Δ

```
Abb Organism
                                                            Position
                                         Accession
                                                                               Genes
Bacillus/Clostridium
                                                                                                           COG2076
  Bsu Bacillus subtilis
                                         NC 000964.1
                                                           + 1375803 1375900 vkkC
                                                                                         COG2076 vkkD
 Bsu Bacillus subtilis
                                         NC 000964.1
                                                            - 3987634 3987722 vxkD
                                                                                         COG1284
 Oih Oceanobacillus ihevensis
                                         NC 004193.1
                                                           - 3401641 3401723
                                                                              OB3264
                                                                                         COG2076 OB3263
                                                                                                           COG2076
 Bha Bacillus halodurans
                                                                                         COG2076 BH0685
                                                                                                           COG2076
                                         NC 002570.1
                                                            - 741877 741966
                                                                              BH0686
                                                            + 586463 586553 TTE0584
                                                                                         COG2252
 Tte Thermoanaerobacter tengcongensis
                                        NC 003869.1
 Gst Geobacillus stearothermophilus
                                                                8552
                                                                        8641 NA
        gnl|OUACGT 1422|bstearo.fasta.screen.Contig257
Cvanobacteria
 Syn Synechocystis
                                         NC 000911.1
                                                            - 801282
                                                                      801389 speB
                                                                                         COG0010
Alpha Proteobacteria
 Rpa Rhodopseudomonas palustris
                                         NZ AAAF01000001.1
                                                           - 3051748 3051838 Rpal2681
                                                                                          OG0715 Rpa12680
                                                                                                          COG0600 Rpa12679 COG1116 Rpa12678 COG3665 Rpa12677 COG3665
 Rle Rhizobium leguminosarum
                                                                 9906
                                                                       10000
                                                                                                ... ?
        gnl|Sanger 216596|rhiz361f07.slk
Beta Proteobacteria
 Bfu Burkholderia fungorum
                                                               41546
                                                                        41664
                                                                              Bcep4105
                                                                                         COG3665
                                                                                                Bcep4104
                                                                                                          COG3665 Bcep4103 COG4770 Bcep4102 COG0154 Bcep4101 COG0600
                                         NZ AAAJ02000045
                                                                               Bcep4100
                                                                                          OG1116
 Bfu Burkholderia fungorum
                                                               44724
                                                                        44857
                                                                              Bcep4109
                                         NZ AAAJ02000045
 Bce Burkholderia cenocepacia
                                                           - 576042 576159
                                                                                          OG3665
                                                                                                 ... ?
    gnl|Sanger 216591|Bcep1157h02.plc
 Neu Nitrosomonas europaea
                                         NC 004757.1
                                                           + 2634433 2634522
                                                                              NE2420
                                                                                         COG4770
 Neu Nitrosomonas europaea
                                                                                         COG0531 NE2418
                                                                                                                             COG3665 NE2416
                                                                                                                                               COG1984
                                         NC 004757.1
                                                           - 2634103 2634191
                                                                              NE2419
                                                                                                           COG3665 NE2417
Gamma Proteobacteria
 Psv Pseudomonas syringae
                                         NC 004578.1
                                                                              PSPT04238
                                                                                                PSPT04239 COG0600 PSPT04240 COG1116 PSPT04241 COG366
                                                                                                                                                      PSPT04242 COG3665
 Pfl Pseudomonas fluorescens
                                         NZ AAAT02000050.1
                                                                       44748 Pflu2166
                                                                                                Pf1u2165
                                                                                                           COG0600 Pflu2164 COG1116 Pflu2163
                                                                                                                                                      Pf1u2162
 Ech Erwinia chrysanthemi
                                                           + 549581
                                                                      549661
        gnl|TIGR 198628|contig:223
 Mde Microbulbifer degradans
                                                                                                                                               COG3665 Mdeq2140
                                         NZ AABI02000012.1 + 100719 100778
                                                                              Mdeq2136
                                                                                              Mdeq2137
                                                                                                           COG0600 Mdeg2138
                                                                                                                             COG1116 Mdeq2139
                                                                                                                                                                COG3665
Epsilon Proteobacteria
 Wsu Wolinella succinogenes
                                         NC 005090.1
                                                           + 1067291 1067378 WS1110
                                                                                               5 WS1111
                                                                                                           COG0600 WS1112
                                                                                                                             COG1116 WS1113
                                                                                                                                                OG3665 WS1114
                                                                                                                                                                 COG3665
COG
                 Description
        BS ycgI Uncharacterized conserved protein
COG366
COG2076
        emrE
                  Membrane transporters of cations and cationic drugs
                  ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components
        ssuA
                 ABC-type nitrate/sulfonate/bicarbonate transport systems, permease component
COG0600
        ssuC
COG111
        ssuB
                 ABC-type nitrate/sulfonate/bicarbonate transport systems, ATPase component
COG4770
                  Acetyl/propionyl-CoA carboxylase, alpha subunit
COG0010
        speB
                 Arginase/agmatinase/formiminoglutamate hydrolase, arginase family
COG1984
                 Allophanate hydrolase subunit 2
        vbaK
COG1284
        BS vdeO
                 Uncharacterized conserved protein
        BS yerM Asp-tRNAAsn/Glu-tRNAGln amidotransferase A subunit and related amidases
COG0154
COG2252
        yqf0
                  Permeases
COG0531
        aniC
                  Amino acid transporters
```

В

Structurey..CUAGGGUUCCq.y.....r.G.cuG.GuCCGAGaG.r..r Consensus Bsu vkkC Bsu vxkD AAUAUUGGAAAGGAUAUGAUAAAAACAGUGGUUUUCUAGGGUUCCGCAAU-----GCAA-----AUUGGACUGUGACCGAGAGAAAAC-ACAUAGCAGC-AUGAUUUAGUUAGAAUUGAAUAUAAUCAUUCGUAAAU<mark>ACUUUCU</mark>AGGGUUCCGCC-----UUAUU------GGUCUG-GUCCGAG<mark>AGAAAGU</mark>-GCAAAGAA Oih **OB3264** UUGCUAUAAUGAGGGGGGAUUAACCGAAUAGCCAAAU<mark>GUUUUCU</mark>AGGGUUCCG<mark>CUUGC----AAG-----GCAAG</mark>GCCUG-GUCCGAG<mark>AGAAAAC</mark>-GCAAAAAAGA-Bha **BH0686** Tte TTE0584 Gst NA AGUUAACUUAAUCAUCCCUAGCUAGGGUAGGGGAUAU<mark>UGUUUCU</mark>AGGGUUCCGAUUCCU-GGUGAUGUG-GGGAAUGGCUG-GUCCGAGAGAAACA-GGCUAG-GGCAGAGAACA-GGCUAG-GGCAGAGAACA-GGCUAG-GGCAGAGAACA-GGCUAG-GGCAGAGAACA-GGCUAG-GGCAGAGAACA-GGCUAG-GGCAGAGAACA-GGCUAG-GGCAGAGAACA-GGCUAG-GGCAGAGAACA-GGCAGAACA-GGCAGAACA-GGCAGAACA-GGCAGAACA-GGCAGAACA-GGCAGAACA-GGCAGAACA-GGCAGAAACA-GGCAGAAACA-GGCAGAAACA-GGCAGAAACA-GGCAGAAACA-GGCAGAAACA-GGCAGAAACA-GGAAACA-GGAAACA-GGAAACA-GGAAACA-GGAAACA-GGAAACA-GGAAACA-GGAAACA-GAAACA-GAAACA-GAAAACA-GAAAACA-GAAACA-GAAAACA-GAAACA-GAAACA-GAAAACA-GAAAACA-GAAAACA-GAAAACA-GAAAACA-GAAACA-GAAAACA-GAAACA-GAAACA-GAAAACA-GAAA Syn speB Rpa Rpa12681 AAUUUGGCACGCACUUUGCUUCGUUAGUUGCAGAGU<mark>UGGUGGCU</mark>AGGGUUCCGCCGUC-----GCAA-----GACGUGGCUG-GUCCGAG<mark>AGCUGCCA-CCGGCAGGC</mark>-------Rle -Bfu Bcep4105 AUAACUGGCCGAGAGGUGCGCAGCGUCGCAUCUUA<mark>GGGAUGCU</mark>AGGGUUCCG<mark>GUUC-----GAGA------GAAC</mark>GUCUG-GUCCGAG<mark>AGCAGCCC</mark>G<mark>GUCC-GCCG</mark>ACAG<mark>GUUCG</mark>AU<mark>UC</mark>GUUCGAU Bfu **Bcep4109** Bce -Neu **NE2420** Neu **NE2419** UCUAGGCAGAUAAGGCAUCAGAAGCACAGUCGUUUCA<mark>CGAAACU</mark>AGGGUUCCG<mark>GCUUUCC</mark>---CAG----<mark>GGAAAGU</mark>GACUG-GUCCGAG<mark>AGUUUCG</mark>-G<mark>GCCGUC</mark>--------Psv PSPT04238 GAGUCAUCACAGGUUCGCGGCACCACAAUUUGCAAUG<mark>GCUGACU</mark>AGGGUUCCG<mark>GCUCGC</mark>----AUCU----<mark>GCGAGU</mark>GGCUG-GUCCGAG<mark>AGUUGGC</mark>-G<mark>ACCUC</mark>-----------------Pfl Pflu2166 Ech -Mde Mdeq2136 GCAACUACUCGGAGUACCUGAACAAUGACGACCAAUGGGUGGCUAGGGUUCCGGCUGU----AAAUAA----ACAGUGACUG-GUCCGAGAGCCAUC-GACCUUCUAAGUGGUAGGCAAU-------AUGUCAUGAGGCUGAAAAGCCUCGAGAUACGCGAACA<mark>GAUGGCU</mark>AGGGUUCCCAUGAUC----GCUU-----GAUCAUG-CUG-GUCCGAG<mark>AGCUAUC</mark>-G<mark>GCCUCU</mark>------------------Wsu **WS1110** Structurey.CACqq..GGGAyAAAAGCCCqGGAGr....... Consensus -AAAUAGAA-----AUGU-----GGGA-CGACUGUCCGGGGGUUUUUUUUGGGAAAAAAGCCCGGGAGAGUCAUCUC-----AUGU------GAGA-CGACUGUCCGGGGUUUUUUUUGUUUUCGG Bsu ykkC ------UUUC-----GUGUUAUG--ACACGG-UGGGAUAAAAGCCCAGGAGUUUCUGCUCUU-----UUUC------GAGAGC-G-UUCUCCUGGGUUUUUUUAUUUGCUA Bsu vxkD ------AGUA------AGUGUUUC-UCCACGG-AGGGAUAAAAGCCCGGGAGAUAŪCACUA-----AGUA------UAGUGGUAUGUCCCGGGUUUUUUGGUUUUUUA Oih **OB3264** -----AUACA-----CGAUAUUUUUC-UCCACGG-AGGGAGAAAGCCCCGGGAGAUAUCG-----AUACA------CGAUAUGUCUCGGGCUUUUUAUAUGGAAA Bha **BH0686** ------------------CCAUAUACC--ACACCUUAGGGAUAAAAGCCCGGGA<mark>GGA-UAG</mark>G-------UUUCAC-------CUAUUCCUGCCGGGCUUAAUUUUUUCAG Tte TTE0584 -----COUNCEC-UACACGG-AGGGACAAAAGCCCGGGAGGAG-----CANUCGUUUCGA-----UCGUUCUCGCGGGCUUUUUUAUUUUCGC Gst NA -<mark>GCCACUAGC</mark>-UACACGG-CGGGACAAAAGCCCGGGAGACUUUAAUGACCAGUGCUUAGGUGUU-GUCAUUAAUAACUACUGGGCAGAUUUUGUUGUUU Svn speB -<mark>U-COUUCGE</mark>ACGCACGG-CGGGACAAAAGCCCGGGAGACCUCGUAAGCCGAGGAAUUGGCAAACGAUGGUCCACGUCAAUUCCUCAUCGCGACCAGAU Rpa Rpa12681 Rle ----UCCUCCCCCGGUGCACGG-CGGGACAAAAGCCCGGGAGACCUCGUAAGCCAAGGGAUUGGCGGCACGAUGGUCAUUGCCGAUCCCUUUUGAAGAAAAGC --CUUUC------AAGECEC-GGGGGAGGG-UCCACGG-AGGGAUAAAAGCCCGGGAGGUCGCGAUGUCGGCCCUCUCACGCUUAUUCCCAACCGAUACCUGAGCCUCAU Bfu Bcep4105 Bfu **Bcep4109** GCAGGUUCCACUCCCCA-UA--CCAAC-GGCCCGUUGCCAC-UACACGG-CGGGACAAAAGCCCGGGAGAUUGGCGAUAGCAAUGUCUAUCGUGCCUCUCCGUGGCCGGCGUUUGUCUUGUGCACAUCGA Bce -Neu NE2420 Neu **NE2419** CAGGGU-UCCACGG-AGGGAUAAAAGCCCGGGAGGUUAUGUUCAAUACAUUAACUACCGGGAGCCAGAGUGGAAAAACUAUCGCGUGUGUGCGCU Psy PSPT04238 --CAGUA------AGU----GGUGUCACGUUG-CUCCU-GGCCGCCUUUUUUCACU --CAGUU------GACCU-UACACGG-CGGGACAAAAGCCCGGGAGACAAGCCACGUUCGCGGUUGCCGUUCCUGUCCGCCCUCGAUCAACUGGAGAAGC Pfl **Pflu2166** Ech ----CUCU-----AUGCAUG-----CUCGC--CGCCCUCCUGCUUUUUUAGUGGUUG Mde Mdeg2136 --UUGCAU-----AUUGG------UAAGAGGGU-UACACGG-CGGGAUAAAAGCCCGGGAGGAUUAAACUGGUGAAAUUGCCAGAAUGCCUCGUGUGAACUUUAUAAAACCAUUUAGGAGA Wsu **WS1110**

yxkD Pre ▶ G136 ► G122 ▶ B. subtilis yxkD G110 ▶ ykkC/yxkD G100 ► 5' gAUUG_G RGAGGGCCCG G89 ► ับบบсธ G74 ► G63 ▶ G51 ▶ G44 ▶ G35 ▶ G18 ►

B. subtilis

