Supplementary Data Set 1:
Riboswitches in eubacteria sense the second messenger c-di-AMP

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Note: the presentation of this supplementary data on novel RNA motifs follows the pattern of our presentation of previously found conserved RNA motifs.

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1 c-di-AMP riboswitch

1.1 Taxa

The taxonomy of each organism containing a putative c-di-AMP riboswitch is listed, with abbreviations identifying each hit (e.g., “Eco-1-1” and “Eco-1-2”). The abbreviations will be used to identify each individual c-di-AMP riboswitch in Section 1.3.
Bacteria Actinobacteria Actinomycetales Corynebacterineae Mycobacteriaceae Mycobacterium Mycobacteriumtuberculosis complex 

Mtu-4-1  Mycobacterium tuberculosis 94_M4241A

Mtu-5-1  Mycobacterium tuberculosis C

Mtu-6-1  Mycobacterium tuberculosis CDC1551

Mtu-7-1  Mycobacterium tuberculosis CPHL_A

Mtu-8-1  Mycobacterium tuberculosis EAS054

Mtu-9-1  Mycobacterium tuberculosis F11

Mtu-10-1  Mycobacterium tuberculosis GM 1503

Mtu-11-1  Mycobacterium tuberculosis H37F

Mtu-12-1  Mycobacterium tuberculosis H37R

Mtu-13-1  Mycobacterium tuberculosis H37Rv

Mtu-14-1  Mycobacterium tuberculosis K85

Mtu-15-1 to Mtu-15-2  Mycobacterium tuberculosis KZN 1435

Mtu-16-1  Mycobacterium tuberculosis KZN 4207

Mtu-17-1  Mycobacterium tuberculosis KZN 605

Mtu-18-1  Mycobacterium tuberculosis KZN R506

Mtu-19-1  Mycobacterium tuberculosis KZN V2475

Mtu-34-1  Mycobacterium tuberculosis KZN str. Haarlem

Mtu-19-1  Mycobacterium tuberculosis SUMu001

Mtu-20-1  Mycobacterium tuberculosis SUMu002

Mtu-21-1  Mycobacterium tuberculosis SUMu003

Mtu-22-1  Mycobacterium tuberculosis SUMu004

Mtu-23-1  Mycobacterium tuberculosis SUMu005

Mtu-24-1  Mycobacterium tuberculosis SUMu006

Mtu-25-1  Mycobacterium tuberculosis SUMu007

Mtu-26-1  Mycobacterium tuberculosis SUMu008

Mtu-27-1  Mycobacterium tuberculosis SUMu009

Mtu-28-1  Mycobacterium tuberculosis SUMu010
Frankia alni  
Fal-1-1 to Fal-1-5  
Bacteria Actinobacteria Actinobacteridae Actinomycetales  
Frankineae Frankiaceae

Ace-1-1 to Ace-1-2  
Bacteria Actinobacteria Actinobacteridae Actinomycetales  
Frankineae Acidothermaceae

Tpa-1-1  
Bacteria Actinobacteria Actinobacteridae Actinomycetales  
Corynebacterineae Tsukamurellaceae

Rjo-1-1 to Rjo-1-3  
Bacteria Actinobacteria Actinobacteridae Actinomycetales  
Corynebacterineae Nocardiaceae

Rer-2-1 to Rer-2-2  
Bacteria Actinobacteria Actinobacteridae Actinomycetales  
Corynebacterineae Nocardiaceae

Frankia sp.  
Fsp-1-1 to Fsp-1-5  
Bacteria Actinobacteria Actinobacteridae Actinomycetales  
Frankineae Frankiaceae

Rer-1-1 to Rer-1-2  
Bacteria Actinobacteria Actinobacteridae Actinomycetales  
Corynebacterineae Nocardiaceae

Req-1-1 to Req-1-2  
Bacteria Actinobacteria Actinobacteridae Actinomycetales  
Corynebacterineae Nocardiaceae

Nfa-1-1  
Bacteria Actinobacteria Actinobacteridae Actinomycetales  
Corynebacterineae Mycobacteriaceae

Mtu-32-1  
Bacteria Actinobacteria Actinobacteridae Actinomycetales  
Mycobacteriaceae Mycobacterium

Mtu-31-1  
Bacteria Actinobacteria Actinobacteridae Actinomycetales  
Mycobacteriaceae Mycobacterium

Mtu-29-1  
Bacteria Actinobacteria Actinobacteridae Actinomycetales  
Mycobacteriaceae Mycobacterium

Fsp-4-1 to Fsp-4-5  
Bacteria Actinobacteria Actinobacteridae Actinomycetales  
Frankineae Frankiaceae

Fsp-3-1 to Fsp-3-8  
Bacteria Actinobacteria Actinobacteridae Actinomycetales  
Frankineae Frankiaceae

Fsp-1-1 to Fsp-1-6  
Bacteria Actinobacteria Actinobacteridae Actinomycetales  
Frankineae Frankiaceae

Sgr-2-1 to Sgr-2-7  
Bacteria Actinobacteria Actinobacteridae Actinomycetales  
Streptomycineae Streptomycetaceae

Sfl-1-1 to Sfl-1-6  
Bacteria Actinobacteria Actinobacteridae Actinomycetales  
Streptomycineae Streptomycetaceae

Sco-1-1 to Sco-1-7  
Bacteria Actinobacteria Actinobacteridae Actinomycetales  
Streptomycineae Streptomycetaceae

Scl-1-1 to Scl-1-5  
Bacteria Actinobacteria Actinobacteridae Actinomycetales  
Streptomycineae Streptomycetaceae

Streptomyces griseus subsp. griseus

Sgr-1-1 to Sgr-1-7  
Bacteria Actinobacteria Actinobacteridae Actinomycetales  
Streptomycineae Streptomycetaceae

Sgr-2-1 to Sgr-2-7  
Bacteria Actinobacteria Actinobacteridae Actinomycetales  
Streptomycineae Streptomycetaceae
Shy-1-1 to Shy-1-3 Bacteria Actinobacteria Actinobacteridae Actinomycetales Streptomycineae Streptomycetaceae *Streptomyces hygroscopicus* ATCC 53653
Shl-1-1 to Shl-1-7 Bacteria Actinobacteria Actinobacteridae Actinomycetales Streptomycineae Streptomycetaceae *Streptomyces lvisans* TK24
Srl-1-1 to Srl-1-7 Bacteria Actinobacteria Actinobacteridae Actinomycetales Streptomycineae Streptomycetaceae *Streptomyces rossosporus* NRRL 11379
Srd-2-1 to Srd-2-7 Bacteria Actinobacteria Actinobacteridae Actinomycetales Streptomycineae Streptomycetaceae *Streptomyces rossosporus* NRRL 15998
Ssc-1-1 to Ssc-1-7 Bacteria Actinobacteria Actinobacteridae Actinomycetales Streptomycineae Streptomycetaceae *Streptomyces scabies* 87.22
Ssp-1-1 to Ssp-1-7 Bacteria Actinobacteria Actinobacteridae Actinomycetales Streptomycineae Streptomycetaceae *Streptomyces sp.* ACT-1
Ssp-2-1 to Ssp-2-6 Bacteria Actinobacteria Actinobacteridae Actinomycetales Streptomycineae Streptomycetaceae *Streptomyces sp.* ACTE
Ssp-3-1 to Ssp-3-3 Bacteria Actinobacteria Actinobacteridae Actinomycetales Streptomycineae Streptomycetaceae *Streptomyces sp.* C
Ssp-7-1 to Ssp-7-5 Bacteria Actinobacteria Actinobacteridae Actinomycetales Streptomycineae Streptomycetaceae *Streptomyces sp.* e14
Ssp-4-1 to Ssp-4-3 Bacteria Actinobacteria Actinobacteridae Actinomycetales Streptomycineae Streptomycetaceae *Streptomyces sp.* Mg1
Ssp-5-1 to Ssp-5-5 Bacteria Actinobacteria Actinobacteridae Actinomycetales Streptomycineae Streptomycetaceae *Streptomyces sp.* SPB74
Ssp-6-1 to Ssp-6-5 Bacteria Actinobacteria Actinobacteridae Actinomycetales Streptomycineae Streptomycetaceae *Streptomyces sp.* SPB78
Sav-1-1 to Sav-1-7 Bacteria Actinobacteria Actinobacteridae Actinomycetales Streptomycineae Streptomycetaceae *Streptomyces azureus* ATCC 29083
Svi-1-1 to Svi-1-4 Bacteria Actinobacteria Actinobacteridae Actinomycetales Streptomycineae Streptomycetaceae *Streptomyces violaceusngu* Tu 4113
Svi-2-1 to Svi-2-7 Bacteria Actinobacteria Actinobacteridae Actinomycetales Streptomycineae Streptomycetaceae *Streptomyces violidochromogenes* DSM 40736
Spr-1-1 to Spr-1-7 Bacteria Actinobacteria Actinobacteridae Actinomycetales Streptosporangineae Streptosporangiaceae *Streptosporangium roseum* DCM 43021
Sro-1-1 to Sro-1-7 Bacteria Actinobacteria Actinobacteridae Actinomycetales Streptosporangineae Streptosporangiaceae *Streptosporangium roseum* DCM 43183
Sro-2-1 to Sro-2-7 Bacteria Actinobacteria Actinobacteridae Actinomycetales Streptosporangineae Streptosporangiaceae *Streptosporangium roseum* DCM 43183
Sro-3-1 to Sro-3-6 Bacteria Actinobacteria Actinobacteridae Actinomycetales Streptosporangineae Streptosporangiaceae *Streptosporangium roseum* DCM 43183
Bacillus sp. m
Bsp-3-1 Bacteria Firmicutes Bacillales Bacillaceae
Bsp-1-1 to Bsp-1-2 Bacteria Firmicutes Bacillales Bacillaceae
Bacillus sp.
Bpu-2-1 to Bpu-2-2 Bacteria Firmicutes Bacillales Bacillaceae
Bacillus pumilus
Bacillus pumilus
Bacillus pseudofirmus
Bps-2-1 to Bps-2-5 Bacteria Firmicutes Bacillales Bacillaceae
Bacillus pseudomycoides DSM 12442
Bacillus pseudomycoides DSM 12442
Bacillus pseudomycoides DSM 12442
Bme-2-1 to Bme-2-5 Bacteria Firmicutes Bacillales Bacillaceae
Bacillus megaterium QM B1555
Bacillus megaterium QM B1555
Bacillus megaterium QM B1555
Bme-1-1 to Bme-1-4 Bacteria Firmicutes Bacillales Bacillaceae
Bacillus megaterium QM B1555
Bacillus megaterium QM B1555
Bacillus megaterium QM B1555
Bps-1-1 Bacteria Firmicutes Bacillales Bacillaceae
Bacillus pumilus SAFR-032
Bacillus pumilus SAFR-032
Bacillus pumilus SAFR-032
Bsp-1-1 to Bsp-1-2 Bacteria Firmicutes Bacillales Bacillaceae
Bacillus sp. B14905
Bacillus sp. B14905
Bacillus sp. B14905
Bsp-2-1 to Bsp-2-6 Bacteria Firmicutes Bacillales Bacillaceae
Bacillus subtilis subsp. spiizizenii ATCC 6633
Bacillus subtilis subsp. spiizizenii ATCC 6633
Bacillus subtilis subsp. spiizizenii ATCC 6633
Bacillus subtilis subsp. spiizizenii ATCC 6633
Bacillus subtilis subsp. spiizizenii ATCC 6633
Bacillus subtilis subsp. spiizizenii ATCC 6633
Bacillus subtilis subsp. spiizizenii ATCC 6633
Bacillus subtilis subsp. spiizizenii ATCC 6633
Bacillus subtilis subsp. spiizizenii ATCC 6633
Bacillus subtilis subsp. spiizizenii ATCC 6633
Bacillus subtilis subsp. spiizizenii ATCC 6633
Bacillus subtilis subsp. spiizizenii ATCC 6633
Bacillus thuringiensis serovar monterrey
Bth-11-1 to Bth-11-4 Bacteria Firmicutes Bacillales Bacillaceae Bacillus Bacilluscereus group

Bacillus thuringiensis serovar konkukian
Bth-8-1 to Bth-8-4 Bacteria Firmicutes Bacillales Bacillaceae Bacillus Bacilluscereus group

Bacillus thuringiensis serovar berliner

Bacillus cytotoxicus
Bcy-1-1 to Bcy-1-3 Bacteria Firmicutes Bacillales Bacillaceae Bacillus Bacilluscereus group

Bacillus mycoides
Bmy-1-1 to Bmy-1-4 Bacteria Firmicutes Bacillales Bacillaceae Bacillus Bacilluscereus group

Bacillus thuringiensis serovar huazhongensis
Bth-7-1 to Bth-7-4 Bacteria Firmicutes Bacillales Bacillaceae Bacillus Bacilluscereus group

Bacillus thuringiensis serovar andalousiensis

Bacillus thuringiensis
Bth-1-1 to Bth-1-4 Bacteria Firmicutes Bacillales Bacillaceae Bacillus Bacilluscereus group

Gth-1-1 Bacteria Firmicutes Bacillales Bacillaceae

Geobacillus thermoglucosidasius

Geobacillus sp.

Gsp-2-1 Bacteria Firmicutes Bacillales Bacillaceae

Geobacillus sp.

Gsp-1-1 Bacteria Firmicutes Bacillales Bacillaceae

Geobacillus sp.

Bacillus thuringiensis str.
Bth-18-1 to Bth-18-4 Bacteria Firmicutes Bacillales Bacillaceae Bacillus Bacilluscereus group

Bacillus thuringiensis serovar tochigiensis
Bth-17-1 to Bth-17-4 Bacteria Firmicutes Bacillales Bacillaceae Bacillus Bacilluscereus group

Bacillus thuringiensis serovar sotto str.
Bth-15-1 to Bth-15-4 Bacteria Firmicutes Bacillales Bacillaceae Bacillus Bacilluscereus group

Bacillus thuringiensis serovar pulsiensis
Bth-13-1 to Bth-13-4 Bacteria Firmicutes Bacillales Bacillaceae Bacillus Bacilluscereus group

Lysinibacillus fusiformis
Lfu-1-1 to Lfu-1-2 Bacteria Firmicutes Bacillales Bacillaceae

Exiguobacterium sp.

Oceanobacillus iheyensis
Oih-1-1 Bacteria Firmicutes Bacillales Bacillaceae

Lsp-2-1 to Lsp-2-2 Bacteria Firmicutes Bacillales Bacillaceae Lysinibacillus sphaericus C3-41

Oli-1 Bacteria Firmicutes Bacillales Bacillaceae Oceanobacillus iheyensis HTE831

Eai-1 Bacteria Firmicutes Bacillales Bacillaceae Bacillus Family XII. IncertaeSedis Eubacterium sibiricum 255-15

Esp-1-1 Bacteria Firmicutes Bacillales Bacillaceae Bacillus Family XII. IncertaeSedis Eubacterium sibiricum 255-15

Meta-1 Bacteria Firmicutes Bacillales Bacillaceae Bacillus Family XII. IncertaeSedis Eubacterium sibiricum 255-15

Bbr-1-1 to Bbr-1-5 Bacteria Firmicutes Bacillales Bacillaceae Brevibacillus brevis NBC 100599

Pcu-1-1 to Pcu-1-7 Bacteria Firmicutes Bacillales Bacillaceae Paenibacillus curtulianoliticus YK9

Pla-1-1 to Pla-1-3 Bacteria Firmicutes Bacillales Bacillaceae Paenibacillus larvae subsp. larvae BRL-230010

Ppq-1-1 to Ppq-1-5 Bacteria Firmicutes Bacillales Bacillaceae Paenibacillus polymyxa E681

Ppq-2-1 to Ppq-2-5 Bacteria Firmicutes Bacillales Bacillaceae Paenibacillus polymyxa SC2

Psp-1-1 to Psp-1-7 Bacteria Firmicutes Bacillales Bacillaceae Paenibacillus polymyxa sp. JDR-2

Psp-2-1 to Psp-2-8 Bacteria Firmicutes Bacillales Bacillaceae Paenibacillus polymyxa sp. oral taxon 786 str. D14

Ath-1-1 to Ath-1-3 Bacteria Firmicutes Clostridiales Anaerocellumgroup Anaerocellum thermophilum DSM 67625

Bhy-1 Bacteria Firmicutes Clostridiales Blautia hydrogenotrophica DSM 10607 (Ruminococcus albus group)

Aor-1-1 Bacteria Firmicutes Clostridiales Akikusalmophilumdi Ostii

Cac-2-1 to Cac-2-2 Bacteria Firmicutes Clostridiales Clostridiales Clostridiales Clostridiales Clostridium acetobutylicum ATCC 824

Cac-1-1 Bacteria Firmicutes Clostridiales Clostridiales Clostridiales Clostridiales Clostridium acetobutylicum DSM 10598

Cbo-1-1 Bacteria Firmicutes Clostridiales Clostridiales Clostridiales Clostridiales Clostridium acetobutylicum AJ-1

Cbo-2-1 to Cbo-2-2 Bacteria Firmicutes Clostridiales Clostridiales Clostridiales Clostridiales Clostridium botulinum A str. ATCC 39397

Cbo-3-1 to Cbo-3-2 Bacteria Firmicutes Clostridiales Clostridiales Clostridiales Clostridiales Clostridium botulinum A str. ATCC 3502

Cbo-4-1 to Cbo-4-2 Bacteria Firmicutes Clostridiales Clostridiales Clostridiales Clostridiales Clostridium botulinum A str. Hall

Cbo-5-1 to Cbo-5-2 Bacteria Firmicutes Clostridiales Clostridiales Clostridiales Clostridiales Clostridium botulinum A str. Kyoto

Cbo-6-1 to Cbo-6-2 Bacteria Firmicutes Clostridiales Clostridiales Clostridiales Clostridiales Clostridium botulinum A3 str. Loch Maree

Cbo-7-1 to Cbo-7-2 Bacteria Firmicutes Clostridiales Clostridiales Clostridiales Clostridiales Clostridium botulinum B str. Okra

Cbo-8-1 to Cbo-8-2 Bacteria Firmicutes Clostridiales Clostridiales Clostridiales Clostridiales Clostridium botulinum B4 str. 657

Cbo-9-1 to Cbo-9-2 Bacteria Firmicutes Clostridiales Clostridiales Clostridiales Clostridiales Clostridium botulinum B5

Cbo-10-1 Bacteria Firmicutes Clostridiales Clostridiales Clostridiales Clostridiales Clostridium botulinum C str. Ekland

Cbo-11-1 Bacteria Firmicutes Clostridiales Clostridiales Clostridiales Clostridiales Clostridium botulinum D str. 1874

Cbo-12-1 to Cbo-12-2 Bacteria Firmicutes Clostridiales Clostridiales Clostridiales Clostridiales Clostridium botulinum F str. Langeland

Cbo-13-1 to Cbo-13-2 Bacteria Firmicutes Clostridiales Clostridiales Clostridiales Clostridiales Clostridium botulinum NCTC 2916

Cca-1-1 to Cca-1-3 Bacteria Firmicutes Clostridiales Clostridiales Clostridiales Clostridiales Clostridium carboxidivorans P7

Cce-1-1 to Cce-1-4 Bacteria Firmicutes Clostridiales Clostridiales Clostridiales Clostridiales Clostridium cellulolyticum H10
Superscript numbers are used to annotate any c-di-AMP riboswitch that has special characteristics (described below). These numeric annotations will be used in Section 1.3. The meaning of the numbers are as follows.

1. Unclear homology. Some mutations in otherwise well conserved nucleotides. A homology search using Infernal with the single sequence and predicted secondary structure as query revealed no homologs with similarly mutated core nucleotides. Therefore, this sequence might be a false positive.

2. Translated BLAST searches suggest that the immediately downstream gene is a transglycosylase.

3. Alignment of P1 stem is unclear.

4. Several mutations in highly conserved nucleotides. Upstream of CHAP domain, TIGR02594. CHAP domains are proposed as amidases that include peptidoglycan hydrolases.

### 1.3 Gene contexts

Each c-di-AMP riboswitch (indicated by “RNA →”) is listed. The surrounding genes for each hit is given. Environmental sequences and some RefSeq entries lack gene annotations, and no genes are listed for such sequences. The direction of each gene is indicated with an arrow (→), and each conserved domain in the gene is colored. Conserved domains associated with more than one c-di-AMP riboswitch are assigned a color; other domains are gray. Information about these conserved domains is given in Section 1.4. The accession number of the sequence containing each c-di-AMP riboswitch is given. Accessions beginning with “NC_” or “NZ_” are RefSeq, while other accession refer to environmental samples. Nucleotide coordinates are given for the 5′ and 3′ boundaries of each. If the 5′ coordinate is greater than the 3′ coordinate, the RNA is present on the reverse-complement strand of the containing genomic DNA sequence. Each hit is denoted by an abbreviation (like “Eco-1-1”) that refers to a taxonomy given in Section 1.1. Superscript numbers refer to annotations listed in Section 1.2.
RNA → Peptidase_M23 (pfam01551) →
RNA → NLPC_P60 (pfam00877) →
hypertension →
RNA → NLPC_P60 (pfam00877) →
RNA → SCRAP12 (SCRAP12) →
RNA → NLPC_P60 (pfam00877) →
RNA → CHAP (pfam02575) →
RNA → NLPC_P60 (pfam00877) →
RNA → Peptidase_C39A (cd00254) →
RNA → NLPC_P60 (pfam00877) →
integral membrane protein →
RNA → Peptidase_C39A (cd00254) →
RNA → NLPC_P60 (pfam00877) →
RNA → SCRAP12 (SCRAP12) →
RNA → SMC (COG1842) →
RNA → SCRAP12 (SCRAP12) →
RNA → LT_surface antigen →
RNA → SMC (COG1196) →
RNA → LT_surface antigen →
RNA → SMC (COG1196) →
RNA → Peptidase_C39A (cd00254) →
RNA → Peptidase_C39A (cd00254) →
integral membrane protein →
RNA → Peptidase_C39A (cd00254) →
RNA → Peptidase_C39A (cd00254) →
RNA → Peptidase_C39A (cd00254) →
RNA → Peptidase_C39A (cd00254) →
RNA → Peptidase_C39A (cd00254) →
RNA → Peptidase_C39A (cd00254) →
RNA → Peptidase_C39A (cd00254) →
RNA → Peptidase_C39A (cd00254) →
| Btu-1-2 | NC_014098.1 | - | 1971255 | 1971133 | RNA $\rightarrow$ hypo$\rightarrow$ KdpA (pfam03814) $\rightarrow$ KdpB (COG2216) $\rightarrow$ KdpC (COG2159) | (shown above) |
| Bme-2-4 | NC_014019.1 | - | 3007759 | 3007626 | RNA $\rightarrow$ RNA $\rightarrow$ (big gap) RNA $\rightarrow$ PoTE (COG0531) $\rightarrow$ CBS_pair_20 (cd04643) |
| Gsp-3-8 | NC_023406.1 | + | 6691699 | 6692154 | RNA $\rightarrow$ PoTE (COG0531) |
| Bps-2-1 | NZ_ACMX01000030.1 | + | 57212 | 57349 | RNA $\rightarrow$ PoTE (COG0531) |
| Bmy-2-1 | NZ_ACMV01000123.1 | + | 5700 | 5837 | RNA $\rightarrow$ PoTE (COG0531) |
| Bmy-3-1 | NZ_ACMW01000041.1 | + | 5728 | 5865 | RNA $\rightarrow$ PoTE (COG0531) |
| Bce-32-1 | NC_011969.1 | + | 1856804 | 1856941 | RNA $\rightarrow$ PoTE (COG0531) |
| Bce-10-1 | NC_011658.1 | + | 1855356 | 1855493 | RNA $\rightarrow$ PoTE (COG0531) |
| Bce-29-1 | NZ_ABDL02000004.1 | + | 314768 | 314906 | RNA $\rightarrow$ PoTE (COG0531) |
| Bce-23-1 | NZ_ACMC01000044.1 | + | 58014 | 58151 | RNA $\rightarrow$ PoTE (COG0531) |
| Bce-39-1 | NZ_ACMLO1000108.1 | + | 9658 | 9794 | RNA $\rightarrow$ PoTE (COG0531) |
| Bce-26-1 | NZ_ACMO01000030.1 | + | 65366 | 65502 | RNA $\rightarrow$ PoTE (COG0531) |
| Bth-3-1 | NZ_ACNK01000040.1 | + | 161017 | 161154 | RNA $\rightarrow$ PoTE (COG0531) |
| Bce-36-1 | NZ_ACMi01000115.1 | + | 16661 | 16798 | RNA $\rightarrow$ PoTE (COG0531) |
| Bce-19-1 | NC_011725.1 | + | 1785230 | 1785367 | RNA $\rightarrow$ PoTE (COG0531) |
| Bce-4-1 | NZ_ACLY01000038.1 | + | 68177 | 68314 | RNA $\rightarrow$ PoTE (COG0531) |
| Bce-46-1 | NZ_ACMa01000037.1 | + | 3037 | 3174 | RNA $\rightarrow$ PoTE (COG0531) |
| Bce-41-1 | NZ_ACMm01000136.1 | + | 63925 | 64062 | RNA $\rightarrow$ PoTE (COG0531) |
| Bth-10-1 | NZ_ACNDO1000048.1 | + | 55519 | 55656 | RNA $\rightarrow$ PoTE (COG0531) |
| Bce-35-1 | NZ_ACMG01000031.1 | + | 12183 | 12321 | RNA $\rightarrow$ PoTE (COG0531) |
| Bce-37-1 | NZ_ACMJ01000037.1 | + | 12185 | 12323 | RNA $\rightarrow$ PoTE (COG0531) |
| Bce-40-1 | NZ_ACMN01000063.1 | + | 12256 | 12394 | RNA $\rightarrow$ PoTE (COG0531) |
| Bce-33-1 | NZ_ACLY01000037.1 | + | 37660 | 37797 | RNA $\rightarrow$ PoTE (COG0531) |
| Bce-17-1 | NC_004722.1 | + | 1762538 | 1762675 | RNA $\rightarrow$ PoTE (COG0531) |
| Bce-28-1 | NC_011772.1 | + | 1739714 | 1739851 | RNA $\rightarrow$ PoTE (COG0531) |
| Bth-1-1 | NC_014171.1 | + | 1788194 | 1788331 | RNA $\rightarrow$ PoTE (COG0531) |
| Bce-27-1 | NZ_AAEK01000005.1 | - | 2073 | 1936 | RNA $\rightarrow$ PoTE (COG0531) |
| Bth-8-1 | NZ_AAJM01000045.1 | + | 1233 | 1370 | RNA $\rightarrow$ PoTE (COG0531) |
| Bce-6-1 | NZ_ABDN02000005.1 | - | 114617 | 114480 | RNA $\rightarrow$ PoTE (COG0531) |
| Bce-15-1 | NZ_ACLT01000044.1 | + | 68977 | 69114 | RNA $\rightarrow$ PoTE (COG0531) |
| Bce-18-1 | NZ_ACLZ01000025.1 | + | 13807 | 13944 | RNA $\rightarrow$ PoTE (COG0531) |
| Bce-22-1 | NZ_ACMB01000042.1 | + | 63402 | 63539 | RNA $\rightarrow$ PoTE (COG0531) |
| Bce-20-1 | NZ_ACMF01000038.1 | + | 148744 | 148881 | RNA $\rightarrow$ PoTE (COG0531) |
| Bce-34-1 | NZ_ACMH01000043.1 | + | 408 | 445 | RNA $\rightarrow$ PoTE (COG0531) |
| Bce-13-1 | NZ_ACMQ01000061.1 | + | 9335 | 9472 | RNA $\rightarrow$ PoTE (COG0531) |
| Bth-17-1 | NZ_ACMY01000048.1 | + | 45777 | 45914 | RNA $\rightarrow$ PoTE (COG0531) |
| Bth-2-1 | NZ_ACMZ01000039.1 | + | 297 | 434 | RNA $\rightarrow$ PoTE (COG0531) |
| Bth-16-1 | NZ_ACNa01000041.1 | + | 210377 | 210514 | RNA $\rightarrow$ PoTE (COG0531) |
| Bth-15-1 | NZ_ACNb01000065.1 | + | 69193 | 69330 | RNA $\rightarrow$ PoTE (COG0531) |
| Bth-12-1 | NZ_ACNc01000068.1 | + | 8467 | 8604 | RNA $\rightarrow$ PoTE (COG0531) |
| Bth-6-1 | NZ_ACNf01000047.1 | + | 10194 | 10331 | RNA $\rightarrow$ PoTE (COG0531) |
| Bth-7-1 | NZ_ACNi01000037.1 | + | 225321 | 225458 | RNA $\rightarrow$ PoTE (COG0531) |
| Bth-4-1 | NZ_ACNL01000060.1 | + | 301 | 438 | RNA $\rightarrow$ PoTE (COG0531) |
| Bwe-1-1 | NC_010184.1 | + | 1778079 | 1779116 | RNA $\rightarrow$ PoTE (COG0531) |
| Bmy-1-1 | NZ_ACMU01000037.1 | + | 105992 | 106129 | RNA $\rightarrow$ PoTE (COG0531) |
| Bce-12-1 | NZ_ACLX01000049.1 | + | 113190 | 113327 | RNA $\rightarrow$ PoTE (COG0531) |
| Bce-8-1 | NZ_ACMs01000086.1 | + | 317 | 454 | RNA $\rightarrow$ PoTE (COG0531) |
| Bce-9-1 | NZ_ACMT01000098.1 | + | 303 | 440 | RNA $\rightarrow$ PoTE (COG0531) |
| Bce-21-1 | NZ_ACDm01000069.1 | + | 61945 | 62082 | RNA $\rightarrow$ PoTE (COG0531) |
| Bce-30-1 | NZ_ACLW01000047.1 | + | 210755 | 210892 | RNA $\rightarrow$ PoTE (COG0531) |
Bce-18-2 NZ_ACLZ01000052.1 + 93584 93715 RNA→ hypo→
Bce-16-2 NC_003909.8 + 3159883 3160014 RNA→ hypo→
Bce-32-2 NC_011906.1 + 3109066 3109197 RNA→ Collagen-like triple helix repeat protein
Bce-10-2 NC_011668.1 + 3146816 3146947 RNA→ collagen-like triple helix repeat protein
Bce-27-2 NZ_AAEK01000001.1 - 145865 145734 RNA→ hypo→
Bce-29-2 NZ_ABDL02000003.1 + 315923 316054 RNA→ hypo→
Bce-23-2 NZ_ACMC01000064.1 + 24617 24748 RNA→ hypo→
Bth-17-2 NZ_ACMY01000080.1 + 36952 37033 RNA→ Collagen-like triple helix repeat protein
Bce-12-2 NZ_ACLX01000071.1 + 44757 44888 RNA→ Collagen-like triple helix repeat protein
Bce-11-2 NZ_ACMP01000084.1 + 19502 19633 RNA→ UPF0066 (pfam01980)
Bmy-1-2 NZ_ACMU01000056.1 + 63812 63943 RNA→ UPF0066 (pfam01980)
Bce-30-2 NZ_ACLW01000070.1 + 28665 28796 RNA→ hypo→
Bce-7-2 NZ_ACMR010000143.1 + 12913 13044 RNA→
Bce-21-2 NZ_ACMO01000099.1 + 11580 11711 RNA→ hypo→
Bce-28-2 NC_011772.1 + 3262817 3262949 RNA→ hypo→
Bth-8-2 NZ_AAJM010000259.1 - 58714 59222 RNA→ Collagen (pfam01391)
Bth-15-2 NZ_ACNB01000107.1 + 13040 13172 RNA→ Collagen-like triple helix repeat protein
Bth-4-2 NZ_ACNL010000115.1 + 23773 23905 RNA→ hypo→
Bth-3-2 NZ_ACNK010000069.1 + 28244 28375 RNA→ hypo→
Bce-17-2 NC_004722.1 + 3306600 3306731 RNA→ Collagen (pfam01391)
Bce-19-2 NC_011725.1 + 3235195 3235326 RNA→ hypo→
Bth-1-2 NC_014171.1 + 3232164 3232295 RNA→ hypo→
Bce-6-2 NZ_ABDA02000002.1 - 412291 412160 RNA→ hypo→
Bce-15-2 NZ_ACLT01000068.1 + 25331 25462 RNA→ hypo→
Bce-4-2 NZ_ACLV01000057.1 + 23342 23473 RNA→ hypo→
Bce-46-2 NZ_ACMH01000076.1 + 30676 30807 RNA→ hypo→
Bce-20-2 NZ_ACMO01000083.1 + 80357 80488 RNA→ hypo→
Bth-16-2 NZ_ACNM01000073.1 + 152350 152481 RNA→ hypo→
Bth-12-2 NZ_ACNQ010000143.1 + 2183 2314 RNA→ hypo→
Bth-2-2 NZ_ACMZ01000083.1 + 2174 2305 RNA→ hypo→
Bth-11-2 NC_011772.1 + 3232164 3232295 RNA→ hypo→
Bth-10-2 NZ_ACMO01000071.1 + 116414 116545 RNA→ hypo→
Bce-33-2 NZ_ACLY01000058.1 + 63147 63278 RNA→ hypo→
Bce-39-2 NZ_ACMO01000142.1 + 12657 12788 RNA→ hypo→
Ban-17-2 NC_005945.1 + 3137592 3137724 RNA→ AdoMet_MTases (cd02440)
Ban-2-2 NC_007530.2 + 3137026 3137158 RNA→ hypo→
Bth-9-2 NC_005957.1 + 3215934 3216066 RNA→ AdoMet_MTases (cd02440)
Bce-25-2 NC_006274.1 + 3187266 3187398 RNA→ AdoMet_MTases (cd02440)
Bce-14-2 NC_011773.1 + 3223700 3223832 RNA→ hypo→
Bth-18-2 NC_008600.1 + 3219382 3219514 RNA→ AdoMet_MTases (cd02440)
Ban-14-2 NC_012581.1 - 1101730 1101598 RNA→ hypo→
Bce-2-2 NC_014272.1 + 3222130 3222262 RNA→ hypo→
Ban-5-2 NC_012659.1 + 3136926 3137058 RNA→ hypo→
Bce-44-2 NC_014535.1 + 3117377 3117269 RNA→ AdoMet_MTases (cd02440)
Ban-12-2 NC_003997.3 + 3136999 3137031 RNA→ hypo→
Ban-11-2 NZ_AAAC02000001.1 + 3601526 3601658 RNA→ AdoMet_MTases (cd02440)
env-1  SRS024580_LANL_scaffold1779  +  39296  39516  RNA→ NLPC_P60 (pfam00877)  →
env-2  SRS063193_LANL_scaffold58934  -  1482  1202  RNA→ NLPC_P60 (pfam00877)  →
env-3  SRS013164_Baylor_scaffold25506  +  1096  1316  RNA→ metagenemark→ NLPC_P60 (pfam00877)  →
env-4  SRS016037_WUGC_scaffold26104  +  830  1050  RNA→ NLPC_P60 (pfam00877)  →
env-5  SRS018439_Baylor_scaffold60860  -  6170  5950  RNA→ NLPC_P60 (pfam00877)  →
env-6  SRS019607_C2763683  +  6284  6504  RNA→ NLPC_P60 (pfam00877)  →
env-7  SRS022077_Baylor_scaffold57405  -  1383  1163  RNA→ NLPC_P60 (pfam00877)  →
env-8  SRS023958_C2069914  +  8917  9137  RNA→ metagenemark→
env-9  SRS044373_C2917542  +  1095  1315  RNA→ NLPC_P60 (pfam00877)  →
env-10 SRS055426_C3295941  +  1123  1346  RNA→ spr (COG3153)  →
env-11 SRS019022_WUGC_scaffold14734  -  32779  32556  RNA→ NLPC_P60 (pfam00877)  →
env-12 SRS019045_WUGC_scaffold41774  +  9834  10057  RNA→ NLPC_P60 (pfam00877)  →
env-13 SRS015791_LANL_scaffold35536  +  147  373  RNA→ metagenemark→
env-14 SRS024318_C3791864  +  201  429  RNA→ NLPC_P60 (pfam00877)  →
env-15 SRS019022_C2648390  +  502  681  RNA→ metagenemark→
env-16 SRS019045_C27739637  +  305  484  RNA→ NLPC_P60 (pfam00877)  →
env-17 SRS016002_WUGC_scaffold47680  -  22183  22207  RNA→ NLPC_P60 (pfam00877)  →
env-18 SRS019122_C5916309  -  312  136  RNA→ metagenemark→
env-19 SRS019126_Baylor_scaffold41641  +  717  893  RNA→ NLPC_P60 (pfam00877)  →
env-20 SRS019127_C1662896  -  312  136  RNA→ metagenemark→
env-21 SRS015537_WUGC_scaffold20201  +  5422  5600  RNA→ NLPC_P60 (pfam00877)  →
env-22 SRS015038_C1880224  +  245  424  RNA→
env-23 SRS019974_C3348413  +  614  438  RNA→ metagenemark→
env-24 SRS021496_Baylor_scaffold60604  -  858  682  RNA→ metagenemark→
env-25 SRS022530_LANL_scaffold8446  -  61111  60935  RNA→ NLPC_P60 (pfam00877)  →
env-26 SRS063288_LANL_scaffold62029  +  2205  2381  RNA→ metagenemark→
env-235  SRS043663_LANL|scaffold|12679   +   4782   4959  RNA→NLPC|P60 (pfam00877)→
env-236  SRS056323_LANL|scaffold|14579   +   382   205  RNA→metagenemark
env-237  SRS024081_LANL|scaffold|47095   -   194   17   RNA→metagenemark
env-238  SRS016225_WUGC|scaffold|17818   +   662   485  RNA→[COG10602]→metagenemark
env-239  SRS016542_C2889230   +   672   849  RNA→metagenemark
env-240  SRS018739_C3659085   +   45   222  RNA→NLPC|P60 (pfam00877)→
env-241  SRS065278_LANL|scaffold|25050   -   966   789  RNA→metagenemark→NLPC|P60 (pfam00877)→
env-242  SRS013948_WUGC|scaffold|14819   +   279   456  RNA→metagenemark→
env-243  SRS017808_Baylor|scaffold|37815   -   1987  1810  RNA→NLPC|P60 (pfam00877)→
env-244  SRS019122_C5904073   +   158   335  RNA→NLPC|P60 (pfam00877)→
env-245  SRS019126_WUGC|scaffold|24561   +   215   392  RNA→NLPC|P60 (pfam00877)→
env-246  SRS018439_Baylor|scaffold|49315   +   715   892  RNA→metagenemark→
env-247  SRS019027_C1961264   -   234   56   RNA→metagenemark→
env-248  SRS018591_WUGC|scaffold|10300   +   3475  3652  RNA→metagenemark→
env-249  SRS018791_WUGC|scaffold|44408   +   1636   1813  RNA→metagenemark→
env-250  SRS044773_WUGC|scaffold|31275   -   180   3   RNA→metagenemark→
env-251  SRS015158_WUGC|scaffold|59161   +   786   950  RNA→NLPC|P60 (pfam00877)→
env-252  SRS016575_C3745194   -   1329  1165  RNA→NLPC|P60 (pfam00877)→
env-253  SRS020226_Baylor|scaffold|20839   +   481   645  RNA→NLPC|P60 (pfam00877)→
env-254  SRS024021_C1890870   -   274   110  RNA→NLPC|P60 (pfam00877)→
env-255  SRS024289_LANL|scaffold|13273   -   3450  3286  RNA→NLPC|P60 (pfam00877)→
env-256  SRS024447_C3925644   +   39   203  RNA→metagenemark→
env-257  SRS015809_C1829138   -   535   371  RNA→metagenemark→
env-258  SRS011098_Baylor|scaffold|48946   +   38   202  RNA→NLPC|P60 (pfam00877)→
env-259  SRS011552_C3411195   +   38   202  RNA→metagenemark→
env-260  SRS011255_Baylor|scaffold|64737   -   1916  1752  RNA→NLPC|P60 (pfam00877)→
env-261  SRS011143_Baylor|scaffold|33912   +   703   867  RNA→metagenemark→NLPC|P60 (pfam00877)→
env-262  SRS013170_Baylor|scaffold|14025   +   39   203  RNA→NLPC|P60 (pfam00877)→
env-263  SRS013533_PGA|scaffold|42446   +   269   433  RNA→metagenemark→
env-264  SRS013723_Baylor|scaffold|83426   -   6747  6583  RNA→NLPC|P60 (pfam00877)→
env-265  SRS013836_C4786000   -   751   587  RNA→NLPC|P60 (pfam00877)→
env-266  SRS013945_C1223075   -   544   380  RNA→metagenemark→
env-267  SRS013949_WUGC|scaffold|61179   +   38   202  RNA→NLPC|P60 (pfam00877)→
env-268  SRS014476_WUGC|scaffold|35730   +   210   374  RNA→metagenemark→
env-269  SRS014578_WUGC|scaffold|38785   -   1242  1078  RNA→NLPC|P60 (pfam00877)→
env-270  SRS015044_WUGC|scaffold|54177   -   519   355  RNA→metagenemark→
env-271  SRS015060_C1532175   -   413   249  RNA→metagenemark→
env-272  SRS015063_WUGC|scaffold|12670   -   2094  2230  RNA→NLPC|P60 (pfam00877)→
env-273  SRS015278_WUGC|scaffold|6973   -   1812   849  RNA→NLPC|P60 (pfam00877)→
env-274  SRS015440_WUGC|scaffold|25966   +   888   1052  RNA→NLPC|P60 (pfam00877)→
env-275  SRS015470_C3286543   +   39   203  RNA→metagenemark→
env-276  SRS015574_C3316164   -   436   272  RNA→metagenemark→
env-277  SRS015755_C1679947   -   1227  1063  RNA→NLPC|P60 (pfam00877)→
env-278  SRS015803_C2592664   +   39   203  RNA→metagenemark→
env-279  SRS015947_C1383587   -   539   375  RNA→metagenemark→
env-280  SRS016039_WUGC|scaffold|16000   +   355   519  RNA→
env-281  SRS016043_WUGC|scaffold|46798   -   5566  5402  RNA→NLPC|P60 (pfam00877)→
env-282  SRS016092_WUGC|scaffold|14296   -   2325  2161  RNA→NLPC|P60 (pfam00877)→
env-283  SRS016200_WUGC|scaffold|47457   +   38   202  RNA→NLPC|P60 (pfam00877)→
env-284  SRS016351_WUGC|scaffold|35767   +   39   203  RNA→NLPC|P60 (pfam00877)→
env-285  SRS016360_C2584971   -   525   361  RNA→metagenemark→
env-286  SRS016746_C2884349   +   38   202  RNA→
| env   | SRS # | Scaffold  | Start | End | Length | RNA →  |
|-------|-------|-----------|-------|-----|--------|--------|
| env-391 | SRS064493_LANL_scaffold_11737 | - | 2392 | 2224 | RNA→NLPC_P60 [pfam00877]→ |
| env-392 | SRS065099_LANL_scaffold_94698 | - | 852 | 684 | RNA→NLPC_P60 [pfam00877]→ |
| env-393 | SRS011255_Baylor_scaffold_52823 | + | 296 | 464 | RNA→NLPC_P60 [pfam00877]→ |
| env-394 | SRS012285_C28866467 | - | 405 | 235 | RNA→metagenemark→ |
| env-395 | SRS013170_Baylor_scaffold_102779 | + | 257 | 425 | RNA→metagenemark→ |
| env-396 | SRS013526_Baylor_scaffold_50311 | + | 443 | 611 | RNA→metagenemark→ |
| env-397 | SRS013723_Baylor_scaffold_93887 | + | 406 | 574 | RNA→NLPC_P60 [pfam00877]→ |
| env-398 | SRS013836_Baylor_scaffold_28604 | - | 850 | 682 | RNA→metagenemark→NLPC_P60 [pfam00877]→ |
| env-399 | SRS014476_WUGC_scaffold_18365 | + | 40 | 208 | RNA→metagenemark→ |
| env-400 | SRS014477_C1631286 | - | 852 | 684 | RNA→NLPC_P60 [pfam00877]→ |
| env-401 | SRS015274_C464466 | + | 77 | 245 | RNA→metagenemark→ |
| env-402 | SRS015278_WUGC_scaffold_17600 | + | 40 | 208 | RNA→NLPC_P60 [pfam00877]→ |
| env-403 | SRS015378_WUGC_scaffold_3764 | + | 188 | 356 | RNA→NLPC_P60 [pfam00877]→ |
| env-404 | SRS015436_C1725737 | - | 483 | 315 | RNA→metagenemark→ |
| env-405 | SRS015440_WUGC_scaffold_58490 | + | 241 | 409 | RNA→metagenemark→ |
| env-406 | SRS015899_WUGC_scaffold_1398 | + | 616 | 784 | RNA→metagenemark→ |
| env-407 | SRS015921_C527678 | - | 489 | 321 | RNA→metagenemark→ |
| env-408 | SRS015989_WUGC_scaffold_23668 | + | 121 | 289 | RNA→metagenemark→ |
| env-409 | SRS016043_C2193660 | - | 585 | 417 | RNA→metagenemark→ |
| env-410 | SRS016092_WUGC_scaffold_3737 | - | 1027 | 859 | RNA→NLPC_P60 [pfam00877]→ |
| env-411 | SRS016349_C1022228 | + | 41 | 209 | RNA→metagenemark→ |
| env-412 | SRS016360_Baylor_scaffold_4334 | + | 845 | 1013 | RNA→metagenemark→ |
| env-413 | SRS016746_Baylor_scaffold_264 | + | 2146 | 1978 | RNA→NLPC_P60 [pfam00877]→ |
| env-414 | SRS017025_Baylor_scaffold_4649 | - | 160 | 328 | RNA→metagenemark→ |
| env-415 | SRS017304_Baylor_scaffold_7891 | + | 223 | 391 | RNA→NLPC_P60 [pfam00877]→ |
| env-416 | SRS017511_C3436658 | + | 40 | 208 | RNA→metagenemark→ |
| env-417 | SRS017533_C4088030 | + | 188 | 356 | RNA→metagenemark→ |
| env-418 | SRS017601_C5396394 | - | 863 | 695 | RNA→metagenemark→NLPC_P60 [pfam00877]→ |
| env-419 | SRS018359_C1200774 | - | 294 | 126 | RNA→metagenemark→ |
| env-420 | SRS019077_WUGC_scaffold_45337 | + | 89 | 257 | RNA→metagenemark→NLPC_P60 [pfam00877]→ |
| env-421 | SRS019225_C1529788 | + | 40 | 208 | RNA→metagenemark→ |
| env-422 | SRS019587_C1048848 | - | 529 | 361 | RNA→metagenemark→ |
| env-423 | SRS019906_C2224822 | + | 40 | 208 | RNA→metagenemark→ |
| env-424 | SRS020334_C2567594 | + | 146 | 314 | RNA→metagenemark→ |
| env-425 | SRS020340_Baylor_scaffold_3834 | + | 334 | 502 | RNA→NLPC_P60 [pfam00877]→ |
| env-426 | SRS020862_C897366 | - | 424 | 256 | RNA→metagenemark→ |
| env-427 | SRS022149_C2883984 | - | 585 | 417 | RNA→metagenemark→ |
| env-428 | SRS022538_C1257786 | + | 43 | 211 | RNA→metagenemark→ |
| env-429 | SRS023595_C7185599 | + | 40 | 208 | RNA→NLPC_P60 [pfam00877]→ |
| env-430 | SRS023987_C1178378 | + | 1172 | 1340 | RNA→metagenemark→ |
| env-431 | SRS024144_LANL_scaffold_27349 | - | 2561 | 2393 | RNA→NLPC_P60 [pfam00877]→ |
| env-432 | SRS024381_LANL_scaffold_27333 | + | 176 | 344 | RNA→metagenemark→ |
| env-433 | SRS024447_C3881828 | - | 424 | 256 | RNA→metagenemark→ |
| env-434 | SRS024561_C2793126 | + | 111 | 279 | RNA→NLPC_P60 [pfam00877]→ |
| env-435 | SRS042984_LANL_scaffold_27330 | + | 334 | 502 | RNA→NLPC_P60 [pfam00877]→ |
| env-436 | SRS043755_WUGC_scaffold_22115 | + | 73 | 241 | RNA→NLPC_P60 [pfam00877]→ |
| env-437 | SRS043772_WUGC_scaffold_31805 | + | 256 | 424 | RNA→metagenemark→ |
| env-438 | SRS045197_WUGC_scaffold_21761 | - | 585 | 417 | RNA→metagenemark→ |
| env-439 | SRS045313_C1357321 | + | 188 | 356 | RNA→NLPC_P60 [pfam00877]→ |
| env-440 | SRS047180_WUGC_scaffold_3456 | - | 1559 | 1391 | RNA→metagenemark→NLPC_P60 [pfam00877]→ |
| env-441 | SRS051941_LANL_scaffold_72646 | - | 340 | 172 | RNA→metagenemark→ |
| env-442 | SRS055401_C2236337 | + | 14 | 182 | RNA→metagenemark→ |
env-495  SRS016575,C3687005  -  414  229 RNA→ metagenemark→
env-496  SRS017139,Baylor,scaffold,25109  +  2279  2464 RNA→ metagenemark→
env-497  SRS017691,Baylor,scaffold,70311  +  1012  1197 RNA→
env-498  SRS022226,C3417582  -  236  53 RNA→
env-499  SRS023938,C2270105  -  300  115 RNA→ metagenemark→
env-500  SRS051378,C1860885  +  702  887 RNA→ metagenemark→
env-501  SRS013836,C4683527  +  229  414 RNA→
env-502  SRS017227,Baylor,scaffold,12437  +  9384  9569 RNA→ NLPC,P60 (pfam00877)→
env-503  SRS047113,C5400941  +  903  1088 RNA→
env-504  SRS043018,C3855509  -  399  213 RNA→ metagenemark→
env-505  SRS051941,LANL,scaffold,75582  +  1282  1468 RNA→
env-506  SRS016092,WUGC,scaffold,14071  -  277  90 RNA→
env-507  SRS065099,LANL,scaffold,48996  -  396  209 RNA→ metagenemark→
env-508  SRS018573,WUGC,scaffold,15803  -  210  23 RNA→
env-509  SRS019024,C912939  +  3  190 RNA→ metagenemark→
env-510  SRS019221,C281677  +  38  225 RNA→
env-511  SRS024144,LANL,scaffold,22453  -  210  23 RNA→
env-512  SRS064809,LANL,scaffold,10667  +  450  637 RNA→ metagenemark→
env-513  SRS017139,C3680389  -  310  123 RNA→
env-514  SRS023938,Baylor,scaffold,19654  +  2117  2304 RNA→ NLPC,P60 (pfam00877)→
env-515  SRS024355,LANL,scaffold,53772  +  699  886 RNA→ NLPC,P60 (pfam00877)→
env-516  SRS047634,LANL,scaffold,78229  +  644  831 RNA→
env-517  SRS015060,WUGC,scaffold,1446  +  380  567 RNA→ metagenemark→
env-518  SRS015745,WUGC,scaffold,4838  -  399  212 RNA→ metagenemark→
env-519  SRS023538,Baylor,scaffold,21549  +  3  190 RNA→ metagenemark→
env-520  SRS018881,WUGC,scaffold,3608  -  212  25 RNA→
env-521  SRS03945,WUGC,scaffold,17476  +  429  616 RNA→ metagenemark→
env-522  SRS014473,C1104999  -  354  167 RNA→ metagenemark→
env-523  SRS015044,WUGC,scaffold,60523  +  443  630 RNA→ metagenemark→
env-524  SRS015154,C734432  +  91  278 RNA→
env-525  SRS015803,C2561781  +  61  248 RNA→ metagenemark→
env-526  SRS015895,WUGC,scaffold,8273  +  418  605 RNA→
env-527  SRS015921,WUGC,scaffold,5142  +  2035  2222 RNA→ metagenemark→
env-528  SRS016529,C3008873  +  17  204 RNA→
env-529  SRS016600,C801105  -  280  93 RNA→
env-530  SRS017533,C4027563  -  424  237 RNA→ metagenemark→
env-531  SRS019029,C3221035  +  9  196 RNA→ metagenemark→
env-532  SRS019129,WUGC,scaffold,42288  -  351  164 RNA→ metagenemark→
env-533  SRS019225,C1500295  +  60  247 RNA→
env-534  SRS019333,WUGC,scaffold,8033  +  555  368 RNA→ metagenemark→
env-535  SRS021960,Baylor,scaffold,1358  +  139  326 RNA→ metagenemark→
env-536  SRS023987,C1174850  +  408  595 RNA→ metagenemark→
env-537  SRS024201,Baylor,scaffold,16504  -  388  201 RNA→ metagenemark→
env-538  SRS024649,LANL,scaffold,8802  +  149  336 RNA→ metagenemark→
env-539  SRS043676,WUGC,scaffold,19054  +  59  246 RNA→ metagenemark→ NLPC,P60 (pfam00877)→
env-540  SRS045313,C1308725  +  116  303 RNA→
env-541  SRS048719,C802909  -  531  344 RNA→ metagenemark→
env-542  SRS051930,C3088385  +  102  289 RNA→
env-543  SRS055450,LANL,scaffold,72191  -  352  165 RNA→ metagenemark→
env-544  SRS056892,C1451957  -  352  165 RNA→ metagenemark→
env-545  SRS058808,LANL,scaffold,43291  +  8  195 RNA→ metagenemark→
env-546  SRS063287,LANL,scaffold,14386  +  606  793 RNA→
| Ensembl Entry | SRS ID   | Start   | End     | Feature   | Description                                      |
|---------------|----------|---------|---------|-----------|-------------------------------------------------|
| env-547       | SRS049268 | 60870   | 350 178 | RNA       | metagenemark                                     |
| env-548       | SRS049318 | 152253  | 297 469 | RNA       | metagenemark                                     |
| env-549       | SRS013252 | 56886   | 553    | RNA       | metagenemark                                     |
| env-550       | SRS015251 | 51213   | 553    | RNA       | metagenemark                                     |
| env-551       | SRS016575 | 56624   | 199 371 | RNA       | metagenemark                                     |
| env-552       | SRS017304 | 1967410 | 19     | RNA       | metagenemark                                     |
| env-553       | SRS018665 | 3643328 | 306    | RNA       | metagenemark                                     |
| env-554       | SRS024087 | 64636   | 156 328 | RNA       | metagenemark                                     |
| env-555       | SRS024144 | 51213   | 297    | RNA       | metagenemark                                     |
| env-556       | SRS045197 | 3521889 | 306    | RNA       | metagenemark                                     |
| env-557       | SRS051244 | 3445828 | 220    | RNA       | metagenemark                                     |
| env-558       | SRS063932 | 3898934 | 447    | RNA       | metagenemark                                     |
| env-559       | SRS011285 | 2948207 | 323    | RNA       | metagenemark                                     |
| env-560       | SRS013950 | 2063634 | 476    | RNA       | metagenemark                                     |
| env-561       | SRS014476 | 41428   | 354    | RNA       | metagenemark                                     |
| env-562       | SRS014578 | 2528240 | 406    | RNA       | metagenemark                                     |
| env-563       | SRS016746 | 41428   | 315    | RNA       | metagenemark                                     |
| env-564       | SRS019029 | 55186   | 292    | RNA       | metagenemark                                     |
| env-565       | SRS019980 | 51213   | 596    | RNA       | metagenemark                                     |
| env-566       | SRS020226 | 3310258 | 292    | RNA       | metagenemark                                     |
| env-567       | SRS024649 | 3602686 | 305    | RNA       | metagenemark                                     |
| env-568       | SRS047113 | 5243061 | 416    | RNA       | metagenemark                                     |
| env-569       | SRS063999 | 81143   | 305    | RNA       | metagenemark                                     |
| env-570       | SRS022536 | 101034  | 477    | RNA       | metagenemark                                     |
| env-571       | SRS022595 | 697796  | 225    | RNA       | metagenemark                                     |
| env-572       | SRS024355 | 4216283 | 370    | RNA       | metagenemark                                     |
| env-573       | SRS065099 | 36079   | 329    | RNA       | metagenemark                                     |
| env-574       | SRS011126 | 4652129 | 305    | RNA       | metagenemark                                     |
| env-575       | SRS013533 | 121249  | 556    | RNA       | metagenemark                                     |
| env-576       | SRS017139 | 97072   | 556    | RNA       | metagenemark                                     |
| env-577       | SRS017691 | 538920  | 646    | RNA       | metagenemark                                     |
| env-578       | SRS020340 | 2954213 | 306    | RNA       | metagenemark                                     |
| env-579       | SRS021477 | 27748   | 472    | RNA       | metagenemark                                     |
| env-580       | SRS022149 | 2825348 | 535    | RNA       | metagenemark                                     |
| env-581       | SRS042984 | 10621   | 306    | RNA       | metagenemark                                     |
| env-582       | SRS055378 | 27249   | 901    | RNA       | metagenemark                                     |
| env-583       | SRS096303 | 16274   | 370    | RNA       | metagenemark                                     |
| env-584       | SRS011343 | 16274   | 515    | RNA       | metagenemark                                     |
| env-585       | SRS016043 | 2079269 | 8      | RNA       | metagenemark                                     |
| env-586       | SRS016200 | 29523   | 285    | RNA       | metagenemark                                     |
| env-587       | SRS018337 | 2356506 | 307    | RNA       | metagenemark                                     |
| env-588       | SRS022890 | 54571   | 214    | RNA       | metagenemark                                     |
| env-589       | SRS043018 | 3719998 | 358    | RNA       | metagenemark                                     |
| env-590       | SRS016331 | 4115711 | 118    | RNA       | metagenemark                                     |
| env-591       | SRS023358 | 3470451 | 265    | RNA       | metagenemark                                     |
| env-592       | SRS024447 | 3766239 | 308    | RNA       | metagenemark                                     |
| env-593       | SRS024649 | 29152   | 301    | RNA       | metagenemark                                     |
| env-594       | SRS063932 | 3819810 | 241    | RNA       | metagenemark                                     |
| env-595       | SRS024381 | 49769   | 323    | RNA       | metagenemark                                     |
| env-596       | SRS011255 | 70812   | 272    | RNA       | metagenemark                                     |
| env-597       | SRS015047 | 20723   | 332    | RNA       | metagenemark                                     |
| env-598       | SRS017304 | 2045    | 253    | RNA       | metagenemark                                     |
env-807  SRS057205,LANL,scaffold_53439  +  709  861 RNA→
env-808  SRS057355,C2296460  +  261  413 RNA→
env-809  SRS057602,LANL,scaffold_15653  -  288  136 RNA→ ← metagenemark
env-810  SRS058366,LANL,scaffold_5649  +  1647  1799 RNA→
env-811  SRS062761,LANL,scaffold_29752  -  274  122 RNA→
env-812  SRS063193,LANL,scaffold_25786  -  300  148 RNA→ ← metagenemark→
env-813  SRS062540,C2314588  +  311  463 RNA→
env-814  SRS015395,C2380068  +  434  586 RNA→
env-815  SRS017713,C3331255  +  435  587 RNA→
env-816  SRS018439,Baylor,scaffold_14613  -  288  136 RNA→
env-817  SRS019974,Baylor,scaffold_38280  -  288  136 RNA→
env-818  SRS022143,WUGC,scaffold_49266  -  564  412 RNA→ ← metagenemark→
env-819  SRS045127,LANL,scaffold_29585  -  279  127 RNA→
env-820  SRS049389,WUGC,scaffold_44162  +  856  1008 RNA→
env-821  SRS020334,Baylor,scaffold_8632  +  1238  1390 RNA→
env-822  SRS063946,C725710  +  420  571 RNA→ ← metagenemark→
env-823  SRS014271,C2919516  +  776  927 RNA→ ← metagenemark→
env-824  SRS017120,Baylor,scaffold_21193  -  287  136 RNA→ ← metagenemark→
env-825  SRS019026,WUGC,scaffold_20761  -  204  53 RNA→
env-826  SRS021496,Baylor,scaffold_59252  +  186  337 RNA→ ← metagenemark→
env-827  SRS024318,LANL,scaffold_21591  -  291  140 RNA→ ← metagenemark→
env-828  SRS014686,C870695  +  194  345 RNA→
env-829  SRS015537,WUGC,scaffold_12163  -  327  176 RNA→ ← metagenemark→
env-830  SRS017713,Baylor,scaffold_9740  +  1138  1289 RNA→ ← NLPC,P60 (pfam00877)→
env-831  SRS013234,Baylor,scaffold_22089  +  1896  2047 RNA→ ← metagenemark→
env-832  SRS015395,WUGC,scaffold_10967  -  72  223 RNA→ ← metagenemark→
env-833  SRS020220,Baylor,scaffold_22748  -  274  123 RNA→ ← metagenemark→
env-834  SRS020334,Baylor,scaffold_17866  -  273  122 RNA→ ← metagenemark→
env-835  SRS021954,Baylor,scaffold_46684  +  422  573 RNA→
env-836  SRS023457,Baylor,scaffold_17159  -  271  120 RNA→ ← metagenemark→
env-837  SRS044373,WUGC,scaffold_50829  +  247  398 RNA→ ← metagenemark→
env-838  SRS051791,LANL,scaffold_10721  -  907  756 RNA→ ← NLPC,P60 (pfam00877)→
env-839  SRS053603,LANL,scaffold_1191  -  728  577 RNA→ ← NLPC,P60 (pfam00877)→
env-840  SRS053854,LANL,scaffold_41417  +  65  216 RNA→ ← NLPC,P60 (pfam00877)→
env-841  SRS054687,LANL,scaffold_16303  -  287  136 RNA→ ← metagenemark→
env-842  SRS015440,C2494351  +  134  285 RNA→
env-843  SRS014578,WUGC,scaffold_53219  -  458  307 RNA→ ← metagenemark→
env-844  SRS012285,Baylor,scaffold_58071  -  273  122 RNA→ ← metagenemark→
env-845  SRS015215,C2518492  +  340  491 RNA→
env-846  SRS015899,C1792485  -  279  128 RNA→ ← metagenemark→
env-847  SRS017139,Baylor,scaffold_85238  -  479  328 RNA→ ← metagenemark→
env-848  SRS018394,C3939873  +  185  336 RNA→ ← metagenemark→
env-849  SRS021477,Baylor,scaffold_57053  -  467  316 RNA→ ← metagenemark→
env-850  SRS023938,Baylor,scaffold_65956  -  541  390 RNA→ ← metagenemark→
env-851  SRS024087,C3433094  +  186  337 RNA→ ← metagenemark→
env-852  SRS024289,LANL,scaffold_40272  +  181  332 RNA→
env-853  SRS016002,WUGC,scaffold_36290  -  466  315 RNA→ ← metagenemark→
env-854  SRS017209,Baylor,scaffold_27434  +  42  193 RNA→
env-855  SRS058356,C1987887  +  42  193 RNA→ ← metagenemark→
env-856  SRS063288,LANL,scaffold_22271  +  325  476 RNA→ ← metagenemark→
env-857  SRS017439,C3822425  -  287  136 RNA→
env-858  SRS016225,WUGC,scaffold_25760  -  193  42 RNA→
| Accession    | Description                      | Start | End   | RNA     | Metagename          |
|--------------|----------------------------------|-------|-------|---------|---------------------|
| SRS022725    | LANL_scaffold_9173               | -     | 561   | 398     | RNA → metagename    |
| SRS023538    | Baylor_scaffold_17267            | +     | 2589  | 2752    | RNA → metagename    |
| SRS025595    | C7010996                         | +     | 218   | 381     | RNA →              |
| SRS023964    | Baylor_scaffold_66014            | -     | 13016 | 12853   | RNA → NLPC_P60      |
| SRS024021    | Baylor_scaffold_11455            | +     | 6593  | 6756    | RNA → NLPC_P60      |
| SRS024289    | LANL_scaffold_42941              | +     | 1816  | 1979    | RNA → NLPC_P60      |
| SRS024381    | LANL_scaffold_28277              | -     | 4753  | 4590    | RNA → NLPC_P60      |
| SRS024447    | C3946289                         | -     | 455   | 292     | RNA → metagename    |
| SRS024649    | C3649189                         | +     | 420   | 583     | RNA → metagename    |
| SRS042984    | C4057433                         | +     | 390   | 553     | RNA → NLPC_P60      |
| SRS043018    | WUGC_scaffold_53541              | +     | 1933  | 2096    | RNA → NLPC_P60      |
| SRS043755    | C2370493                         | +     | 577   | 740     | RNA → metagename    |
| SRS043772    | WUGC_scaffold_20147              | +     | 351   | 514     | RNA → metagename    |
| SRS045197    | WUGC_scaffold_54492              | +     | 1620  | 1783    | RNA → NLPC_P60      |
| SRS045153    | C1328403                         | +     | 222   | 385     | RNA → NLPC_P60      |
| SRS047100    | WUGC_scaffold_29617              | +     | 575   | 738     | RNA → NLPC_P60      |
| SRS047113    | LANL_scaffold_77949              | -     | 1269  | 1160    | RNA → NLPC_P60      |
| SRS047265    | WUGC_scaffold_21708              | +     | 1458  | 1621    | RNA → NLPC_P60      |
| SRS047634    | C4427416                         | +     | 553   | 716     | RNA →              |
| SRS049268    | LANL_scaffold_16588              | +     | 1462  | 1625    | RNA → NLPC_P60      |
| SRS051244    | C3397963                         | -     | 282   | 119     | RNA → metagename    |
| SRS051941    | C4068888                         | -     | 466   | 303     | RNA → metagename    |
| SRS052604    | C1789241                         | +     | 352   | 515     | RNA →              |
| SRS052876    | C2120887                         | -     | 202   | 39      | RNA →              |
| SRS053584    | C2093820                         | -     | 1269  | 1160    | RNA → NLPC_P60      |
| SRS054430    | C2083433                         | -     | 282   | 119     | RNA → metagename    |
| SRS054653    | LANL_scaffold_38508              | -     | 1211  | 1048    | RNA → NLPC_P60      |
| SRS054776    | C1546144                         | -     | 226   | 63      | RNA →              |
| SRS055378    | LANL_scaffold_91193              | +     | 1550  | 1713    | RNA → metagename    |
| SRS055401    | C2347232                         | -     | 472   | 309     | RNA → metagename    |
| SRS058053    | LANL_scaffold_84471              | -     | 1569  | 1406    | RNA → NLPC_P60      |
| SRS058808    | C2888121                         | -     | 448   | 285     | RNA → metagename    |
| SRS063215    | C2273020                         | +     | 1583  | 1746    | RNA →              |
| SRS063603    | C4204425                         | -     | 217   | 54      | RNA →              |
| SRS063999    | LANL_scaffold_90125              | -     | 964   | 801     | RNA → NLPC_P60      |
| SRS064449    | LANL_scaffold_56898              | +     | 1774  | 1937    | RNA → NLPC_P60      |
| SRS064493    | LANL_scaffold_13455              | -     | 38145 | 37982   | RNA → NLPC_P60      |
| SRS065099    | LANL_scaffold_51896              | -     | 2767  | 2930    | RNA → NLPC_P60      |
| SRS0712285   | Baylor_scaffold_65460             | -     | 4368  | 4205    | RNA → NLPC_P60      |
| SRS071739    | Baylor_scaffold_106465            | -     | 1152  | 989     | RNA → NLPC_P60      |
| SRS079280    | Baylor_scaffold_19536            | +     | 696   | 859     | RNA → NLPC_P60      |
| SRS024355    | C4298096                         | +     | 572   | 735     | RNA → NLPC_P60      |
| SRS025508    | SUL1                               | -     | 3305  | 3177    | RNA → STAS_SulP_like_sulfate_transporter (cd07042) → hypo |
| SRS025703     |                                     | -     | 742   | 614     | RNA → SUL1 (COG0659) → |
| SRS030394    | Cons10394                        | -     | 2017  | 1891    | RNA → hypo          |
| LWA1N626        |                                   | -     | 122   | 298     | RNA → hypo          |
| LWA1N602     |                                   | -     | 122   | 298     | RNA → hypo          |
| MA55A        |                                   | -     | 129   | 209     | RNA → hypo          |
| DCYCP1344   |                                   | -     | 508   | 359     | RNA → hypo          |
| B3all_c     |                                   | -     | 2479  | 2359    | RNA → PotE (COG0531) → COG2317 (COG2317) → |
| B3all_c     |                                   | -     | 7551  | 7428    | RNA → PotE (COG0531) → TomB family C-terminal domain → |
| B3all_c     |                                   | +     | 1346  | 1544    | RNA → GT1Sucrose_synthase (cd03800) → |
| env | ch | contig | start | end | name | position | RNA → | Cons | annotation |
|-----|----|--------|-------|-----|-------|----------|--------|-----|------------|
| env-1319 | B3 | all | - | 420 | 295 | RNA → ← hypo | B3 All_e | Cons119611 - 420 295 |
| env-1320 | A5 | c1 | Cons30106 | + | 5545 | 5682 | RNA → hypo | A5_C1 | TIGR00113 → |
| env-1321 | FRSSGG | Sequence000017119 | + | 495 | 633 | RNA → PosE | TIGR00531 → |
| env-1322 | GBAN | final | - | 341 | 204 | RNA → hypo | GBAN | COG00000333 |
| env-1323 | sg4i | contig03433 | + | 430 | 569 | RNA → hypo | TIGR00531 → |
| env-1324 | MA55A | contig00112 | + | 200 | 330 | RNA → hypo | MA55A | Contig112 - 200 330 |
| env-1325 | FNTS | GJ87FRN01EUCFW | + | 22 | 173 | RNA → hypo | FNTS | Contig112 - 22 173 |
| env-1326 | Cons15790 | + | 200 | 330 | RNA → hypo | Cons15790 | Contig112 - 200 330 |
| env-1327 | FNTS | GKA24FP01BJMS | - | 350 | 136 | RNA → hypo | FNTS | Contig112 - 350 136 |
| env-1328 | FNTS | GJ87FRN01IIG3Y | - | 200 | 330 | RNA → hypo | FNTS | Contig112 - 200 330 |
| env-1329 | FNTS | GJ87FRN01IIXQX | - | 200 | 330 | RNA → hypo | FNTS | Contig112 - 200 330 |
env-1526 FNTS067_GKA24FP01BAOCG + 140 275 RNA→ hypo→
env-1527 FNTS067_GKA24FP01C1Y16 - 163 30 RNA→
env-1528 FNTS067_GKA24FP01EVTF5 - 170 18 RNA→ hypo→
env-1529 PRSSGFv2_Sequence0000049712 + 633 746 RNA→ PG_binding_1 (pfam01471)→
env-1530 PRSSGFv2_Sequence0000031906 + 351 472 RNA→ hypo→
env-1531 ACOFG987_F36MELC01D9K1S + 41 154 RNA→ PG_binding_1 (pfam01471)→
env-1532 ASLM90b_GN81PCX02HEEOE - 311 147 RNA→ hypo→
env-1533 topACOD_FV90NF401BDSQI - 299 155 RNA→
env-1534 topACOD_F9509CU02GWX61 + 65 209 RNA→ hypo→ hypo→
env-1535 FNTS067_GJ87FRN01A7W5D - 260 104 RNA→ hypo→
env-1536 scaffold877_2_O2.UC-18 + 628 767 RNA→ hypo→
env-1537 scaffold41962_1_V1.CD-12 + 124 267 RNA→ Na_Pro_sym (TIGR02121)→
env-1538 FNTS_GKKEVUV02HXHWN + 93 249 RNA→ hypo→
env-1539 DCiCpGBGc198499 - 183 38 RNA→
env-1540 A5_c1_Cons78508 - 1140 981 RNA→
env-1541 GBANfinal_FHN120P03QM4MF - 424 257 RNA→ spore_SleB (TIGR02869)→
env-1542 FNTS_GKKEVUV01BGYQK + 41 194 RNA→ hypo→
env-1543 FNTS_GKKEVUV02J6L1I + 151 318 RNA→ hypo→
env-1544 P3_CLC_Cons136658 + 333 489 RNA→ hypo→
env-1545 ZhangC00857_1 - 164 28 RNA→
env-1546 A2_c1_Cons15230 + 214 364 RNA→ hypo→ hypo→
env-1547 botACOD_FV90NF402I4N1Z - 255 126 RNA→ hypo→
env-1548 A5_c1_Cons9234 + 589 736 RNA→ hypo→
env-1549 FNTS067_GKA24FP01C0NGA - 150 2 RNA→
env-1550 P3_CLC_Cons16885 + 534 662 RNA→ hypo→
env-1551 FNTS067_GJ87FRN01AFO6F - 169 37 RNA→ hypo→
env-1552 A5_c1_Cons101191 + 322 185 RNA→ hypo→
env-1553 A5_c1_Cons84081 + 875 738 RNA→ hypo→
env-1554 B13_all_c_Cons79562 + 4995 4859 RNA→ hypo→
env-1555 A5_c1_Cons811 - 482 346 RNA→
env-1556 ASMM170b_GM97KZC01BGF2Y + 146 291 RNA→
env-1557 A5_c1_Cons32245 - 1167 1019 RNA→ Peptidase_M23 (pfam01551)→
env-1558 A5_c1_Cons30632 + 1947 2098 RNA→ hypo→
env-1559 A5_c1_Cons105912 + 623 774 RNA→ hypo→
env-1560 2033473052 - 155 2 RNA→
env-1561 A5_c1_Cons79188 + 1332 1478 RNA→
env-1562 botACOD_GAKN62C01CU8HH - 304 167 RNA→ hypo→
env-1563 A5_c1_Cons66383 + 121 472 RNA→ hypo→
env-1564 A5_c1_Cons54154 + 493 644 RNA→ PG_binding_1 (pfam01471)→ SCAD_SBCAD (cd01158)→
env-1565 HCF12C_J21183 - 199 54 RNA→
env-1566 LWFCAGLZZ6Z001CM8GC + 130 251 RNA→
env-1567 BDMC2_contig15757 - 3602 3474 RNA→ KdpA (pfam03814)→ KdpB (COG2216)→
env-1568 BDMC2_contig12827 - 169 41 RNA→ KdpA (pfam03814)→
env-1569 BDMC2_contig10162 + 195 323 RNA→ hypo→
env-1570 BDMC2_contig16269 - 1072 1199 RNA→
env-1571 LWFCAn_GLO1YSU01C5GAR + 52 148 RNA→ hypo→
env-1572 PCEOT_FS8BFFD02D0PER + 257 390 RNA→ hypo→
env-1573 2033268912 - 301 182 RNA→
env-1574 TB18AUG2009H_c634 + 1923 2049 RNA→ LT_GEWL (cd00254)→
env-1575 PBDC2_contig36377 - 253 117 RNA→
env-1576 TB03JUN2009H_c3815 - 408 284 RNA→ hypo→
env-1577 TB18AUG2009H_c391 + 3379 3503 RNA→ PotE (COG0531)→
env-1733 scaffold60855_1_V1.CD-11 + 10306 10436 RNA → HATPase_c (cd00075) HisKA (cd00082) →
env-1734 444165.3.07861 + 1754 1884 RNA → metagenemark →
env-1735 444164.3.06833 - 1563 1436 RNA → KdpD (pfam02702) →
env-1736 CAM_READ_0099621053 + 301 429 RNA → HATPase_c (cd00075) HisKA (cd00082) →
env-1737 444165.3.13299 + 1062 1189 RNA → OpuBB (COG1174) →
env-1738 CAM_READ_0099942719 + 74 199 RNA →
env-1739 444164.3.48393 - 336 211 RNA → metagenemark →
env-1740 CAM_READ_009567587 - 242 118 RNA →
env-1741 CAM_READ_0099778655 - 264 138 RNA → ← metagenemark →
env-1742 444165.3.50505 + 118 244 RNA →
env-1743 444165.3.29609 - 3277 3151 RNA → metagenemark → PAS (cd00130) HAMP (cd06225) → HisKA (cd00082) →
env-1744 PBDC2_contig21384 - 695 545 RNA → LysM (cd00118) spore_SleB (TIGR02869) →
env-1745 PRSSGFv2_Sequence000001278 + 9445 9566 RNA → NLPC_P60 (pfam00877) PG_binding_1 (pfam01471) →
env-1746 BMHBC_133015 - 152 18 RNA → ← hypo →
env-1747 MA40A_contig11243 + 36 149 RNA → ← hypo →
env-1748 PRSSGFv2_Sequence0000015855 - 1366 1816 RNA → eurate_synth_like_1_2 (cd00119) →
env-1749 MA55A_contig03486 + 210 335 RNA → ← hypo →
env-1750 PBDC2_GBB5CE401CPP2R_left + 158 289 RNA →
env-1751 LWFCa_GLZZ6Z001CB8KR + 7 139 RNA → ← hypo →
env-1752 LWFCa_GLZZ6Z001EiF6P + 107 242 RNA →
env-1753 2016935643 - 206 71 RNA →
env-1754 PBDC2_FISUTAU01CF00Q - 398 253 RNA → PG_binding_1 (pfam01471) →
env-1755 LWAnN_GIDYKCY01ESFAZ - 185 55 RNA →
env-1756 FNTS_GKKEVU02JRS08 + 6 134 RNA →
env-1757 taComm3_FFOP7019_x1 + 310 433 RNA →
env-1758 PRSSGFv2_Sequence000003322 + 5413 5528 RNA → Radical_SAM (cd01335) →
env-1759 MA55A_contig03336 + 18 145 RNA → →
env-1760 PRSSGFv2_Sequence000004191 + 1065 1195 RNA → Porto (COG0531) →
env-1761 BMHBC_2646 - 258 390 RNA → Amino acid permease →
env-1762 PRSSGFv2_Sequence000004191 + 3542 3682 RNA → kup (COG3158) → ← hypo →
env-1763 BMHBC_84036 - 2809 2677 RNA → kup (COG3158) → kup (COG3158) →
env-1764 LWFCa_N_G009JKT02FJX8Q - 298 175 RNA →
env-1765 PCEOT_F164ET01DT07C + 75 198 RNA →
env-1766 LWFCa_GLO1YSU01DC1KQE - 263 141 RNA → ← hypo →
env-1767 LWFCa_N_G009JKT02JMKQB + 126 249 RNA →
env-1768 LWFCa_contig05684 - 446 321 RNA → kup (COG3158) →
env-1769 LWFCa_GLO1YSU01ATNSX + 152 277 RNA → ← hypo →
env-1770 comb11_contig95278 + 1690 1565 RNA → kup (COG3158) → kup (COG3158) →
env-1771 comb22_contig05476 - 1690 1565 RNA → kup (COG3158) → kup (COG3158) →
env-1772 LWFCa_GLZZ6Z001CAT4P - 262 148 RNA → ← hypo →
env-1773 LWFCa_GLQ6A01Q1OSVR - 219 98 RNA → ← hypo →
env-1774 LWFCa_GLZZ6Z001DC19P + 100 224 RNA →
env-1775 LWSC_GLQAYWI02GBV09 - 192 68 RNA → ← hypo →
env-1776 LWSC2_GGWJX9X02GBDHL + 239 113 RNA →
env-1777 LWSC_GLQAYWI02JVR7V + 97 221 RNA → ← hypo →
env-1778 LWSC_GLQAYWI02FXOCM - 255 130 RNA → ← hypo →
env-1779 LWSC_GLQAYWI02HUKWD + 135 260 RNA → ← hypo →
env-1780 lwComb_BCG036405_201 - 359 231 RNA →
env-1781 LWSC_GFMCQXZ02F8CA2 - 360 235 RNA → kup (COG3158) →
env-1782 LWSC2_GGBSFT02H7086 - 166 37 RNA → ← hypo →
env-1783 LWSC_GLQAYWI02HMTM1 + 140 267 RNA → ← hypo →
env-1784 2031582183 + 760 883 RNA → ← hypo →
env-1785 GXP7IEG01ED91V + 27 146 RNA→
env-1786 lwComb_BHFI11741_g1 + 317 432 RNA→ Amino acid transporters→
env-1787 2014738123 - 353 233 RNA→
env-1788 ANASMEcb_4085297_CG351 - 354 233 RNA→ hypo→
env-1789 PBDC2_contig40830 - 6262 6143 RNA→ DapB (COG0289)→
env-1790 PBDC2_FISUTAU01DIYI + 138 255 RNA→
env-1791 PBDC2_GBB5CE401ELM9Z_right - 247 130 RNA→
env-1792 FNTS_GKEVUV02HODON - 298 141 RNA→ hypo→
env-1793 FNTS067_GJ87FRN01AEVGH + 142 289 RNA→ ← hypo
env-1794 DCrCPGB_r494539 + 99 247 RNA→
env-1795 FNTS067_GJ87FRN01E4CGQ - 179 23 RNA→ ← hypo
env-1796 FNTS067_GJ87FRN01ETK5F - 294 141 RNA→ ← hypo
env-1797 FNTS067_GJ87FRN01C3HA9 + 182 340 RNA→ → hypo
env-1798 FNTS067_GKA24FP01BOY9V - 269 114 RNA→ → hypo
env-1799 DCrCPGB_r559396 + 254 414 RNA→ → hypo
env-1800 DCrCPGB_r245916 + 187 347 RNA→ ← hypo
env-1801 FNTS067_GJ87FRN01CGQEZ - 323 166 RNA→ ← hypo
env-1802 FNTS_GKEVUV01B3SJ8A + 131 287 RNA→ → hypo
env-1803 DCrCPGB_r740967 + 82 235 RNA→
env-1804 FNTS067_GKA24FP01DSGH5 + 94 249 RNA→ ← hypo
env-1805 MA55A_contig00235 + 2580 2726 RNA→ Radical_SAM [cd01335] → DRE_TIM_Re_CS (cd07947)→
env-1806 BMHBC_209013 + 5510 5627 RNA→ DapB (COG0289)→
env-1807 BMHBC_164527 - 989 860 RNA→ Radical_SAM [cd01335] → DRE_TIM_Re_CS (cd07947)→
env-1808 MA55A_contig05039 + 429 548 RNA→ DapB (COG0289)→
env-1809 MA55A_contig00617 - 163 40 RNA→ ← hypo
env-1810 MA55A_contig01245 - 3842 3719 RNA→ ← hypo
env-1812 MA55A_contig00306 + 406 519 RNA→ NAD Gly3P dh N (pfam01210) → B12-binding like (cd02065) → Glm_e (cd00245)→
env-1811 MA55A_contig00306 + 651 766 (shown above)
env-1813 MA55A_contig001245 + 135 287 RNA→
env-1815 MA55A_contig00617 - 163 40 RNA→ ← hypo
env-1816 MA55A_contig01245 - 3842 3719 RNA→ ← hypo
env-1817 MA55A_contig00306 + 406 519 RNA→ NAD Gly3P dh N (pfam01210) → B12-binding like (cd02065) → Glm_e (cd00245)→
env-1818 MA55A_contig00617 - 163 40 RNA→ ← hypo
env-1819 MA55A_contig01245 - 3842 3719 RNA→ ← hypo
env-1820 MA55A_contig00306 + 406 519 RNA→ NAD Gly3P dh N (pfam01210) → B12-binding like (cd02065) → Glm_e (cd00245)→
env-1821 MA55A_contig00617 - 163 40 RNA→ ← hypo
env-1822 MA55A_contig00306 + 406 519 RNA→ NAD Gly3P dh N (pfam01210) → B12-binding like (cd02065) → Glm_e (cd00245)→
env-1823 MA55A_contig00306 + 406 519 RNA→ NAD Gly3P dh N (pfam01210) → B12-binding like (cd02065) → Glm_e (cd00245)→
env-1824 MA55A_contig00306 + 406 519 RNA→ NAD Gly3P dh N (pfam01210) → B12-binding like (cd02065) → Glm_e (cd00245)→
env-1825 MA55A_contig00306 + 406 519 RNA→ NAD Gly3P dh N (pfam01210) → B12-binding like (cd02065) → Glm_e (cd00245)→
env-1826 MA55A_contig00306 + 406 519 RNA→ NAD Gly3P dh N (pfam01210) → B12-binding like (cd02065) → Glm_e (cd00245)→
env-1827 MA55A_contig00306 + 406 519 RNA→ NAD Gly3P dh N (pfam01210) → B12-binding like (cd02065) → Glm_e (cd00245)→
1.4 Conserved domains

Conserved domains found in protein-coding genes listed in Section 1.3 are listed, with the first sentence in their description from the Conserved Domain Database. Conserved domains associated with more than one c-di-AMP riboswitch are assigned a color, while others are shown in gray. The number in parentheses is the number of occurrences of the given gene.
**cd00075** (6) Histidine kinase-like ATPases; This family includes several ATP-binding proteins for example: histidine kinase, DNA gyrase B, topoisomerases, heat shock protein HSP90, phytochrome-like ATPases and DNA mismatch repair proteins.

**cd00082** (7) Histidine Kinase A (dimerization/phosphoacceptor) domain; Histidine Kinase A dimers are formed through parallel association of 2 domains creating 4-helix bundles; usually these domains contain a conserved His residue and are activated via trans-autophosphorylation by the catalytic domain of the histidine kinase.

**cd00118** (101) Lysin domain; found in a variety of enzymes involved in bacterial cell wall degradation.

**cd00130** (5) PAS domain; PAS motifs appear in archaea, eubacteria and eukarya.

**cd00134** (4) Bacterial periplasmic transport systems use membrane-bound complexes and substrate-bound, membrane-associated, periplasmic binding proteins (PBPs) to transport a wide variety of substrates, such as, amino acids, peptides, sugars, vitamins and inorganic ions.

**cd00156** (9) Signal receiver domain; originally thought to be unique to bacteria (CheY, OmpR, NtrC, and PhoB), now recently identified in eukaryotes ETR1 Arabidopsis thaliania; this domain receives the signal from the sensor partner in a two-component system; contains a phosphoacceptor site that is phosphorylated by histidine kinase homologs; usually found N-terminal to a DNA binding effector domain; forms homodimers.

**cd00165** (1) S4/Hsp/ tRNA synthetase RNA-binding domain; The domain surface is populated by conserved, charged residues that define a likely RNA-binding site; Found in stress proteins, ribosomal proteins and RNA synthetases; This may imply a hitherto unrecognized functional similarity between these three protein classes.

**cd00189** (3) Tetra-tricopeptide repeat domain; typically contains 34 amino acids [WLF]-X(2)-[LML]-[GAS]-X(2)-[YLF]-X(8)-[ASE]-X(3)-[FYL]-X(2)-[ASL]-X(4)-[PKE]

**cd00215** (13) Coenzyme B12-dependent glutamate mutase epsilon subunit-like family; contains proteins similar to Clostridium coclearium glutamate mutase (Gln) and Streptomyces tendae Tu901 NIKV.

**cd00254** (25) Lytic Transglycosylase (LT) and Goose Egg White Lysozyme (GEWL) domain.

**cd00267** (2) ABC (ATP-binding cassette) transporter nucleotide-binding domain; ABC transporters are a large family of proteins involved in the transport of a wide variety of different compounds, like sugars, ions, peptides, and more complex organic molecules.

**cd00293** (5) Usp: Universal stress protein family.

**cd00318** (1) Phosphofructokinase, a key regulatory enzyme in glycolysis, catalyzes the phosphotransferase from 6-phosphate to fructose-1,6-biphosphate.

**cd00323** (1) Urease alpha-subunit; Urease is a nickel-dependent metalloenzyme that catalyzes the hydrolysis of urea to form ammonia and carbon dioxide.

**cd00359** (1) Urease gamma-subunit; Urease is a nickel-dependent metalloenzyme that catalyzes the hydrolysis of urea to form ammonia and carbon dioxide.

**cd00351** (1) Coenzyme B12-dependent-methylmalonyl coenzyme A (CoA) mutase (MCM)-like family; contains proteins similar to MCM, and the large subunit of Streptomyces coenzyme B12-dependent iso-1-propionyl-CoA mutase (ICM).

**cd00567** (1) Acyl-CoA dehydrogenase.

**cd00609** (1) Acetyl ornithine aminotransferase family.

**cd00625** (1) Anion permease ArsB/NhaD.

**cd00655** (1) Trans-Isoamyl Diphosphate Synthetase head-to-tail.

**cd00712** (11) Glutamine amidotransferases class-II (GATase) asparagine synthase.

**cd00735** (2) MoaE family.

**cd00761** (1) Glycosyltransferase family A (GT-A) includes diverse families of glycosyl transferases with a common GT-A type structural domain.

**cd00838** (1) metallophosphatase superfamily, metallophosphatase domain.

**cd00987** (1) PDZ domain of tryspin-like serine proteases, such as DegP/HtrA, which are oligomeric proteases involved in heat-shock response, chaperone function, and apoptosis.

**cd01029** (2) The substrate-binding domain of an ABC-type nickel/oligopeptide-like import system contains the type 2 periplasmic binding fold.

**cd01095** (2) Permease SLC13 (solute carrier 13).

**cd01155** (1) Short chain acyl-CoA dehydrogenases and eukaryotic short/branched chain acyl-CoA dehydrogenases.

**cd01128** (1) TRZ/ATZ family contains enzymes from the atrazine degradation pathway and related hydrolases.

**cd01133** (31) Radical SAM superfamily.

**cd01142** (3) Haloacid dehalogenase-like hydrolases.

**cd01365** (1) Glycosyltransferases catalyze the transfer of sugar moieties from activated donor molecules to specific acceptor molecules, forming glycosidic bonds.

**cd01891** (1) TypA (tyrosine phosphorylated protein A)/BipA subfamily.

**cd01991** (11) The C-terminal domain of Asparagine Synthase B.

**cd02021** (9) Thiamine pyrophosphate (TPP) family, Pyruvate oxidase (POX) subfamily, TPP-binding module; composed of proteins similar to Lactobacillus plantarum POX, which plays a key role in controlling acetate production under aerobic conditions.

**cd02035** (1) ArsA ATPase function as an efflux pump located on the inner membrane of the cell.

**cd02065** (14) B12 binding domain (B12-BD).

**cd02440** (17) S-adenosylmethionine-dependent methyltransferases (SAM or AdoMet-MTase), class I; AdoMet-MTases are enzymes that use S-adenosyl-L-methionine (SAM or AdoMet) as a substrate for methyltransfer, creating the product S-adenosyl-L-homocysteine (AdoHcy).

**cd02541** (1) Prokaryotic UGPase catalyses the synthesis of UDP-glucose.

**cd02549** (5) A sub-family of peptidase family C39.

**cd02874** (1) Cortical fragment-lytic enzyme (CFLE) is a peptidoglycan hydrolase involved in bacterial endospore germination.

**cd02883** (7) Nudix hydrolase is a superfamily of enzymes found in all three kingdoms of life, bacterial endospore germination.

**cd02922** (31) Radical SAM superfamily.

**cd03255** (1) This family is comprised of MJ0796 ATP-binding cassette, macrolide-specific ABC-type efflux carrier (MacAB), and proteins involved in cell division (FtsE), and release of lipoproteins from the cytoplasmic membrane (LolCDE).
cd03257  (2) The ABC transporter subfamily specific for the transport of dipeptides, oligopeptides (OppD), and nickel (NikDE).
cd03262  (4) HisP and GlnQ are the ATP-binding components of the bacterial periplasmic histidine and glutamine permeases, respectively.
cd03278  (1) Barmotin is a tight junction-associated protein expressed in rat epithelial cells which is thought to have an important regulatory role in tight junction barrier function.
cd03293  (7) NrtD and SsuB are the ATP-binding subunits of the bacterial ABC-type nitrate and sulfonate transport systems, respectively.
cd03294  (1) This family comprises the glycine betaine/L-proline ATP binding subunit in bacteria and its equivalents in archaea.
cd03295  (6) OpuCA is a the ATP binding component of a bacterial solute transporter that serves a protective role to cells growing in a hyperosmolar environment.
cd03318  (1) Enolase: Enolases are homodimeric enzymes that catalyse the reversible dehydration of 2-phospho-D-glycerate to phosphoenolpyruvate as part of the glycolytic and gluconeogenesis pathways.
cd03379  (1) Carbonic anhydrases (CA) are zinc-containing enzymes that catalyse the reversible hydration of carbon dioxide in a two-step mechanism in which the nucleophilic attack of a zinc-bound hydroxide ion on carbon dioxide is followed by the regeneration of an active site by ionization of the zinc-bound water molecule and removal of a proton from the active site.
cd03380  (1) DNA Polymerase IV/Kappa.
cd03601  (9) BipA,TyPA,Jl: domain II of BipA (also called TypA) having homology to domain II of the elongation factors (EFs) EF-G and EF-Tu.
cd03710  (1) BipA,TyPA,C: a C-terminal portion of BipA or TypA having homology to the Cterminal domains of the elongation factors EF-G and EF-2.
cd03783  (3) Trehalose-6-Phosphate Synthase (TPS) is a glycosyltransferase that catalyses the synthesis of alpha, alpha-1,1-trehalose-6-phosphate from glucose-6-phosphate using a UDP-glucose donor.
cd03791  (1) This family is most closely related to the GT1 family of glycosyltransferases.
cd03800  (9) This family is most closely related to the GT1 family of glycosyltransferases.
cd03801  (3) This family is most closely related to the GT1 family of glycosyltransferases and named after YggM in Bacillus licheniformis about which little is known.
cd04301  (7) N-Acyltransferase superfamily: Various enzymes that characteristically catalyse the transfer of an acyl group to a substrate.

cd04583  (1) This cd contains two tandem repeats of the cystathionine beta-synthase (CBS pair) domains in association with the ABC transporter OpuCA.
cd04590  (2) This cd contains two tandem repeats of the cystathionine beta-synthase (CBS pair) domains associated with the CorC/HlyC domain.
cd04643  (2) The CBS domain, named after human CBS, is a small domain originally identified in cystathionine beta-synthase and is subsequently found in a wide range of different proteins.
cd04732  (1) HisA.
cd05379  (12) SCP_bacterial: SCP-like extracellular protein domain, as found in bacteria and archaea.
cd06113  (3) Citrate synthase (CS) catalyzes the condensation of acetyl coenzyme A (AcCoA) and oxalacetate (OAA) to form citrate and coenzyme A (CoA), the first step in the oxidative citric acid cycle (TCA or Krebs cycle).
cd06171  (1) Sigma70, region (SR) 4 refers to the most C-terminal of four conserved domains found in Escherichia coli (Ec) sigma70, the main housekeeping sigma, and related sigma-factors (SFs).
cd06261  (29) Transmembrane subunit (TM) found in Periplasmic Binding Protein (PBP)-dependent ATP-Binding Cassette (ABC) transporters which generally bind type 2 PBPs.
cd06558  (1) This domain superfamily is found in a variety of structurally related metalloproteins, including the type I extradiol dioxygenases, glyoxalase I and a group of antibiotic resistance proteins.
cd07039  (9) Pyrimidine (PYR) binding domain of POX.
cd07042  (2) Sulphate Transporter and Anti-Sigma factor antagonist domain of SulP-like sulfate transporters, plays a role in the function and regulation of the transport activity, proposed general NTP binding function.
cd07043  (1) Sulphate Transporter and Anti-Sigma factor antagonist domain of anti-anti-sigma factors, key regulators of anti-sigma factors by phosphorylation.
cd07182  (1) bacterial Ribonuclease HIII-like.
cd07377  (2) Winged helix-turn-helix (WHTH) DNA-binding domain of the GntR family of transcriptional regulators.
cd07819  (1) Ligand-binding SRPBCC domain of an uncharacterized subfamily of proteins.
cd07947  (15) Clostridium kluyveri Re-citrate synthase and related proteins, catalytic TIM barrel domain.
cd08103  (5) Alanyl-tRNA synthetase [Translation, ribosomal structure and biogenesis]
cd09245  (1) Exopolyphosphatase [Nucleotide transport and metabolism / Inorganic ion transport and metabolism]
cd10210  (10) Dihydrodipicolinate reductase [Amino acid transport and metabolism]
cd10305  (1) Aminopeptidase N [Amino acid transport and metabolism]
cd10415  (2) Kef-type K+ transport systems, membrane components [Inorganic ion transport and metabolism]
cd10531  (113) Amino acid transporters [Amino acid transport and metabolism]
cd10566  (1) rRNA methylases [Translation, ribosomal structure and biogenesis]
cd10569  (36) K+ transport systems, NAD-binding component [Inorganic ion transport and metabolism]
cd10578  (2) Glycerol-3-phosphate dehydrogenase [Energy production and conversion]
cd10903  (3) Na+/proline symporter [Amino acid transport and metabolism / General function prediction only]
| COG10194 (9) Lipoproteins [Cell envelope biogenesis, outer membrane] |
|-----------------|---------------------------------------------------------------|
| COG10833 (1) Amino acid transporters [Amino acid transport and metabolism] |
| COG10555 (1) Na+/H+ antiporter NhaD and related arsenite permeases [Inorganic ion transport and metabolism] |
| COG11141 (1) Ferredoxin [Energy production and conversion] |
| COG11174 (3) ABC-type proline/glycine betaine transport systems, permease component [Amino acid transport and metabolism] |
| COG11396 (1) Chromosome segregation ATPases [Cell division and chromosome partitioning] |
| COG12124 (2) Predicted sugar nucleotide transferases [Cell envelope biogenesis, outer membrane] |
| COG1277 (4) ABC-type transport system involved in multi-copper enzyme maturation, permease component [General function prediction only] |
| COG1285 (2) Uncharacterized membrane protein [Function unknown] |
| COG1313 (1) Predicted sugar nucleotidyltransferases [Cell envelope biogenesis, outer membrane] |
| COG1328 (3) Pentapeptide repeats containing protein [Function unknown] |
| COG1392 (1) Phosphate transport regulator (distant homolog of PhoU) [Inorganic ion transport and metabolism] |
| COG1509 (3) Lysine 2,3-aminomutase [Amino acid transport and metabolism] |
| COG1574 (1) Predicted metal-dependent hydrolase with the TIM-barrel fold [General function prediction only] |
| COG1759 (2) Uncharacterized protein containing LysM domain [Function unknown] |
| COG1772 (6) Periplasmic glycine betaine/choline-binding (lipo) protein of an ABC-type transport system [Inorganic ion transport and metabolism] |
| COG1842 (1) Phage shock protein A (IM30), suppresses sigma54-dependent transcription [Transcription / Signal transduction mechanisms] |
| COG1877 (2) Trehalose-6-phosphatase [Carbohydrate transport and metabolism] |
| COG2060 (1) K+-transporting ATPase, A chain [Inorganic ion transport and metabolism] |
| COG2183 (3) ABC-type proline/glycine betaine transport systems, periplasmic components [Amino acid and metabolism] |
| COG2159 (1) Predicted metal-dependent hydrolase of the TIM-barrel fold [General function prediction only] |
| COG2205 (1) Osmosensitive K+ channel histidine kinase [Signal transduction mechanisms] |
| COG2216 (88) High-affinity K+ transport system, ATPase chain B [Inorganic ion transport and metabolism] |
| COG2218 (2) Uncharacterized protein conserved in bacteria [Function unknown] |
| COG2317 (1) Zn-dependent carboxypeptidase [Amino acid transport and metabolism] |
| COG2343 (1) Uncharacterized protein conserved in bacteria [Function unknown] |
| COG2365 (20) K+-transporter [Inorganic ion transport and metabolism] |
| COG2439 (3) NaP-type Na+/-H+ and K+/-H+ antiporters with a unique C-terminal domain [Inorganic ion transport and metabolism] |
| COG3409 (3) Putative peptidoglycan-binding domain-containing protein [Cell envelope biogenesis, outer membrane] |
| COG3523 (9) Uncharacterized protein conserved in bacteria [Function unknown] |
| COG3528 (14) Uncharacterized protein conserved in bacteria [Function unknown] |
| COG3773 (2) Cell wall hydrolyses involved in spore germination [Cell envelope biogenesis, outer membrane] |

**pfam**

- pfam00692 (2) C-type lysozyme/alpha-lactalbumin family.
- pfam01160 (1) Cyclophilin type peptidyl-prolyl cis-trans isomerase/CLD.
- pfam03784 (10) Sodium/dicarboxylate symporter family.
- pfam05582 (2) Universal stress protein family.
- pfam05873 (575) NlpC/P60 family.
- pfam06092 (1) Sec-independent protein translocase protein (TatC).
- pfam06959 (2) Mechanosensitive ion channel.
- pfam07999 (1) Sodium/hydrogen exchanger family.
- pfam0806 (2) CDP-alcohol phosphatidyltransferase.
- pfam01145 (3) SPFH domain / Band 7 family.
- pfam01240 (14) NAD-dependent glycerol-3-phosphate dehydrogenase N-terminal.
- pfam01391 (3) Collagen triple helix repeat (20 copies).
- pfam01433 (3) Peptidase family M48.
- pfam01464 (1) Transglycosylase SLT domain.
- pfam01471 (95) Putative peptidoglycan binding domain.
- pfam01551 (79) Peptidase family M23.
- pfam01943 (1) Poly saccharide biosynthesis protein.
- pfam01980 (2) Uncharacterized protein family UPF0066.
- pfam02519 (1) B12 binding domain.
- pfam02611 (2) AraC-like ligand binding domain.
- pfam02517 (15) NAD/NADP octopine/nopaline dehydrogenase, alpha-helical domain.
- pfam02702 (1) Osmosensitive K+ channel His kinase sensor domain.
- pfam03446 (2) NAD binding domain of 6-phosphoglucose dehydrogenase.
- pfam03652 (9) Uncharacterized protein family (UPF0081).
- pfam03814 (93) Potassium-transporting ATPase A subunit.
- pfam04069 (1) Substrate binding domain of ABC-type glycine betaine transport system.
- pfam04150 (1) Plant Basic Secretory Protein.
- pfam05103 (1) DivIVA protein.
- pfam05110 (2) Sucrose-6P-phosphate phosphohydrolase.
- pfam05262 (2) CHAP domain.
- pfam05791 (30) Bacillus haemolytic enterotoxin (HBL).
- pfam06135 (9) Bacterial protein of unknown function (DUF965).
- pfam06154 (1) Protein of unknown function (DUF970).
- pfam06210 (2) Amylo-alpha-1,6-glucosidase.
- pfam06339 (1) Ectoine synthase.
- pfam06721 (4) 3D domain.
- pfam06737 (160) Transglycosylase-like domain.
- pfam06792 (1) Uncharacterized protein family (UPF0236).
- pfam07182 (8) Cell Wall Hydrolase.
- pfam07501 (3) G5 domain.
- pfam07834 (1) Copper amine oxidase N-terminal domain.
- pfam07854 (1) Protein of unknown function (DUF1646).
pfam07859 (1) alpha/beta hydrolase fold.
pfram08239 (34) Bacterial SH3 domain.
pfram08242 (1) Methyltransferase domain.
pfram08365 (1) NPCBM/NEW2 domain.
pfram08472 (1) Sucrose-6-phosphate phosphohydrolase C-terminal.
TIGR01045 (2) Uncharacterized conserved protein (DUF2294).
pfram11256 (1) Protein of unknown function (DUF3055).
pfram11258 (3) Protein of unknown function (DUF3151).
pfram11574 (8) Protein of unknown function (DUF3235).
pfram12439 (1) Glycogen debranching enzyme N terminal.
PRK13914 (1) invasion associated secreted endopeptidase; Provisional
SCRAP12 (11) Self-Cleaving Ribozyme Associated Protein number 12
SCRAP27 (2) Self-Cleaving Ribozyme Associated Protein number 27
SCRAP33 (1) Self-Cleaving Ribozyme Associated Protein number 33
SCRAP4 (1) Self-Cleaving Ribozyme Associated Protein number 4
SCRAP41 (1) Self-Cleaving Ribozyme Associated Protein number 41
smart00287 (2) Bacterial SH3 domain homologues.
smart00342 (2) helix-turn-helix, arabinose operon control protein.
TIGR02028 (2) dihydrodipicolinate reductase.
TIGR00064 (1) signal recognition particle-docking protein FtsY.
TIGR00090 (6) rare lipoprotein A.
TIGR00053 (1) glutamine synthetase, type I.
TIGR00085 (1) trehalose-phosphatase.
TIGR00744 (1) ROK family protein (putative glucokinase).
TIGR00909 (1) amino acid transporter.
TIGR00931 (1) Na+ / H+ antiporter NhaC.
TIGR00932 (1) transporter, monovalent cation: proton antiporter-2 (CPA2) family.
TIGR00933 (32) potassium uptake protein, TrkH family.
TIGR00137 (4) nitrate ABC transporter, permease protein.
TIGR01311 (2) glycerol kinase.
TIGR02121 (1) sodium/proline symporter.
TIGR02161 (4) chromosome segregation protein SMC, common bacterial type.
TIGR02189 (1) chromosome segregation protein SMC, primarily archaeal type.
TIGR02408 (1) ectoine hydroxylase.
TIGR02594 (3) conserved hypothetical protein TIGR02594.
TIGR02859 (73) spore cortex-lytic enzyme.
TIGR02884 (1) delta-lactam-biosynthetic de-N-acetylase.
TIGR02899 (1) spore coat assembly protein SafA.
TIGR02929 (2) putative PEP-CTERM system TPR-repeat lipoprotein.