG1883						

Cyanobacteria

| Nos | *Nostoc* | NC_003272.1 | + | 2037117 | 2037211 | *alr1698* | COG2119 | | | | | | |

Alpha Proteobacteria

| Ccr | *Caulobacter crescentus* | NC_002696.2 | − | 2571360 | 2571465 | *CC2370* | COG2119 | | | | | | |

Beta Proteobacteria

| Rso | *Ralstonia solanacearum* | NC_003295.1 | − | 997656 | 997775 | *RSc0949* | COG0861 | | | | | | |
| Rso | *Ralstonia solanacearum* | NC_003295.1 | + | 2274752 | 2274883 | *RSc2100* | COG2119 | | | | | | |

Gamma Proteobacteria

Eco	*Escherichia coli*	NC_000913.1	+	1903494	1903590	*b1821*	COG1971						
Eco	*Escherichia coli*	NC_000913.1	+	3236021	3236135	*ygjT*	COG0861						
Pae	*Pseudomonas aeruginosa*	NC_002516.1	−	3265282	3265372	*PA2910*	COG1971						
Ppu	*Pseudomonas putida*	NC_002947.3	−	875969	876104	*PP0760*	COG2119						
Psy	*Pseudomonas syringae*	NC_004578.1	−	1255691	1255806	*PSPTO1145*	COG2119						
Psy	*Pseudomonas syringae*	NC_004578.1	+	4244896	4244988	*PSPTO3755*	COG1971						
Sen	*Salmonella enterica*	NC_003198.1	+	1853550	1853646	*STY1963*	COG1971						
Sen	*Salmonella enterica*	NC_003198.1	+	3249576	3249690	*STY3404*	COG0861						
Sty	*Salmonella typhimurium*	NC_003197.1	+	1931945	1932041	*yebN*	COG1971						
Sty	*Salmonella typhimurium*	NC_003197.1	+	3392075	3392189	*ygjT*	COG0861						
Sfl	*Shigella flexneri*	NC_004337.1	−	1443956	1444052	*yebN*	COG1971						
Sfl	*Shigella flexneri*	NC_004337.1	+	3228618	3228732	*ygjT*	COG0861						
Son	*Shewanella oneidensis*	NC_004347.1	−	1112147	1112263	*SO1071*	COG2119						
Vch	*Vibrio cholerae* chr I	NC_002505.1	+	20094	20199	*VC0022*	COG2119						
Vch	*Vibrio cholerae* chr II	NC_002506.1	+	484083	484181	*VCA0546*	COG0861						
Vvu	*Vibrio vulnificus* chr I	NC_004459.1	−	990603	990713	*VV10988*	COG2119						
Vvu	*Vibrio vulnificus* chr II	NC_004460.1	+	268169	268307	*VV20239*	COG0861						
Vvu	*Vibrio vulnificus* chr II	NC_004460.1	−	559562	559653	*VV20505*	COG0530						
Xax	*Xanthomonas axonopodis*	NC_003919.1	+	4930332	4930424	*XAC4192*	COG1971						
Xax	*Xanthomonas axonopodis*	NC_003919.1	+	5161397	5161491	*ygjT*	COG0861						
Xca	*Xanthomonas campestris*	NC_003902.1	+	4836456	4836549	*XCC4075*	COG1971						
Xca	*Xanthomonas campestris*	NC_003902.1	+	5057779	5057873	*ygjT*	COG0861						
Ype	*Yersinia pestis*	NC_003143.1	−	1999981	2000102	*YPO1754*	COG1971						

Actinobacteria

Blo	*Bifidobacterium longum*	NC_004307.1	+	1260972	1261083	*pacL2*	COG0474						
Cef	*Corynebacterium efficiens*	NC_004369.1	−	1962455	1962574	*CE1859*	COG0861						
Cgl	*Corynebacterium glutamicum*	NC_003450.2	+	1548576	1548716	*Cgl1469*	COG1971	*Cgl1470*	COG0798				
Cgl	*Corynebacterium glutamicum*	NC_003450.2	−	2072953	2073094	*Cgl1967*	COG0861						
Cgl	*Corynebacterium glutamicum*	NC_003450.2	−	2677230	2677318	*NCgl2442*	-------	*Cgl2528*	COG1321				
Mtu	*Mycobacterium tuberculosis*	NC_000962.1	+	4322182	4322263	*Rv3848*	COG2119						
Sco	*Streptomyces coelicolor*	NC_003888.1	−	2517535	2517629	*SCC8A.05c*	COG2119						

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COG	Gene	Description
COG0861	*terC*	possibly involved in tellurium resistance
COG0474	*mgtA*	Cation transport ATPases
COG1971	-	Predicted membrane protein
COG2119	-	Predicted membrane protein
COG0168	*trkG*	Trk-type K+ transport systems, membrane components
COG1883	-	Na+-transporting methylmalonyl-CoA/oxaloacetate decarboxylase, beta subunit
COG0586	*dedA*	Uncharacterized membrane-associated protein
COG0798	*ACR3*	Arsenite efflux pump ACR3 and related permeases
COG0530	*yrbG*	Ca2+/Na+ antiporter
COG3339	-	Conserved hypothetical
COG0515	*BS_yabT*	Serine/threonine protein kinases
COG1321	*troR*	Mn-dependent transcriptional regulator

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Structure  ........<<<<<<<<......<<<<<<<<<<<<<<<<<<<<<<<<...>>>>>>>>>>>>>>>>><<<<.<<<<.......<<<<<<<<<<<<<<<<<...>>>>>>>>>>>>>>>>>>>>
Consensus  .........gGGGAGUAgcy.........................RUCR.CAy...Y.r...........................y.
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Org	Gene	Sequence
Ban	*BA0809*	AAAAUUGUGUAUAUAAAGGGGAGUAGACU--------UAUUAC-------------AGUAA--AGUCGUCAUU-ACAGGG--------------AGAAA-----------------CCCU
Ban	*BA1322*	AAUAGCAUAUCUCCAAAGGGGAGUAGCU-UCCAAGAA-------UAU--------UUCUUGGAAACAA-AGUCGUCAUU-ACGUAGAAAC-----------------UUA--------GUUCUUC
Bha	*BH2553*	ACUACAUAG-CUUUAAGGGGAGUAGCU-------------AAUUAC---------AAUAA-AGUCGUCAUG-ACAGGGAU------------CUCCCAUAA---------AUCCCU
Bsu	*ykoY*	UUUCUUGAAAUCCAAAGGGGAGUAGCG-UCCGGAA--------UGUA--------UUCCGGAAACAA-AGUCGUCAUU-UCAUGGAU------------UGU------------AUCCAU
Bsu	*yybP*	AAAAUGAACACUCCAAAGGGGAGUAGCU-------------AGUCG-AGUCGUCAUU-ACGGGACA------------AGG------------UGUCCU
Cpe	*CPE0333*	AUAUCUAUUGUGUUAAGGGGAGUAGUU------------GCAAGC-UAUAA-UAUCAACAUC-GCGGUUAAC------------GAAA-------------GUU-ACC
Cpe	*CPE0535*	AACUUUGUUUCCAUAUGAGGGAGUAGUUA-GCUCA-------AGUUGAA-------UGAGUGAUUA-AGUCAACAAA-UUGACCAAA---------GAGC--------UUUGGUC
Dha	*Desu0831*	AAAAUAUUAGUCCAAAGGGGAGUAGCU--------------GUAC---------AGCAA-AGUCGUCAUUCACGGACU------------AAA---------AGUCC
Lla	*yoaB*	AACAUAAAAUUUCCAAAGGGGAGUAGCG-UCGGU---------AAG--------ACCGAAACAA-AGUCGUCAUU-ACGUGAG------------AUU--------CUCAC
Lpl	*pacL2*	CUUACGAUACAAUCAUAUGAGGGAGUAGCUA-GCAGAA-------AUA--------UUCUGCGGCAA-UAUCGUCAGC-AAGA--------------AGCCAA----------------UC
Lin	*lin0990*	CUUUGACAAAUGUCAGAGGGGAGUAGCG-CUGAUUAG--------CUU--------UUAAUCAGGAUAA-AGUCGUCAUU-ACAUGAUA------------GAGA----------UAUCAU
Lmo	*lmo0991*	CUUUGACAAAUGUCAGAGGGGAGUAGCG-CUGAUUAG--------CUU--------UUAAUCAGGAUAA-AGUCGUCAUU-ACAUGAUA------------GAGA----------UAUCAU
Oih	*OB3036*	ACUUAUAGCAAAUUAAAGGGGAGUAGCU---------------GUACA-------UUUAA-AGUCGUCAUU-ACGAGA--------------UUUAA-------------UCUC
Oih	*OB1286*	UUGAAAUAAAUCCCAAAGGGGAGUAGCU--------------UAAU---------AGCAGCUGUCACAUU-ACGAGA--------------GAAA--------------UCCU
Sau	*SA0878*	UAUGGCAUUUUGUCAGAGGGGAGUAACUU-AAGAAUCAU---------GACCGUAUAA---------AUGAUUCGACACUU-UAUCGUCAUU-ACGAAG------------AUAU------------CUUC
Sep	*SE0721*	AUGACAAAACUGUCAGAGGGGAGUAACUU-GAGAAUAGUUAUUGAAUGCAUUUAAACUGA-UAAUAACUAUUCAA-CACUU-UGUCGUCAUU-ACGAAGA-----------UAAG-----------UCUUC
Sag	*SAG0514*	CAAUGAUUAACAUAUCAAGGGGAGUAGCAG-ACGG--------------UUUA--------CCGUGGCAA-UGUCGUCAUU-ACGAAA--------------GAAA--------------UUUC
Smu	*SMU.723*	UAUAUGAAAGAGGGGAGUAGCG-GCGG--------------UUUUG--------CCUGGAG-UGUCGUCAUU-ACGAAA--------------CUGU--------------UUUC
Spn	*SP1551*	UAUAAUGGUACUACUCAAGGGGAGUAGCUG-GCAG-------------AAAC--------CUGUAGUAG-UGUCGUCAUU-CCGAAUUUUAUGCU------GAAA------AGUAUGCU-UUC
Spy	*pacL*	UAAUGGUUAUUAUAUCAAGGGGAGUAGCAG-ACGG--------------CUAG--------CCGUAUG-UAUCGUCAUU-ACGGAAU------------UUCG------------GUUUC
Tte	*MgtA4*	UUUCUUUUCUGGUAAAGGGGAGUAACUC-----------------UAAAU-------CAAUC-AGUCGUCAUG-ACGGC--------------UUUUU--------------GCC
Tte	*OadB*	AAAACAUAACAUAAAGGGGAGUAGCU---GCCACA-------GUA--------UGUGGUUUAACC-UGUCGUCAUU-ACGGAA------------AUU------------UUCUC
Nos	*alr1698*	UUUUAUUCUGAUAAGAAGGGGAGUAGCU---GCUGGC-----------AAAA--------GCCAGUACAUCUG-AAUCAACAUA-CUGGC------------GAUGA----------GCC
Ccr	*CC2370*	AAACGCCGCCCACCUUUGGGGAGUAGCCG-CCCGC-------------GUCUAUCA----------GCGGCCCCG-CCGUCAACACA-CUUGAUCU---------UCC---------GGAUCA
Rso	*RSc0949*	AUGCCGACUUCCUCAAAGGGGAGUAGCUC-GGGGGUU--------CUUC--------AGCCCAGGCAC-GAUCGUCAUG-ACGAAGC-----------GCAC-----------GCUUC
Rso	*RSc2100*	UAAUGCCGGCUUCCAUUUGGGGAGUAGCU-GCCUUGAGG-------CAAUGC--------UCCGGGCACG-CGUCAACAGA-CUGAGCGUUCGUCGUC----------GCAAU---------GGAGGACGGUUU
Eco	*b1821*	AGGUUGCGCCCUCCAUUUGGGGAGUAGCCG-AUUUCC--------AGAUUCC--------GGAAAUGUACG-UGUCAACAUA-CUCGUU-----------GCAA-----------AACG
Eco	*ygjU*	ACUUUGUUACCUGCAAAGGGGAGUAACUU-UUUU--------CAUUG--------CCGGUCGAUCGUCAUU-ACGAUGUGU-----------GAAAA----------ACACAUC
Pae	*PA2910*	UGCUGCCGGCCUUCCUUGGGGAGUAGCU-GCCGUCA-------CCCGU--------UGACGGCGCGCU-GGUCAACAUU-CUUGGCA-----------ACC-----------UGCCA
Ppu	*PP0760*	GAAUCCGCACCGUCCUUGGGGAGUAGCUC-CCC--------ACCCA--------GCUCGUCCGGCACG-GAUCAACAUU-CUGGC-----------CACA-----------GACCA
Psy	*PSPUO1145*	GAAUCCGCUCCGUCCUUAGGGGAGUAGUCU-CCCACGACG-------CCA--------UGCUCGUCCGGCACG-UAUCAACAUU-CUGGGUC---------CUCA---------GACCA
Psy	*PSPUO3755*	UAGUGACGGCCCUUUGUUGGGGAGUAGCCU-GUUC-GUGAC-------CCCG--------GUCACUGAGCGUCG-UAUCAACAUU-CUCGGCA----------GCA----------UGCCG
Sen	*SUY1963*	AUGUUGCGCCGUCAAUUAGGGGAGUAGCCG-AUUUCC--------AGACUCC--------GGAAAUGUACG-UGUCAACAUA-CUCGUU-----------GCAA-----------AACG
Sen	*SUY3404*	ACUUUGUUACCGCAAAGGGGAGUAACUU-CAUUG--------CCGGUCGAUCGUCAUU-ACGAUGUG---------UGCAAAAC--------CACAUC
Sty	*yebN*	AUGUUGCGCCGUCAAAGGGGAGUAGCCG-AUUUCCAG--------ACU--------CCGGAAAUGUACG-UGUCAACAUA-CUCGUU-----------GCAA-----------AACG
Sty	*ygjU*	ACUUUGUUACCGCAAAGGGGAGUAACUU-CAUUG--------CCGGUCGAUCGUCAUU-ACGAUGUG----------UGCAAAAC---------CACAUC
Sfl	*yebN*	AGGUUGCGCCCUCAUUUGGGGAGUAGCCG-AUUUCCAG--------AUU--------CCGGAAAUGUACG-UAUCAACAUA-CUCGUU-----------GCAA-----------AACG
Sfl	*ygjU*	ACUUUGUUACCUGCAAAGGGGAGUAACUU-CAUUG--------CCGGUCGAUCGUCAUU-ACGAUGAGUG---------AAAAA--------C-CACAUC
Son	*SO1071*	AUGCCCAUCUCGCUUCGGGGAGUAGCUAA-CUGGAUUUCGA-------GCCA--------UCGAUCUCUAGGUGUGAA-CGUCAACAUU-CUUGGC------------CGCAU------------GCCA
Vch	*VC0022*	GAAUUCGCUCCGUCUUUGGGGGAGUAGCUG-GUCUCUAAGUU-------UUC--------AACUUGGUGAUUCACA-CAUCAACAUU-UUGGGUA----------CUCAU----------UACCA
Vch	*VCA0546*	UAGAAUGGCGACGUUUUGGGGGAGUAGUCG-CC--------UUA--------GGUUUAUU-UGUCGUCAUC-ACGUUGAGU----------UUC----------ACUCAAC
Vvu	*VV10988*	GAAUUCGCCGUGUCUUUGGGGGAGUAGCUUA-CUGGAUGAAAA-------GCCA--------UUUUCAUCGAGUUCACCGUCAACAUU-ACCAAAU---------CCAAAU---------CACCA
Vvu	*VV20239*	UACAAUAUCGAACGUCUUUGGGGAGUAGUUA-GC--------GUAA--------GUUUAUU-UGUCGUCAUC-UCGUUAGGC----------CAAA----------GCCUUUC
Vvu	*VV20505*	UAGAAUAGCGCCGUUAAGGGGAGUAGCCU-UCCUCA--------UGGUU--------UGAGGAGUGAA-UAUCACAGUCUCGAGC-----------UUAAU-----------GCUUG
Xax	*XAC4192*	UACACUGCGCGCCCCUUGGGGAGUAGCCU-GCUUUCG--------UCAU--------CGAAAGCGCCUG-CAUCAACAUA-CUCGGC------------CAGUGC------------GCCG
Xax	*ygjU*	CAGAACGGGCCGCAGAGGGGAGUAGCU------------CCCAG--------CGUUGUCGCCGUCAUU-ACGAGCC-GC--------CAUGU-------GCAGCGUC
Xca	*XCC4075*	ACACUGCGCGCCCCUUGGGGAGUAGCCU-GCUUCCA--------GUCGA--------UGGAUGCGCCG-CAUCAACAUA-CUCGGC------------CGUUGC------------GCCG
Xca	*ygjU*	CAGAAUCGGCCGCAGAAGGGGAGUAGCUC------------CCAG--------CGUUGUCGCCGUCAUU-ACGAGC-CCUG------------CCUGU-----------CAGGCGUC
Ype	*YPO1754*	AGGUUGCGCCGUUC-AUGGGGAGUAGCCG-GUUUCUG--UGC-AUAUUAUUCAU-AAUAUAUUGGCAAG-CAGAAACGCCCG-UAUCAACAUA-CUCGUUUCA--------UUUAUU--------UGAAACG
Blo	*pacL2*	AACUGAACUAACCAUGAGGGAGUAGACA-GCAUUGCGGCGAA-GGGC----UCG--GCCC-AAACCGCAAUGU-GGCAUUGAUCGUCAUU-ACGGCCGUCGGC------------AGUUC----------GUU-ACGGUC
Cef	*CE1859*	UUUCUUUCGUAAUAUGAGGGAGUAGCCC------------GUUCAC----------GGCAUUGAUCGUCAAC-ACGGAGGGCAUCUGGUUCACCGUUAGAGU-GGCCGGAUGGAUGAU-UCC
Cgl	*Cgl1469*	ACCACAUUCCAUUUGGAGGGGAGUAGUUC-CA-ACAAAGGCGA-------UCUGAC--------UCGUUUUUGUUCGAGGUAU-GUUCGACAUACUGGAGCAAG--------UUCAC--------CUUGCUC
Cgl	*Cgl1967*	AGUUUUCCCGUAUUGGAGGGGAGUAGCCCC-----------------ACAAGC-------AGCGUUGAUCGUCAAC-ACGGAAAUCA-AACUUUAAA------GAA------UUUUAGGUUGUGAAUUCC
Cgl	*NCgl2442*	CGAUGUCUGUUGCUGAAGGGGAGUAGCU-GACAAA--------CGCGUUGUCAACAUA-CUGGCACGCA-----------AGAUC-----------UGUGUACC
Mtu	*Rv3848*	CUGGGGACGUUAGCAGAGGGGAGUAGUC------------CCGAA--------UCGUCGAGCGUCAACAUA-CUGGC--------------GAAAA--------------GCC
Sco	*SCC8A.05*	CUAUGGACGGCGCAGAGGGGAGUAGCU--------------CUUCG-------CCGGACCGUCAACAUA-CUGCUCAG------------CCCGC------------CUGAGC
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Structure  >>>>  >>>>  <<<<<<<<<<<<<<<<<<<<<<<<<<<...  >>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>  >>>>>....  >>>>>>>>>.................................
Consensus  YGGY..........  GGCAACG.......................UUU.......................................rgYRAGACc........................
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		Sequence
Ban	BA0809	CGGCU-UUAUU-GGCAACG----------------------------CGUUGUU---AGGAGAGACCCUUACCA--------GCAA----------------------UGGUAAAGGCCCCUUAUU
Ban	BA1322	CGGCU-UUGUU-GGCAU-------------------UUUCAUUACAU---------AUGUC-UAGCAGACCUUUGCC----------UAUUAAC--------------GGCAGAGGUCUUUUUUA
Bha	BH2553	CGGCU-UUAUU-GGCAAC---------------GGAUAUACG-----------GUUGUC-UAGCAGACCUUUACC--------AAAUGG--------------UGGUAAAGGUCUUUUCCUAU
Bsu	ykoY	CGGCU-UUGUU-GGCAUG-------------CCUGAAUU-----------CAUGUC-UAGCAGACCUUUGCC---------UUUAUGUC------------GGCAAAGGUCUUUUUUGCA
Bsu	yybP	CGGCU-UUGCU-GGCAAU--------------------CUC--------------UAGC-UAGCGAGACCUUUGCCAAAU----------AUUUUGGUGAAGGCGUCUUUAUUU
Cpe	CPE0333	UGGUA-UUAUA-CACCA----------------------AUU------------UGGU--UACAAGACUUUUAAU-------AUAAUCUAAGGA-------AUUUAAGGUAUUUUAUGU
Cpe	CPE0535	UGGCU-UAAUC-----------------------------UUAAA------------UAGC-GAGACUUAUAUGCAGU-----UUUU-------GCUAUAUAGGUCUUUUUUAU
Dha	Desu0831	CGGCU-UUGUU-GGCAAC-----------------ACA-----------GUUGUU-AGCGAGACCUUUGCCC---------AUCC---------GGGUAAAGGUUUUUUUUA
Lla	yoaB	CGGCU-UUGUU-GACAUAC-------------------GUAUGU-UAGC-GAGACCUUUGCCAG------UUUGAUAU-----CCAUAAUGGUCAUUUUA
Lpl	pacL2	CGGUA-UUGUC---------------------------UUAAA--------------UAGUGACUUAUGUAUGUUCACACAAUUUUGCGUGCAUACAUGAGUCUCAUUUUCUAUC
Lin	lin0990	CGGUU-UUAUC-ACAUUUA-----------------ACUU-----------UAAAUGU-UAGC-GAGACCUUUGCCU--------UUAU-----GGGCAGGUCUCGCUUUUUGUU
Lmo	lmo0991	CGGUU-UUAUC-ACAUUUA-----------------ACUU-----------UAAAUGU-UAGCGAGACCUUUGCCU----------UUAC-----GGGCAGGUCUCGCUUUUUUGUU
Oih	OB3036	CGGCU-UUAUA-UGGCAAC-----------------GACC-----------GUUGUU-AGCGAGACCUUUACC-ACUA----CCA----UUAGUAGGUAAAGGCCGUCUUUUUUACG
Oih	OB1286	CGGCA-CUGCU-GGCAACGAAU---------------UAU----------AUU-GUUGCU-UGCGAGACCUUUGCUCA----AUUUAG----UGGGCAAAGGUCUCUUUUUGAC
Sau	SA0878	CGGUA-AAGUG-GGCAAU----------------------UUAA------------AUUGUC-UAGCGAGACCUUUGCUA-------UUUUAU----UAGCAUAGGUCUCUUUUUGAC
Sep	SE0721	CGGUA-AAGUG-GGCAA----------------------AAAUA-----------UUGCU-AAGUGAGACCUUUGCUA-------UUAAAU----UAGCAUAGGUCUCUUUAUUUGU
Sag	SAG0514	CGGCG-UUGUC----------------------------UUAAA------------CAGC-GAGACUUGUUU-----------CAUA----------UAACAGGUUUCUUU
Smu	SMU.723	CGGCA-ACAU-A------------------------UUAAA-----------UAGC-GAGACUUGUUUAA-----------UUA---------UUAAACAGGUCUUUCUUU
Spn	SP1551	CGGGC-CUAUC----------------------------UUAAA------------CAGC-GAGACUUGUUA----------UGAU----------UAACAGGUUUCUUUU
Spy	pacL	CGGUA-CAAUC----------------------------UUAAA------------CAGC-GAGACUUGUUA----------AGAAAA---------UAAACAGGUCUUUUUAUUU
Tte	MgtA4	CGGCA-GAUUC-AGCA----------------------GAUAA-----------UGC--GAGUGAGACCUUUACUUUGUGG------AUUA------CUACAAGAUGAGACCUUUUUUCAU
Tte	OadB	CGGCA-GGUUA-GAAACUCC-------------GGAC-----------GGAGUAUA-GAGCGAGACCUUUAUAGAG-----GUAAA----UAC-CACUAUAUAGGUCUUGCUUUUGUAUG
Nos	alr1698	UGGUU-CAGGU-GACAACUA-------------GAAAA----------UAUUUGG-AAGCGAGACCUUC-ACUAAGUUCACAUUUAAGAUGUG-GCUUGGUGGGGUCUUUUGGCAU
Ccr	CC2370	UGGCG-CGGGU-AAGGGAAGC---------GGACUUGAA-------GCUUCCUU--GGCGAGACCAAUGGCGCGAUCGUCAUCCGGGCCGGGUGGGGUAUCGACGCUAUUGGCA
Rso	RSc0949	UGGUC-GUGCC-GGCAUCCG-CAGGU-----UCCUG-----------GCCUGCGG-UGUC-GAGCAGACGAGUCGCGGCAAUCCAUGGUCUGCAAAGCGUCUCGCCCAGCCUUCAUG
Rso	RSc2100	UGGUA-CAUUCCA-AUCCUGGGUGC---------CCC----------GCACCC-GG-UGAGCGCCUGGCCGAGACACGCCCUUUCCGGACAGGGCGGGGAAAGGUGCCAUUGGUUCG
Eco	b1821	UGGCA-CGUAG-GGACUGAA----------------------UACU----------AGGC-GAGACCAUAUGCACAUCAAUCGCUAUGCCUGCAUGAACGCGAAAACCAUCACGGCU
Eco	ygjU	CGGUC-ACCGG-GCAACCCGAAAGGAAUACG-------------CAGA----------GGUAUUCCUUUUUUGUUGU-AAGUGAGACCUU-GCCGGAAGGCGAGGUCUAUGCAUAAAAAGCAGCGGCUGGACGUCUUC
Pae	PA2910	UGGCC-AGCGU-AUCC-----------------------AACC---------GGAU-UGGUGAGACCAACGACAUUCCUGCGCCGAAGCCGGGCCGCGGGGUCAUGCGUUGACUCA
Ppu	PP0760	UGGCG-CGUGC-GACCCGCCAUGCACGCCUGCAUGG----------GAUCCGCAUAGACGGAUCGAGGGUU-UGACAGACACGCACACCUUAACGGGCGCGGGAGGUCGUACGUGUCUAUAGCC
Psy	PSPU01145	UGGUA-CGUGC-GACC-CGGAAUCCG-------------CUCAGA--------GGA-UCAGUGACAGACCUAUGACGAACACCUUACCCGGGCGGGGAGGUCGUACGUGUCUAUAGCC
Psy	PSPU03755	UGGUA-CGAAC-ACC------------------------UUCU----------GGU-UGGCGAGACCAACGAUGCAUCCAUGCCUAAAGUCGGGCGUGUGGUUGCGUCGUUGACUCA
Sen	SUY1963	UGGCG-CGUAG-GGACCAGC--------------CGCC----------GCUGGGC-AGGCGAGACCA-UAGGCGCAUCACUGCUGUGUAUUUCGUCACAGAAUGGCGACAUGCAU
Sen	SUY3404	CGGUC-ACCGG-GCAGCCAUAAAGGAAUGCG-------------UCAG----------GCUGGGC-AAGUGAGACCUU-GCCGGAAUGGCAAGGUCUAUGCAUAAAAAGCAGCGGCUAAUGCCAUUCG
Sty	yebN	UGGCG-CGUAG-GGACCAGC--------------CGCC----------GCUGGGC-AGGCGAGACCA-UAGGCGCAUCACUGCUGUGUAUUUCGUCACAGAAUGGCGACAUGCAU
Sty	ygjU	CGGUC-ACCGG-GCAGCCAUAAAGGAAUGCG-------------UCAG----------GCUGGGC-AAGUGAGACCUU-GCCGGAAUGGCAAGGUCUAUGCAUAAAAAGCAACGGCUAAUGCCAUUCG
Sfl	yebN	UGGCA-CGUAG-GACUGAA----------------------GACU----------UUCAGUC-AGGCGAGACCAUAUGCACAUCAAUCGCUAUGCCUGCAUGAACGCGAAAACCAUCGCGGC
Sfl	ygjU	CGGUC-ACCGG-GCAACCCGAAAGGAAUACG-------------CAGA----------CGUAUUCCUUUUUUGUUGU-AAGUGAGACCUU-GCCGGAAGGCGAGGUCUAUGCAUAAAAAGCAGCGGCUGACGUCUUC
Son	SO1071	UGGUG-UUCAC-AG-CAAAUC-------------------AUC----------GAUUUGUCUU-GCAAGACCUGAGCACAAUAACCGCACCUAGGGGUGGACGGUCAUUGUGCUUAUGUCA
Vch	VC0022	UGGUG-UGUGA-GACCUGA----------------------GCCU----------UCAGGUU-UAGCAGACCUAGACAAACAACGCGAACUGGGGAUAGGGCGUGAUUGUUUGUCUACGGUU
Vch	VCA0546	CGGCA-AAUUA-UUAAGCUCUGAAUC---------------CAA----------GUUCAACGCUU-CGACGAGACCAACGCAUUCAAUACUGCAUUUGUUGCAGGAAUCAUUGGUAUGCGGAAGGU
Vvu	VV10988	UGGCG-UUCGAC-ACUUGGA---------------------GCCU----------UUAAUGUGAUUUAGCAGACCUAGACAAACAACGACAACCUGGGGUGGGGGGUGU
Vvu	VV20239	CGGCA-AAUAA-AGGUGAGUU--ACCCUCUCUUUGUUUCU-UUGUCAUCAACAGAAACAGAGAAAGCAUUCCAGUUCACUU-CAACGAGACCAA-CGCAUUCACAUACACAGUACAGAAAUUAGGAACGAUUCUGUCGCGAUUUG
Vvu	VV20505	UGGUA-UUCAC-GUUC----------------------AUCU----------GUUC-UGGCGAGACCUUAAGCAAAGUUUGAAUUUGGGUAGCAAUUCGAACUUUGCUUUGGGUUAAG
Xax	XAC4192	UGGUG-CAGGC-AACC----------------------AGUUUC---------GGUC-UGGCGAGACCAGCGGCAUGCGUGCACGACGACGGUUGGGCGCGGGCGCAUGCCGUUGUGAC
Xax	ygjU	CGGUG-CAACG-GCAACCGGUC--------------CCG----------GCCGGUUGC-GAGCGAGACCUUCGCCGCGCAGGCGAAGGUCCGUCACCCGGAAUCCACGAUUUCCGUGUC
Xca	XCC4075	UGGUG-CGGGC-AACCA----------------------CUCU----------UGGGU-UGGCGAGACCAGCGGCAUGCGUGCACGACGAUGGUUGGGCGCGGGCGCAUGCCGUUGUGA
Xca	ygjU	CGGUG-CAACG-GCAACCGGC---------------CCG----------GCCGGUUGC-GAGCGAGACCUUC-GCCGCGCAGGCGAAGGUCCGUCACCCGGAAUCCACGAUUUCCGUGU
Ype	YPO1754	UGGUA-CGGGC-AGCC----------------------AGGUAA---------GGUU-GCGAGACCAUAGACACGUAGCUCCGUCGUUAGGUUGGGGGUGGGUUACGUGUAUAUGG
Blo	pacL2	UGGCU-UGCC----------------------------UUAAA----------UGAC-UGCAUGUACCGGAUGCAUGCGUAUGUCAAAUC
Cef	CE1859	CGGUC-AUGUC-GGCCCACCG---------------GAAA----------CG-CGGGU-GGGGGAGACCUCCGGUUCUU--AAACGACAAUC--------AAGAACCGGAGGUUCUUUUUCUAU
Cgl	Cgl1469	CCGGC-AUACCA-CCUGAAC----AAGGCCUU-----------AAAAA----------GGGGCUUUAUCGGUUCAGGCGAGCGAGACCUUCGGCGUUCACUUCGCCGGGGUCAUUUUUUUAUGCCCAGGCACGGCU
Cgl	Cgl1967	CGGUC-ACACU-GCCCAUUUGUUUUUCAGAUGCAU-------GUUAG----------AUGCGU-UGAGGGACAA----GGGU-GGGGGAGACCUCCGGUUCUU-AAAUUGUCUAACC-AGAAACCGGAGGUUCUUUUUUGUCA
Cgl	NCgl2442	CCGCC-ACGUG-CCUA----------------------AAAC----------UAGGUGAGACCUUCGACCGAUGUUCGAUGACGUGGUCGUCAACGCGUCGAAAGUU
Mtu	Rv3848	CGGCU-GGCGA-ACCGUU------------------UGAUACC---------AACGGU-GGGC-GAGACCUUCGACCGAUGUUCGAUGACGUGGUCGUCAACGCGUCGAAAGUU
Sco	SCC8A.05	CGGCG-CCCGG-AGGCAGGCCUCG-----------UGCG----------CGAGGCGGGCC--AGCGAGACCUUCGGCAAGCAGUGCAGCGCCCGGUGCCGUACGGCCAGGGGUGAAUCCGUGUG

C

B. subtilis yybP

yybP/ykoY