Supplementary Tables

Evaluating the genetic capacity of Mycoplasmas for coenzyme A biosynthesis in a search for new anti-mycoplasma targets

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Supplementary Table 1 NCBI accession numbers for the nucleotide sequences of *Mycoplasma* genomes analysed and the genomic location of their annotated CoA biosynthetic genes

| Mycoplasma species               | NCBI accession number | PanK type III | CoaBC         | PPAT         | DPCK         |
|----------------------------------|-----------------------|---------------|---------------|--------------|--------------|
| *M. agalactiae* PG2              | NC_009497.1^          | 37520-38281   | complement (40704-41141) | 161810-162232 (locus tag: MAG_RS00720) | complement (784004-784576) (locus tag: MAG_RS03375) |
| *M. alligatoris* A21JP2          | NZ_ADNC0000000000.1*  | complement (52254-53027) | complement (50239-50694) | complement (32640-33086) | complement (10188-10745) (locus tag: MAG_RS004280) (contig: NZ_ADNC01000002.1) |
| *M. alvi* ATCC 29626             | NZ_INJ0000000000.1*   | 7192-7998     | 28237-28989   | 6078-7205    | complement (40704-41141) (locus tag: MAG_RS00720) (contig: NZ_ADNC01000002.1) |
| *M. anatis* 1340                 | NZ_AFJ0000000000.1*   | 28237-28989   | 27107-28261   | 18799-19230  | complement (10188-10745) (locus tag: MAG_RS004280) |
| *M. arginini* ATCC 23838         | NZ_AUH0000000000.1*   | complement (27614-28354) | complement (32640-33086) | complement (32640-33086) | complement (10188-10745) (locus tag: MAG_RS004280) |
| *M. bovigenitalium* 51080        | NZ_AP017902.1^        | 7192-7998     | 28237-28989   | 27107-28261 | complement (10188-10745) (locus tag: MAG_RS004280) (contig: NZ_ADNC01000002.1) |
| *M. bovis* 08M                   | NZ_CP019639.1^        | 6078-7205     | 28237-28989   | 27107-28261 | complement (10188-10745) (locus tag: MAG_RS004280) |
| *M. bovoculi* M165/69            | NZ_CP007154.1^        | 133462-133884 | 133462-133884 | 133462-133884 | complement (10188-10745) (locus tag: MAG_RS004280) |
| *M. buteonis* ATCC 51371         | NZ_AP017902.1^        | complement (27614-28354) | complement (32640-33086) | complement (32640-33086) | complement (10188-10745) (locus tag: MAG_RS004280) |
| *M. capricolum* subsp. capricolum ATCC 27343 | NC_007633.1^          | complement (28147-281869) | complement (32640-33086) | complement (32640-33086) | complement (10188-10745) (locus tag: MAG_RS004280) |
| *M. capricolum* subsp. capripneumoniae | NZ_CP019061.1^        | complement (28147-281869) | complement (32640-33086) | complement (32640-33086) | complement (10188-10745) (locus tag: MAG_RS004280) |
| *M. clostridiiformis* ST-6       | NZ_CP007521.1^        | complement (28147-281869) | complement (32640-33086) | complement (32640-33086) | complement (10188-10745) (locus tag: MAG_RS004280) |
| *M. citreus* UFS3                 | NZ_AJFS0000000000.1*  | complement (30033-30464) | complement (30033-30464) | complement (30033-30464) | complement (10188-10745) (locus tag: MAG_RS004280) |
| *M. capricolum* subsp. capripneumoniae | NZ_CP019061.1^        | complement (28147-281869) | complement (32640-33086) | complement (32640-33086) | complement (10188-10745) (locus tag: MAG_RS004280) |
| *M. coli* ATCC 35278             | NZ_INJY0000000000.1*  | complement (199287-199715) | complement (199287-199715) | complement (199287-199715) | complement (10188-10745) (locus tag: MAG_RS004280) |
| *M. columbinum* ATCC 29257       | NZ_JONY0000000000.1*  | complement (28147-281869) | complement (32640-33086) | complement (32640-33086) | complement (10188-10745) (locus tag: MAG_RS004280) |

[^]: Accession number with GenBank link.
| Mycoplasma species       | NCBI accession number          | PanK type III              | CoaBC            | Genomic location                                                                 |
|-------------------------|--------------------------------|---------------------------|-----------------|----------------------------------------------------------------------------------|
| M. columborae ATCC 29258 | NZ_JNJZ00000000.1*            | complement (1358-2179)   | complement (2167-3300) | (contig: NZ_JNJZ01000000.1) (locus tag: T404_RS02275)                            |
|                         |                               |                           |                  | (locus tag: T404_RS02280) (contig: NZ_JNJZ01000008.1)                            |
| M. conjunctivae HRC/581T | NC_012806.1^                 |                           | complement (56507-57325) | (contig: NZ_JAHB01000000.1) (locus tag: T404_RS0100350)                            |
|                         |                               |                           |                  | (locus tag: T404_RS0100355) (contig: NZ_JAHB01000001.1)                            |
| M. crocodyli MP145      | NC_014014.1^                 |                           | complement (29628-30404) | (contig: NZ_JNJZ01000008.1) (locus tag: T404_RS02275)                            |
|                         |                               |                           |                  | (locus tag: T404_RS02280) (contig: NZ_JNJZ01000008.1)                            |
| M. dispar ATCC 27140    | NZ_CP007229.1^                |                           | complement (56507-57325) | (contig: NZ_JAHB01000000.1) (locus tag: T404_RS0100350)                            |
|                         |                               |                           |                  | (locus tag: T404_RS0100355) (contig: NZ_JAHB01000001.1)                            |
| M. felis ATCC 23391     | NZ_JNKA00000000.1*            |                           | complement (7696-8109)   | (contig: NZ_JNKA01000000.1) (locus tag: T404_RS0100350)                            |
|                         |                               |                           |                  | (locus tag: T404_RS0100355) (contig: NZ_JNKA01000001.1)                            |
| M. fermentans PG18      | NC_021002.1*                  |                           | complement (240477-249095) | (contig: NZ_JNKA01000008.1) (locus tag: T404_RS0100350)                            |
|                         |                               |                           |                  | (locus tag: T404_RS0100355) (contig: NZ_JNKA01000001.1)                            |
| M. gallinarum Mgn_IPT   | NZ_LVLH00000000.1*            |                           | complement (20875-21315) | (contig: NZ_LVLH01000000.1) (locus tag: T404_RS0100350)                            |
|                         |                               |                           |                  | (locus tag: T404_RS0100355) (contig: NZ_LVLH01000001.1)                            |
| M. gallinarum str. R(low)| NC_004829.2^                 |                           | complement (56507-57325) | (contig: NZ_LVLH01000000.1) (locus tag: T404_RS0100350)                            |
|                         |                               |                           |                  | (locus tag: T404_RS0100355) (contig: NZ_LVLH01000001.1)                            |
| M. genitalium G37       | NC_000908.2^                  |                           | complement (56507-57325) | (contig: NZ_LVLH01000000.1) (locus tag: T404_RS0100350)                            |
|                         |                               |                           |                  | (locus tag: T404_RS0100355) (contig: NZ_LVLH01000001.1)                            |
| M. hyopneumoniae 1      | NC_007295.1^                  |                           | complement (7696-8109)   | (contig: NZ_LVLH01000000.1) (locus tag: T404_RS0100350)                            |
|                         |                               |                           |                  | (locus tag: T404_RS0100355) (contig: NZ_LVLH01000001.1)                            |
| M. hyorhinis HUB-1      | NC_014448.1^                  |                           | complement (7696-8109)   | (contig: NZ_LVLH01000000.1) (locus tag: T404_RS0100350)                            |
|                         |                               |                           |                  | (locus tag: T404_RS0100355) (contig: NZ_LVLH01000001.1)                            |
| M. imitans ATCC 51306   | NZ_JADI00000000.1*            |                           | complement (56507-57325) | (contig: NZ_LVLH01000000.1) (locus tag: T404_RS0100350)                            |
|                         |                               |                           |                  | (locus tag: T404_RS0100355) (contig: NZ_LVLH01000001.1)                            |
| Mycoplasma species | NCBI accession number | PanK type III | CoaBC | Genomic location | PPAT | DPCK |
|--------------------|-----------------------|---------------|-------|------------------|------|------|
| *M. iners* ATCC 19705 | NZ_JNJW00000000.1* | | | | complement (3298-3741) (locus tag: T395_RS0102600) (contig: NZ_JNJW01000012.1) | complement (13826-14398) (locus tag: T395_RS0102195) (contig: NZ_JNJW01000007.1) |
| *M. iowae* 695 | CP033512^v | Complement (670158-670934) (locus tag: EER00_02695) | | | 329605-330027 (locus tag: MSB_RS01360) | 109349-109906 (locus tag: MSB_RS00465) |
| *M. leachii* PG50 | NC_014751.1^ | | | | complement (725838-726569) (locus tag: MMOB_RS03205) | complement (726554-727636) (locus tag: MMOB_RS03210) |
| *M. leonicaptivi* ATCC 49890 | NZ_JHWE00000000.1* | | | | complement (349967-350389) (locus tag: MLC_RS01385) | complement (101826-102374) (locus tag: MLC_RS03135) |
| *M. mobile* 163K | NC_006908.1^ | complement (80872-81600) (locus tag: MMOB_RS03205) | | | complement (329605-330027) (locus tag: MSB_RS01360) | 109349-109906 (locus tag: MSB_RS00465) |
| *M. molare* ATCC 27746 | NZ_JHGW00000000.1* | | | | 312742-313164 (locus tag: MSC_0272) | 114548-115117 (locus tag: MSC_0096) |
| *M. mycoides* subsp. capri LC str. 95010 | NC_015431.1^ | | | | complement (726554-727636) (locus tag: MMOB_RS03210) | complement (725838-726569) (locus tag: MMOB_RS03205) |
| *M. mycoides* subsp. mycoides SC str. PG1 | NC_005364.2^ | | | | complement (349967-350389) (locus tag: MLC_RS01385) | complement (101826-102374) (locus tag: MLC_RS03135) |
| *M. opalescens* ATCC 27921 | NZ_JOOB00000000.1* | | | | complement (80872-81600) (locus tag: MMOB_RS03205) | complement (725838-726569) (locus tag: MMOB_RS03205) |
| *M. ovipneumoniae* SC01 | NZ_AFHO00000000.1* | | | | complement (179214-179984) (locus tag: X558_RS0103155) (contig: NZ_KK365982.1) | complement (179214-179984) (locus tag: X558_RS0103155) (contig: NZ_KK365982.1) |
| *M. penetrans* HF-2 | NC_004432.1^ | complement (1332546-1333313) (locus tag: MYPE_RS05220) | | | complement (1285586-1286308) (locus tag: MYPE_RS04950) | complement (1285586-1286308) (locus tag: MYPE_RS04950) |
| *M. pirum* MPI25960 | NZ_AZH00000000.1* | complement (1379214-179984) (locus tag: X558_RS0103155) (contig: NZ_KK365982.1) | | | complement (175096-175551) (locus tag: X558_RS0103155) (contig: NZ_KK365982.1) | 171820-172404 (locus tag: X558_RS04315) (contig: NZ_KK365981.1) |
| *M. pneumoniae* M129 | NC_000912.1^ | | | | | 458998-459600 |
| Mycoplasma species       | NCBI accession number | Genomic location | PanK type III       | CoaBC          | PPAT          | DPCK          |
|--------------------------|-----------------------|------------------|---------------------|----------------|---------------|---------------|
|                          |                       |                  |                     |                |               |               |
| *M. primatum* ATCC 25948 | NZ_JNJV00000000.1*    | complement (242058-242879) (locus tag: Q349_RS011120) (contig: NZ_JNIZ01000003.1) |                     |                |               |               |
| *M. pulmonis* UAB CTIP   | NC_002771.1^          | complement (570749-571423) (locus tag: MYPU_RS02370) |                     |                |               |               |
| *M. putrefaciens* KS1    | NC_015946.1^          | complement (615746-616171) (locus tag: MPUT_RS02695) |                     |                |               |               |
| *M. simbae* ATCC 49888  | NZ_JNIG00000000.1*    | complement (23328-23756) (locus tag: T329_RS0101755) (contig: NZ_JNJG01000001.1) |                     |                |               |               |
| *M. sturni* DSM 22021    | NZ_JNIZ00000000.1*    | complement (8415-9167) (locus tag: MS53_RS00030) |                     |                |               |               |
| *M. synoviae* 53         | NC_007294.1^          | complement (9143-10297) (locus tag: MS53_RS00035) |                     |                |               |               |
| *M. testudinis* ATCC 43263 | NZ_JHXT00000000.1*   | complement (1820-2566) (locus tag: T384_RS0104425) (contig: NZ_JHXT010000017.1) |                     |                |               |               |
| *M. yeatsii* GM274B      | NZ_CP007520.1^        | complement (512943-513365) (locus tag: MYE_RS02185) (contig: NZ_JHXT010000017.1) |                     |                |               |               |
| Mycoplasma sp. Ms02      | CP081302^             | complement (858351-858929) (locus tag: K4L35_03330) |                     |                |               |               |

^Complete genome (deposited to NCBI)
*Incomplete genome (deposited to NCBI)
## Supplementary Table 2  NCBI accession numbers for 16S rRNA gene sequences and protein sequences of the CoA biosynthesis pathway enzymes

| Mycoplasma species | 16S rRNA gene NCBI accession number | PanK Type III protein | CoaBC protein NCBI accession number | PPAT protein NCBI accession number | DPKC protein NCBI accession number |
|-------------------|-------------------------------------|-----------------------|-------------------------------------|-------------------------------------|-------------------------------------|
| M. agalactiae      | NR_118811.1                         |                       |                                     |                                     |                                     |
| M. alligatoris     | NR_041844.1                         |                       |                                     |                                     |                                     |
| M. alvi            | NR_025985.1                         |                       |                                     |                                     |                                     |
| M. anatis          | NR_113689.1                         |                       |                                     |                                     |                                     |
| M. arginini        | NR_041743.1                         |                       |                                     |                                     |                                     |
| M. bovis           | NR_102850.1                         |                       |                                     |                                     |                                     |
| M. bovoculi        | NR_121731.1                         |                       |                                     |                                     |                                     |
| M. buteonis        | NR_025177.1                         |                       |                                     |                                     |                                     |
| M. californicum    | NR_029166.1                         |                       |                                     |                                     |                                     |
| M. canis           | NR_113676.1                         |                       |                                     |                                     |                                     |
| M. capricolum subsp. caprilucum | NR_074664.1                      |                       |                                     |                                     |                                     |
| M. capricolum subsp. capripneumoniae | NR_118795.1                      |                       |                                     |                                     |                                     |
| M. collis          | NR_114636.1                         |                       |                                     |                                     |                                     |
| M. columbinum      | NR_025063.1                         |                       |                                     |                                     |                                     |
| M. columborale     | NR_025179.1                         |                       |                                     |                                     |                                     |
| M. conjunctivae    | NR_044781.1                         |                       |                                     |                                     |                                     |
| M. cricetuli       | NR_025180.1                         |                       |                                     |                                     |                                     |
| M. crocodyli       | NR_074301.1                         |                       |                                     |                                     |                                     |
| M. bovigenitalium  | NR_113690.1                         |                       |                                     |                                     |                                     |
| M. conjunctivae    | NR_044781.1                         |                       |                                     |                                     |                                     |
| M. crocodyli       | NR_074301.1                         |                       |                                     |                                     |                                     |

| Protein | Accession Numbers |
|---------|-------------------|
| M. agalactiae PG2 | WP_011949321.1 | M. agalactiae PG2 | WP_011949819.1 |
| M. alligatoris A21JP2 | WP_005683755.1 | M. alligatoris A21JP2 | WP_005683611.1a |
| M. alvi ATCC 29626 | WP_033159884.1 | M. alvi ATCC 29626 | WP_033159717.1a |
| M. anatis 1340 | WP 006886261.1 | M. anatis 1340 | WP 006886260.1a |
| M. arginini ATCC 23838 | WP_020003050.1 | M. arginini ATCC 23838 | WP_020003049.1 |
| M. bovis 08M | WP_013456618.1 | M. bovis 08M | WP_014829984.1 |
| M. bovoculi M165/69 | WP_029355460.1 (HADf) |
| M. buteonis ATCC 51371 | WP_036452417.1 | M. buteonis ATCC 51371 | WP_036451916.1a |
| M. californicum ST-6 | WP_038561568.1 | M. californicum ST-6 | WP_038561049.1 |
| M. canis UF33 | WP_004796179.1 | M. canis UF33 | WP_004796406.1a |
| M. capricolum ATCC 27343 | WP_011387120.1 | M. capricolum subsp. capricolum ATCC 27343 | ABC01831.1 |
| M. collis ATCC 35278 | WP_033161390.1 | M. collis ATCC 35278 | WP_033160863.1 |
| M. columbinum ATCC 29257 | WP_006608789.1 | M. columbinum ATCC 29257 | WP_029891912.1 |
| M. columborale ATCC 29258 | WP_036434680.1 | M. columborale ATCC 29258 | WP_036434731.1 |
| M. conjunctivae HRC/581T | WP_041594472.1 | M. conjunctivae HRC/581T | WP_012751785.1 (HADf) |
| M. crocodyli MP145 | WP_013054470.1 | M. crocodyli MP145 | WP_013054324.1 |
| Mycoplasma species | 16S rRNA gene | PanK Type III protein | CoaBC protein | PPAT protein | DPCK protein |
|--------------------|----------------|----------------------|---------------|-------------|--------------|
| M. dispar          | NR_025182.1    |                      |               |             |              |
| M. felifascium     | NR_025963.1    |                      |               |             |              |
| M. felis           | NR_029174.1    |                      |               |             |              |
| M. fermentans      | NR_113683.1    |                      |               |             |              |
| M. flocculare      | NR_036954.1    |                      |               |             |              |
| M. gallinaceum     | NR_025913.1    | AKA50150,1a           | AKA50149,1a   |             |              |
| M. gallinarum      | NR_113687.1    |                      |               |             |              |
| M. gallisepticum   | NR_104952.1    |                      |               |             |              |
| M. genitalium      | NR_074611.1    |                      |               |             |              |
| M. huomocans       | AY529641.1     |                      |               |             |              |
| M. hominis         | NR_041881.1    |                      |               |             |              |
| M. hypneumoniae    | NR_121689.1    |                      |               |             |              |
| M. hyorhinius      | NR_041845.1    |                      |               |             |              |
| M. imitans         | NR_025912.1    |                      |               |             |              |
| M. iners           | NR_025064.1    |                      |               |             |              |
| M. iowae           | NR_044669.2    | M. iowae 695         | M. iowae 695 | QHG89842    | M. iowae 695 |
| M. leachii         | NR_044773.1    |                      |               |             |              |
| M. leonicaptivi    | NR_025965.1    |                      |               |             |              |
| M. lipofaciens     | NR_025065.1    |                      |               |             |              |
| M. mobile          | NR_074620.1    | M. mobile 163K       | M. mobile 163K | WP_011265111.1 | M. mobile 163K | WP_011265112.1 | M. mobile 163K | WP_011265096.1b | M. mobile 163K | WP_011265097.1 |
| M. molare          | NR_114637.1    | M. molare ATCC 27746 |               | WP_027123244.1 | M. molare ATCC 27746 | WP_027123383.1 | M. molare ATCC 27746 | WP_027123123.1 |
| Mycoplasma species                  | 16S rRNA gene | PanK Type III protein | CoaBC protein | PPAT protein | DPCK protein |
|-------------------------------------|----------------|-----------------------|---------------|--------------|--------------|
| M. mycoides subsp. capri LC        | NR_118794.1    | M. mycoides subsp. capri LC | WP_013729412.1 | M. mycoides subsp. capri LC str. 95010 | WP_013729251.1 |
| M. mycoides subsp. mycoides SC     | NR_074703.1    | M. mycoides subsp. mycoides SC | NP_975271.1 | M. mycoides subsp. mycoides SC str. PG1 | NP_975106.1 |
| M. opalescens                      | NR_025067.1    | M. opalescens ATCC 27921 | WP_029906491.1 | M. opalescens ATCC 27921 | WP_029906184.1 |
| M. ovipneumoniae                   | NR_025989.1    | M. ovipneumonia SC01 |            |              |              |
| M. mycoides subsp. mycoides SC     | NR_118794.1    | M. mycoides subsp. mycoides SC | WP_013729412.1 | M. mycoides subsp. mycoides SC str. 95010 | WP_013729251.1 |
| M. mycoides subsp. capri LC        | NR_118794.1    | M. mycoides subsp. capri LC | WP_013729412.1 | M. mycoides subsp. capri LC str. 95010 | WP_013729251.1 |
| M. mycoides subsp. mycoides SC     | NR_074703.1    | M. mycoides subsp. mycoides SC | NP_975271.1 | M. mycoides subsp. mycoides SC str. PG1 | NP_975106.1 |
| M. opalescens                      | NR_025067.1    | M. opalescens ATCC 27921 | WP_029906491.1 | M. opalescens ATCC 27921 | WP_029906184.1 |
| M. ovipneumoniae                   | NR_025989.1    | M. ovipneumonia SC01 |            |              |              |
| M. mycoides subsp. mycoides SC     | NR_118794.1    | M. mycoides subsp. mycoides SC | WP_013729412.1 | M. mycoides subsp. mycoides SC str. 95010 | WP_013729251.1 |
| M. mycoides subsp. capri LC        | NR_118794.1    | M. mycoides subsp. capri LC | WP_013729412.1 | M. mycoides subsp. capri LC str. 95010 | WP_013729251.1 |
| M. opalescens                      | NR_025067.1    | M. opalescens ATCC 27921 | WP_029906491.1 | M. opalescens ATCC 27921 | WP_029906184.1 |
| M. ovipneumoniae                   | NR_025989.1    | M. ovipneumonia SC01 |            |              |              |
| M. mycoides subsp. mycoides SC     | NR_118794.1    | M. mycoides subsp. mycoides SC | WP_013729412.1 | M. mycoides subsp. mycoides SC str. 95010 | WP_013729251.1 |
| M. mycoides subsp. capri LC        | NR_118794.1    | M. mycoides subsp. capri LC | WP_013729412.1 | M. mycoides subsp. capri LC str. 95010 | WP_013729251.1 |
| M. opalescens                      | NR_025067.1    | M. opalescens ATCC 27921 | WP_029906491.1 | M. opalescens ATCC 27921 | WP_029906184.1 |
| M. ovipneumoniae                   | NR_025989.1    | M. ovipneumonia SC01 |            |              |              |
| M. mycoides subsp. mycoides SC     | NR_118794.1    | M. mycoides subsp. mycoides SC | WP_013729412.1 | M. mycoides subsp. mycoides SC str. 95010 | WP_013729251.1 |
| M. mycoides subsp. capri LC        | NR_118794.1    | M. mycoides subsp. capri LC | WP_013729412.1 | M. mycoides subsp. capri LC str. 95010 | WP_013729251.1 |
| M. opalescens                      | NR_025067.1    | M. opalescens ATCC 27921 | WP_029906491.1 | M. opalescens ATCC 27921 | WP_029906184.1 |
| M. ovipneumoniae                   | NR_025989.1    | M. ovipneumonia SC01 |            |              |              |

*Annotated as hypothetical protein
*Annotated as putative protein
*Bifunctional HAD-like/dephospho-coenzyme A kinase protein

ORF = open reading frame
**Supplementary Table 3:** The related organisms used in the phylogenetic analyses and the NCBI accession numbers of their respective CoA biosynthetic proteins

| Organism                      | PanK type III   | CoaBC       | PPAT       | DPCK       |
|-------------------------------|-----------------|-------------|------------|------------|
| B. coahuilensis m2-6          | WP_010169518.1 | WP_082688052.1 | WP_059282518.1 | WP_059283260.1 |
| C. innocuum I46              | ASU20925.1      | ASU20926.1 | ASU18107.1 | ASU18339.1 |
| L. fermentum IFO 3956        | -               | WP_012391452.1 | BAG26942.1 | BAG27651.1 |
| S. pneumoniae N              | CKG77743.1      | -           | CKE32357.1 | CKG66021.1 |

**Supplementary Table 4** PanK CDD results

| Query            | Hit type  | ID region start | ID region end | E-Value | Accession              | Short name                          | Superfamily                          | Definition                                      |
|------------------|-----------|-----------------|---------------|---------|------------------------|-------------------------------------|---------------------------------------|------------------------------------------------|
| M. alligatoris   | non-specific | 9              | 190           | 8.15e-17 | pfam03309              | Pan_kinase                          | cl17037                               | Type III pantothenate kinase                   |
|                  | superfamily  | 9              | 190           | 8.15e-17 | c17037                 | NBD_sugar-kinase_HSP70_actin_superfamily | -                                     | Nucleotide-Binding Domain of the sugar kinase/HSP70/actin superfamily |
|                  | non-specific  | 9              | 249           | 1.80e-15 | PRK13320               | PRK13320                            | c17037                               | pantothenate kinase                           |
|                  | non-specific  | 8              | 190           | 5.16e-11 | COG1521                | CoaX                                | cl17037                               | Pantothenate kinase type III                   |
|                  | non-specific  | 7              | 253           | 3.09e-10 | PRK13321               | PRK13321                            | c17037                               | pantothenate kinase                           |
|                  | non-specific  | 8              | 190           | 7.94e-10 | TIGR00671              | baf                                 | cl17037                               | pantothenate kinase, type III                  |
|                  | non-specific  | 9              | 190           | 2.26e-05 | PRK13318               | PRK13318                            | cl17037                               | pantothenate kinase                           |
|                  | non-specific  | 8              | 229           | 4.00e-05 | PRK13324               | PRK13324                            | cl17037                               | pantothenate kinase                           |
| M. alvi          | non-specific  | 9              | 197           | 2.86e-26 | pfam03309              | Pan_kinase                          | cl17037                               | Type III pantothenate kinase                   |
|                  | superfamily  | 9              | 197           | 2.86e-26 | c17037                 | NBD_sugar-kinase_HSP70_actin_superfamily | -                                     | Nucleotide-Binding Domain of the sugar kinase/HSP70/actin superfamily |
|                  | non-specific  | 9              | 247           | 1.01e-17 | PRK13320               | PRK13320                            | c17037                               | pantothenate kinase                           |
|                  | non-specific  | 9              | 255           | 1.05e-17 | COG1521                | CoaX                                | cl17037                               | Pantothenate kinase type III                   |
| Species         | Type       | Accession | Accession | Accession | Description                                      |
|-----------------|------------|-----------|-----------|-----------|-------------------------------------------------|
|                 | non-specific | 8         | 196       | 7.61e-17  | PRK13321                                        | pantothenate kinase |
|                 | non-specific | 9         | 255       | 6.31e-13  | PRK13318                                        | pantothenate kinase |
|                 | non-specific | 9         | 225       | 8.06e-12  | TIGR00671                                      | pantothenate kinase, type III |
|                 | non-specific | 8         | 256       | 3.44e-07  | PRK13324                                        | pantothenate kinase |
|                 | specific    | 9         | 156       | 5.96e-05  | cd00012                                         | Nucleotide-Binding Domain of the sugar kinase/HSP70/actin superfamily |
|                 | non-specific | 1         | 225       | 0.000472  | PRK13326                                        | pantothenate kinase |
|                 | non-specific | 1         | 247       | 0.00078   | PRK13331                                        | pantothenate kinase |
|                 | specific    | 10        | 249       | 8.45e-22  | COG1521                                         | pantothenate kinase type III |
|                 | non-specific | 10        | 249       | 8.45e-22  | c117037                                         | Nucleotide-Binding Domain of the sugar kinase/HSP70/actin superfamily |
|                 | non-specific | 10        | 205       | 9.42e-21  | pfam03309                                      | Type III pantothenate kinase |
|                 | non-specific | 10        | 246       | 3.67e-17  | PRK13320                                        | pantothenate kinase |
|                 | non-specific | 10        | 241       | 5.97e-14  | TIGR00671                                      | pantothenate kinase, type III |
|                 | specific    | 10        | 250       | 1.08e-11  | PRK13318                                        | pantothenate kinase |
|                 | non-specific | 8         | 239       | 4.15e-06  | PRK13326                                        | pantothenate kinase |
|                 | non-specific | 10        | 249       | 0.000186  | PRK13324                                        | pantothenate kinase |
|                 | non-specific | 5         | 198       | 1.60e-06  | pfam03309                                      | Type III pantothenate kinase |
|                 | specific    | 5         | 198       | 1.60e-06  | c117037                                         | Nucleotide-Binding Domain of the sugar kinase/HSP70/actin superfamily |
|                 | non-specific | 5         | 234       | 3.26e-06  | PRK13320                                        | pantothenate kinase |
|                 | non-specific | 5         | 235       | 6.44e-06  | TIGR00671                                      | pantothenate kinase, type III |
|                 | non-specific | 5         | 234       | 8.74e-06  | COG1521                                         | Pantothenate kinase type III |
|                 | non-specific | 6         | 209       | 1.18e-12  | pfam03309                                      | Type III pantothenate kinase |
| superfamily                  | 6  | 209 | 1.18e-12 | c117037 | NBD_sugar-kinase_HSP70_actin superfamily | - | Nucleotide-Binding Domain of the sugar kinase/HSP70/actin superfamily |
|-----------------------------|----|-----|----------|--------|----------------------------------------|---|------------------------------------------|
| non-specific                | 3  | 232 | 5.53e-10 | COG1521 | CoaX                                    | c117037 | Pantothenate kinase type III               |
| non-specific                | 4  | 233 | 1.26e-06 | TIGR00671 | baf                                   | c117037 | pantothenate kinase, type III             |
| non-specific                | 1  | 235 | 0.000122 | PRK13320 | PRK13320                                | c117037 | pantothenate kinase                        |
| non-specific                | 4  | 223 | 0.00372  | PRK13321 | PRK13321                                | c117037 | pantothenate kinase                        |
| non-specific                | 4  | 233 | 5.58e-10 | COG1521  | CoaX                                    | c117037 | Pantothenate kinase type III               |
| M. crateruli               | 4  | 233 | 5.58e-10 | c117037 | NBD_sugar-kinase_HSP70_actin superfamily | - | Nucleotide-Binding Domain of the sugar kinase/HSP70/actin superfamily |
| non-specific                | 112| 234 | 1.08e-06 | TIGR00671 | baf                                   | c117037 | pantothenate kinase, type III             |
| non-specific                | 5  | 209 | 9.25e-05 | pfam03309 | Pan_kinase                             | c117037 | Type III pantothenate kinase              |
| non-specific                | 189| 249 | 0.004086 | PRK13320 | PRK13320                                | c117037 | pantothenate kinase                        |
| M. crocodyli               | 14 | 195 | 3.44e-15 | pfam03309 | Pan_kinase                             | c117037 | Type III pantothenate kinase              |
| superfamily                | 14 | 195 | 3.44e-15 | c117037 | NBD_sugar-kinase_HSP70_actin superfamily | - | Nucleotide-Binding Domain of the sugar kinase/HSP70/actin superfamily |
| non-specific                | 14 | 253 | 1.86e-13 | TIGR00671 | baf                                   | c117037 | pantothenate kinase, type III             |
| non-specific                | 13 | 256 | 1.91e-13 | COG1521  | CoaX                                    | c117037 | Pantothenate kinase type III               |
| M. gallinaceum             | 12 | 257 | 6.11e-13 | PRK13320 | PRK13320                                | c117037 | pantothenate kinase                        |
| non-specific                | 14 | 253 | 1.58e-07 | PRK13321 | PRK13321                                | c117037 | pantothenate kinase                        |
| non-specific                | 14 | 248 | 5.79e-06 | PRK13324 | PRK13324                                | c117037 | pantothenate kinase                        |
| M. crateruli               | 9  | 195 | 5.46e-16 | pfam03309 | Pan_kinase                             | c117037 | Type III pantothenate kinase              |
| superfamily                | 9  | 195 | 5.46e-16 | c117037 | NBD_sugar-kinase_HSP70_actin superfamily | - | Nucleotide-Binding Domain of the sugar kinase/HSP70/actin superfamily |
| non-specific                | 6  | 245 | 3.79e-15 | COG1521  | CoaX                                    | c117037 | Pantothenate kinase type III               |
| non-specific                | 6  | 245 | 1.22e-09 | PRK13320 | PRK13320                                | c117037 | pantothenate kinase                        |
| non-specific                | 9  | 196 | 7.81e-08 | TIGR00671 | baf                                   | c117037 | pantothenate kinase, type III             |
| M. iowae | M. mobile | M. mobile |
|---|---|---|
| non-specific | non-specific | non-specific |
| 6 | 248 | 4.54e-07 | PRK13318 | PRK13318 | c17037 | pantothenate kinase |
| 7 | 245 | 3.06e-06 | PRK13321 | PRK13321 | c17037 | pantothenate kinase |
| 6 | 212 | 0.000497 | PRK13324 | PRK13324 | c17037 | pantothenate kinase |
| non-specific | non-specific | non-specific |
| 6 | 204 | 3.30e-26 | pfam03309 | Pan_kinase | c17037 | Type III pantothenate kinase |
| 6 | 204 | 3.30e-26 | c17037 | NBD_sugar-kinase_HSP70_actin superfamily | - | Nucleotide-Binding Domain of the sugar kinase/HSP70/actin superfamily |
| 4 | 251 | 1.33e-20 | COG1521 | CoaX | c17037 | Pantothenate kinase type III |
| 5 | 191 | 3.98e-17 | PRK13318 | PRK13318 | c17037 | pantothenate kinase |
| 2 | 252 | 2.04e-13 | PRK13320 | PRK13320 | c17037 | pantothenate kinase |
| 5 | 198 | 2.95e-08 | PRK13324 | PRK13324 | c17037 | pantothenate kinase |
| non-specific | non-specific | non-specific |
| 5 | 191 | 8.10e-08 | PRK13321 | PRK13321 | c17037 | pantothenate kinase |
| non-specific | non-specific | non-specific |
| 6 | 249 | 3.70e-15 | TIGR00671 | baf | c17037 | pantothenate kinase, type III |
| 3 | 197 | 4.16e-45 | pfam03309 | Pan_kinase | c17037 | Type III pantothenate kinase |
| 3 | 197 | 4.16e-45 | c17037 | NBD_sugar-kinase_HSP70_actin superfamily | - | Nucleotide-Binding Domain of the sugar kinase/HSP70/actin superfamily |
| non-specific | non-specific | non-specific |
| 1 | 235 | 3.89e-38 | COG1521 | CoaX | c17037 | Pantothenate kinase type III |
| non-specific | non-specific | non-specific |
| 1 | 240 | 1.19e-27 | PRK13318 | PRK13318 | c17037 | pantothenate kinase |
| 1 | 240 | 6.36e-26 | PRK13321 | PRK13321 | c17037 | pantothenate kinase |
| 3 | 236 | 7.86e-25 | TIGR00671 | baf | c17037 | pantothenate kinase, type III |
| non-specific | non-specific | non-specific |
| 1 | 235 | 1.87e-14 | PRK13320 | PRK13320 | c17037 | pantothenate kinase |
| 3 | 217 | 3.77e-11 | PRK13326 | PRK13326 | c17037 | pantothenate kinase |
| non-specific | non-specific | non-specific |
| 1 | 219 | 5.53e-10 | PRK13324 | PRK13324 | c17037 | pantothenate kinase |
| non-specific | non-specific | non-specific |
| 3 | 236 | 1.08e-07 | PRK13331 | PRK13331 | c17037 | pantothenate kinase |
| non-specific | non-specific | non-specific |
| 118 | 241 | 2.91e-07 | PRK13322 | PRK13322 | c17037 | pantothenate kinase |
| Non-Specific | Specific | M. molare | M. penetrans |
|-------------|----------|-----------|--------------|
| 93          | 8        | 3.66e-05  | 1.60e-05     |
| 235         | 254      | COG1521   | pfam03309    |
| PRK13328    | PRK13328 | COaX      | Pan_kinase   |
| c17037      | c17037   | c17037    | c17037       |
| Pantothenate kinase | Pantothenate kinase | NBD_sugar-kinase_HSP70_actin superfamily | Type III pantothenate kinase |
| 93          | 8        | 2.00e-03  | 2.72e-16     |
| 236         | 255      | PRK13320  | PRK13320     |
| PRK13333    | PRK13333 | PRK13320  | PRK13320     |
| c17037      | c17037   | c17037    | c17037       |
| Pantothenate kinase | Pantothenate kinase | NBD_sugar-kinase_HSP70_actin superfamily | Type III pantothenate kinase |
| 93          | 8        | 0.007289  | 0.007289     |
| 236         | 255      | STKc_HIPK1| STKc_HIPK1   |
| cd14228     | cd14228  | c21453    | c21453       |
| 93          | 8        | 7.15e-18  | 7.15e-18     |
| 228         | 222      | TIGR00671 | TIGR00671    |
| PRK13321    | PRK13321 | PRK13326  | PRK13326     |
| c17037      | c17037   | c17037    | c17037       |
| Pantothenate kinase | Pantothenate kinase | NBD_sugar-kinase_HSP70_actin superfamily | Type III pantothenate kinase |
| 93          | 8        | 1.39e-15  | 1.39e-15     |
| 213         | 222      | PRK13318  | PRK13318     |
| PRK13318    | PRK13318 | PRK13318  | PRK13318     |
| c17037      | c17037   | c17037    | c17037       |
| Pantothenate kinase | Pantothenate kinase | NBD_sugar-kinase_HSP70_actin superfamily | Type III pantothenate kinase |
| 93          | 8        | 6.27e-10  | 6.27e-10     |
| 231         | 222      | PRK13333  | PRK13333     |
| PRK13333    | PRK13333 | PRK13333  | PRK13333     |
| c17037      | c17037   | c17037    | c17037       |
| Pantothenate kinase | Pantothenate kinase | NBD_sugar-kinase_HSP70_actin superfamily | Type III pantothenate kinase |
| 93          | 8        | 8.31e-08  | 8.31e-08     |
| 212         | 222      | PRK13321  | PRK13321     |
| PRK13321    | PRK13321 | PRK13321  | PRK13321     |
| c17037      | c17037   | c17037    | c17037       |
| Pantothenate kinase | Pantothenate kinase | NBD_sugar-kinase_HSP70_actin superfamily | Type III pantothenate kinase |
| 93          | 8        | 1.20e-05  | 1.20e-05     |
| 219         | 222      | PRK13324  | PRK13324     |
| PRK13324    | PRK13324 | PRK13324  | PRK13324     |
| c17037      | c17037   | c17037    | c17037       |
| Pantothenate kinase | Pantothenate kinase | NBD_sugar-kinase_HSP70_actin superfamily | Type III pantothenate kinase |
| 93          | 8        | 1.45e-05  | 1.45e-05     |
| 222         | 222      | PRK13320  | PRK13320     |
| PRK13320    | PRK13320 | PRK13320  | PRK13320     |
| c17037      | c17037   | c17037    | c17037       |
| Pantothenate kinase | Pantothenate kinase | NBD_sugar-kinase_HSP70_actin superfamily | Type III pantothenate kinase |
| 93          | 8        | 0.00397   | 0.00397      |
| 226         | 226      | PRK13326  | PRK13326     |
| PRK13326    | PRK13326 | PRK13326  | PRK13326     |
| c17037      | c17037   | c17037    | c17037       |
| Pantothenate kinase | Pantothenate kinase | NBD_sugar-kinase_HSP70_actin superfamily | Type III pantothenate kinase |
| 93          | 8        | 1.56e-33  | 1.56e-33     |
| 193         | 193      | pfam03309 | pfam03309    |
| PRK13318    | PRK13318 | PRK13318  | PRK13318     |
| c17037      | c17037   | c17037    | c17037       |
| Pantothenate kinase | Pantothenate kinase | NBD_sugar-kinase_HSP70_actin superfamily | Type III pantothenate kinase |
|                         | 9    | 227  | 0.00134 | PRK13326 | PRK13326 | c17037 | pantothenate kinase |
|-------------------------|------|------|---------|----------|----------|-------|---------------------|
| non-specific            | 126  | 193  | 0.001658| PRK13331 | PRK13331 | c17037 | pantothenate kinase |
| non-specific            | 9    | 193  | 1.71e-16| pfam03309|          |       |                     |
| superfamily             |      |      |         |          |          |       |                     |
| non-specific            | 9    | 217  | 5.01e-13| COG1521  | CoaX     | c17037 | Pantothenate kinase type III |
| non-specific            | 9    | 227  | 1.27e-12| TIGR00671| baf      | c17037 | pantothenate kinase, type III |
| non-specific            | 9    | 253  | 3.76e-12| PRK13320 | PRK13320 | c17037 | pantothenate kinase |
| non-specific            | 8    | 193  | 1.85e-06| PRK13321 | PRK13321 | c17037 | pantothenate kinase |
| non-specific            | 9    | 193  | 1.12e-05| PRK13318 | PRK13318 | c17037 | pantothenate kinase |
| specific                | 1    | 224  | 7.06e-60| COG1521  | CoaX     | c17037 | Pantothenate kinase type III |
| superfamily             |      |      |         |          |          |       |                     |
| non-specific            | 5    | 216  | 1.95e-18| TIGR00671| baf      | c17037 | pantothenate kinase, type III |
| non-specific            | 3    | 203  | 1.78e-13| pfam03309|          |       |                     |
| superfamily             |      |      |         |          |          |       |                     |
| non-specific            | 1    | 216  | 1.45e-11| PRK13321 | PRK13321 | c17037 | pantothenate kinase |
| non-specific            | 1    | 216  | 4.25e-10| PRK13320 | PRK13320 | c17037 | pantothenate kinase |
| non-specific            | 1    | 224  | 6.07e-07| PRK13318 | PRK13318 | c17037 | pantothenate kinase |
| non-specific            | 121  | 216  | 0.000398| PRK13333 | PRK13333 | c17037 | pantothenate kinase |
| non-specific            | 6    | 209  | 5.47e-09| pfam03309|          |       |                     |
| superfamily             | 6    | 209  | 5.47e-09| c17037   |          |       |                     |
| non-specific            | 4    | 211  | 2.00e-05| PRK13320 | PRK13320 | c17037 | pantothenate kinase |
| non-specific            | 6    | 264  | 2.17e-05| COG1521  | CoaX     | c17037 | Pantothenate kinase type III |
| non-specific            | 6    | 260  | 7.24e-05| TIGR00671| baf      | c17037 | pantothenate kinase, type III |
| Organism        | Non-specific | Gene | e-Value | Description                                                                 | E-value | GenBank Accession ID | BLASTX Description                                           |
|-----------------|--------------|------|---------|--------------------------------------------------------------------------------|---------|----------------------|--------------------------------------------------------------|
| **M. synoviae** | 10           | 249  | 2.74e-21| COG1521 Pantothenate kinase type III superfamily                              | 0.01    | PRK13324             | Type III pantothenate kinase                                 |
|                 | 10           | 249  | 2.74e-21| e17037 NBD_sugar-kinase_HSP70_actin superfamily                              |         | PRK13320             | Type III pantothenate kinase                                 |
|                 | 10           | 205  | 3.32e-21| pfam03309 Pan_kinase                                                           | 0.01    | PRK13318             | Type III pantothenate kinase                                 |
|                 | 10           | 246  | 1.13e-17| PRK13320 PRK13320                                                              | 0.01    | PRK13326             | Type III pantothenate kinase                                 |
|                 | 10           | 241  | 2.91e-14| TIGR00671 baf                                                                  | 0.01    | PRK13318             | Type III pantothenate kinase                                 |
|                 | 8            | 239  | 4.27e-06| PRK13326 PRK13326                                                              | 0.01    | PRK13324             | Type III pantothenate kinase                                 |
|                 | 10           | 249  | 0.000354| PRK13324 PRK13324                                                              | 0.01    | PRK13318             | Type III pantothenate kinase                                 |
|                 | 5            | 242  | 1.90e-38| PRK13318 PRK13318                                                              | 0.01    | PRK13322             | Type III pantothenate kinase                                 |
|                 | 5            | 242  | 1.90e-38| e17037 NBD_sugar-kinase_HSP70_actin superfamily                              |         | PRK13326             | Type III pantothenate kinase                                 |
|                 | 5            | 238  | 1.17e-37| PRK13320 PRK13320                                                              | 0.01    | PRK13320             | Type III pantothenate kinase                                 |
|                 | 5            | 201  | 1.90e-37| pfam03309 Pan_kinase                                                           | 0.01    | PRK13320             | Type III pantothenate kinase                                 |
|                 | 5            | 242  | 3.20e-36| COG1521 CoaX                                                                  | 0.01    | PRK13318             | Type III pantothenate kinase                                 |
|                 | 5            | 241  | 1.68e-26| TIGR00671 baf                                                                  | 0.01    | PRK13320             | Type III pantothenate kinase                                 |
| **M. testudinis** | 4            | 242  | 2.53e-19| PRK13320 PRK13320                                                              | 0.01    | PRK13326             | Type III pantothenate kinase                                 |
|                 | 5            | 246  | 6.96e-17| PRK13326 PRK13326                                                              | 0.01    | PRK13318             | Type III pantothenate kinase                                 |
|                 | 5            | 240  | 8.26e-17| PRK13324 PRK13324                                                              | 0.01    | PRK13320             | Type III pantothenate kinase                                 |
|                 | 9            | 236  | 1.30e-12| PRK13313 PRK13313                                                              | 0.01    | PRK13322             | Type III pantothenate kinase                                 |
|                 | 1            | 240  | 5.88e-10| PRK13322 PRK13322                                                              | 0.01    | PRK13320             | Type III pantothenate kinase                                 |
|                 | 8            | 243  | 6.43e-10| PRK13333 PRK13333                                                              | 0.01    | PRK13328             | Type III pantothenate kinase                                 |
|                 | 100          | 236  | 0.000424| PRK13328 PRK13328                                                              | 0.01    | PRK13324             | Type III pantothenate kinase                                 |
## Supplementary Table 5 PanK InterPro results

| Mycoplasma species | Amino acid region | Database | Database ID | Database signature description | ID region start | ID region end | InterPro IDb | ID typea | Gene Ontology (GO) termc |
|--------------------|-------------------|----------|-------------|---------------------------------|---------------|-------------|-------------|----------|--------------------------|
| M. alligatoris      | 253               | Gene3D   | G3DSA:3.30.420.40 |                                | 4             | 134         |             |          |                          |
|                     |                   | PANTHER  | PTHR34265   | Type III pantothen kinase       | 9             | 251         | IPR004619   | F        | GO:0004594               |
|                     |                   | Pfam     | PF03309     |                                  | 8             | 193         | IPR004619   | F        | GO:0004594               |
|                     |                   | SUPERFAMILY | SSF53067  |                                  | 123           | 244         |             |          |                          |
|                     |                   | SUPERFAMILY | SSF53067  |                                  | 8             | 116         |             |          |                          |
|                     |                   | TIGRFAM  | TIGR00671   | baf: pantothenate kinase, type III | 8             | 224         | IPR004619   | F        | GO:0004594               |
| M. alvi             | 257               | Gene3D   | G3DSA:3.30.420.40 |                                | 1             | 84          |             |          |                          |
|                     |                   | CDD      | cd00012     | NBD_sugar-kinase_HSP70_actin    | 127           | 252         |             |          |                          |
|                     |                   | Gene3D   | G3DSA:3.30.420.40 |                                | 102           | 257         |             |          |                          |
|                     |                   | Hamap    | MF 01274    | Type III pantothen kinase [coaX]. | 7             | 256         | IPR004619   | F        | GO:0004594               |
|                     |                   | PANTHER  | PTHR34265   | Type III pantothen kinase       | 8             | 255         | IPR004619   | F        | GO:0004594               |
|                     |                   | Pfam     | PF03309     | Type III pantothen kinase       | 9             | 202         | IPR004619   | F        | GO:0004594               |
|                     |                   | SUPERFAMILY | SSF53067  |                                  | 9             | 121         |             |          |                          |
|                     |                   | SUPERFAMILY | SSF53067  |                                  | 9             | 121         |             |          |                          |
|                     |                   | TIGRFAM  | TIGR00671   | baf: pantothenate kinase, type III | 9             | 228         | IPR004619   | F        | GO:0004594               |
| M. anatis           | 268               | Gene3D   | G3DSA:3.30.420.40 |                                | 102           | 257         |             |          |                          |
|                     |                   | CDD      | cd00012     | NBD_sugar-kinase_HSP70_actin    | 3             | 143         |             |          |                          |
|                     |                   | Pfam     | PF03309     | Type III pantothen kinase       | 8             | 173         | IPR004619   | F        | GO:0004594               |
|                     |                   | SUPERFAMILY | SSF53067  |                                  | 7             | 114         |             |          |                          |
| M. arginini         | 250               | Gene3D   | G3DSA:3.30.420.40 |                                | 94            | 250         |             |          |                          |
|                     |                   | Hamap    | MF 01274    | Type III pantothen kinase [coaX]. | 8             | 250         | IPR004619   | F        | GO:0004594               |
|                     |                   | PANTHER  | PTHR34265   | Type III pantothen kinase       | 10            | 249         | IPR004619   | F        | GO:0004594               |
|                     |                   | Pfam     | PF03309     | Type III pantothen kinase       | 10            | 206         | IPR004619   | F        | GO:0004594               |
|                     |                   | SUPERFAMILY | SSF53067  |                                  | 126           | 249         |             |          |                          |
|                     |                   | SUPERFAMILY | SSF53067  |                                  | 9             | 120         |             |          |                          |
|                     |                   | TIGRFAM  | TIGR00671   | baf: pantothenate kinase, type III | 10            | 234         | IPR004619   | F        | GO:0004594               |
| M. bateonis          | 246               | Gene3D   | G3DSA:3.30.420.40 |                                | 1             | 100         |             |          |                          |
|                     |                   | Gene3D   | G3DSA:3.30.420.40 |                                | 101           | 240         |             |          |                          |
|                     |                   | Pfam     | PF03309     | Type III pantothen kinase       | 104           | 273         |             |          |                          |
| M. columborale      | 273               | Gene3D   | G3DSA:3.30.420.40 |                                | 5             | 198         | IPR004619   | F        | GO:0004594               |
|                     |                   | PANTHER  | PTHR34265   | Type III pantothen kinase       | 5             | 271         | IPR004619   | F        | GO:0004594               |
|                     |                   | Pfam     | PF03309     | Type III pantothen kinase       | 5             | 209         | IPR004619   | F        | GO:0004594               |
|                     |                   | SUPERFAMILY | SSF53067  |                                  | 129           | 235         |             |          |                          |
| M. cricetuli        | 272               | Gene3D   | G3DSA:3.30.420.40 |                                | 97            | 272         |             |          |                          |
|                     |                   | PANTHER  | PTHR34265   | Type III pantothen kinase       | 4             | 242         | IPR004619   | F        | GO:0004594               |
|                     |                   | Pfam     | PF03309     | Type III pantothen kinase       | 4             | 209         | IPR004619   | F        | GO:0004594               |
|                     |                   | SUPERFAMILY | SSF53067  |                                  | 133           | 242         |             |          |                          |
|                     |                   | SUPERFAMILY | SSF53067  |                                  | 4             | 124         |             |          |                          |
| M. crocodyli        | 258               | Gene3D   | G3DSA:3.30.420.40 |                                | 108           | 258         |             |          |                          |
|                     |                   | Hamap    | MF 01274    | Type III pantothen kinase [coaX]. | 12            | 257         | IPR004619   | F        | GO:0004594               |
| M. crocodyli        | 258               | PANTHER  | PTHR34265   | Type III pantothen kinase       | 14            | 256         | IPR004619   | F        | GO:0004594               |
|                     |                   | Pfam     | PF03309     | Type III pantothen kinase       | 13            | 203         | IPR004619   | F        | GO:0004594               |
| Mycoplasma species | Amino acid region | Database | Database ID | Database signature description | ID region start | ID region end | InterPro ID | ID type | Gene Ontology (GO) term |
|-------------------|------------------|----------|-------------|-------------------------------|----------------|---------------|-------------|--------|------------------------|
| M. gallinaceum    | 248              | Gene3D   | G3DSA:3.30.420.40 | SSF53067 | baf: pantothenate kinase, type III | 128            | 250          | IPR004619 | F      | GO:0004594             |
|                   |                  | PANTHER  | PTHR34265   | SSF53067 | Type III pantothenate kinase | 6              | 245          | IPR004619 | F      | GO:0004594             |
|                   |                  | Pfam     | PF03309     | SSF53067 | Type III pantothenate kinase | 6              | 196          | IPR004619 | F      | GO:0004594             |
|                   | 258              | Gene3D   | G3DSA:3.30.420.40 | SSF53067 | baf: pantothenate kinase, type III | 7              | 206          | IPR004619 | F      | GO:0004594             |
| M. iowae          | 243              | Hamap    | MF_01274    | SSF53067 | Type III pantothenate kinase [coaX] | 4              | 252          | IPR004619 | F      | GO:0004594             |
|                   |                  | Pfam     | PF03309     | SSF53067 | Type III pantothenate kinase | 5              | 204          | IPR004619 | F      | GO:0004594             |
|                   |                  | SUPERFAMILY | SSF53067   | SSF53067 | Type III pantothenate kinase | 5              | 114          | IPR004619 | F      | GO:0004594             |
| M. mobile         | 243              | Hamap    | MF_01274    | SSF53067 | Type III pantothenate kinase [coaX] | 1              | 236          | IPR004619 | F      | GO:0004594             |
|                   |                  | Pfam     | PF03309     | SSF53067 | Type III pantothenate kinase | 1              | 198          | IPR004619 | F      | GO:0004594             |
|                   |                  | SUPERFAMILY | SSF53067   | SSF53067 | Type III pantothenate kinase | 1              | 114          | IPR004619 | F      | GO:0004594             |
| M. molare         | 242              | Hamap    | MF_01274    | SSF53067 | Type III pantothenate kinase [coaX] | 7              | 228          | IPR004619 | F      | GO:0004594             |
|                   |                  | Pfam     | PF03309     | SSF53067 | Type III pantothenate kinase | 8              | 203          | IPR004619 | F      | GO:0004594             |
|                   |                  | SUPERFAMILY | SSF53067   | SSF53067 | Type III pantothenate kinase | 8              | 203          | IPR004619 | F      | GO:0004594             |
| M. penetrans      | 255              | Hamap    | MF_01274    | SSF53067 | Type III pantothenate kinase [coaX] | 8              | 229          | IPR004619 | F      | GO:0004594             |
|                   |                  | Pfam     | PF03309     | SSF53067 | Type III pantothenate kinase | 8              | 233          | IPR004619 | F      | GO:0004594             |
|                   |                  | SUPERFAMILY | SSF53067   | SSF53067 | Type III pantothenate kinase | 9              | 233          | IPR004619 | F      | GO:0004594             |
| M. pirum          | 256              | Hamap    | MF_01274    | SSF53067 | Type III pantothenate kinase [coaX] | 120             | 254          | IPR004619 | F      | GO:0004594             |
|                   |                  | Pfam     | PF03309     | SSF53067 | Type III pantothenate kinase | 123             | 254          | IPR004619 | F      | GO:0004594             |
|                   |                  | SUPERFAMILY | SSF53067   | SSF53067 | Type III pantothenate kinase | 9              | 231          | IPR004619 | F      | GO:0004594             |
| Mycoplasma species | Amino acid region | Database | Database ID | Database signature description | ID region start | ID region end | InterPro IDa | ID typeb | Gene Ontology (GO term)c |
|--------------------|------------------|----------|------------|--------------------------------|---------------|-------------|--------------|----------|--------------------------|
| M. pulmonis        | 224              | Gene3D   | G3DSA:3.30.420.40 | Type III pantothenate kinase | 96            | 222         | IPR004619    | F        | GO:0004594               |
|                    |                  | PANTHER  | PTHR34265  |                                 | 1             | 217         | IPR004619    | F        | GO:0004594               |
|                    |                  | Pfam     | PF03309    |                                 | 3             | 203         | IPR004619    | F        | GO:0004594               |
|                    |                  | SUPERFAMILY| SSF53067  | Type III pantothenate kinase | 121           | 218         |              |          |                          |
|                    |                  | SUPERFAMILY| SSF53067  |                                 | 1             | 118         |              |          |                          |
|                    |                  | TIGRFAM  | TIGR00671  | bafl: pantothenate kinase, type III | 4             | 217         | IPR004619    | F        | GO:0004594               |
| M. sturni          | 273              | Gene3D   | G3DSA:3.30.420.40 | Type III pantothenate kinase | 100           | 273         |              |          |                          |
|                    |                  | Pfam     | PF03309    |                                 | 6             | 210         | IPR004619    | F        | GO:0004594               |
|                    |                  | Phobius  | CYTOPLASMIC_DOMAIN | Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm. | 217           | 273         |              |          |                          |
|                    |                  | Phobius  | TRANSMEMBRANE | Region of a membrane-bound protein predicted to be embedded in the membrane. | 196           | 216         |              |          |                          |
|                    |                  | Phobius  | NON_CYTOPLASMIC_DOMAIN | Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region. | 1             | 195         |              |          |                          |
|                    |                  | SUPERFAMILY| SSF53067  |                                 | 130           | 237         |              |          |                          |
|                    |                  | TMHMM    | TMhelix    | Region of a membrane-bound protein predicted to be embedded in the membrane. | 194           | 216         |              |          |                          |
| M. synoviae        | 250              | Gene3D   | G3DSA:3.30.420.40 | Type III pantothenate kinase [coaX]. | 94            | 250         |              |          |                          |
|                    |                  | Hamap    | MF_01274   |                                 | 8             | 250         | IPR004619    | F        | GO:0004594               |
|                    |                  | PANTHER  | PTHR34265  |                                 | 10            | 249         | IPR004619    | F        | GO:0004594               |
|                    |                  | Pfam     | PF03309    |                                 | 10            | 206         | IPR004619    | F        | GO:0004594               |
|                    |                  | SUPERFAMILY| SSF53067  | Type III pantothenate kinase | 9             | 120         |              |          |                          |
|                    |                  | SUPERFAMILY| SSF53067  |                                 | 126           | 249         |              |          |                          |
|                    |                  | TIGRFAM  | TIGR00671  | bafl: pantothenate kinase, type III | 10            | 234         | IPR004619    | F        | GO:0004594               |
| M. testudinis       | 248              | Gene3D   | G3DSA:3.30.420.40 | Type III pantothenate kinase [coaX]. | 92            | 246         |              |          |                          |
|                    |                  | Hamap    | MF_01274   |                                 | 3             | 244         | IPR004619    | F        | GO:0004594               |
|                    |                  | PANTHER  | PTHR34265  |                                 | 5             | 242         | IPR004619    | F        | GO:0004594               |
|                    |                  | Pfam     | PF03309    |                                 | 5             | 196         | IPR004619    | F        | GO:0004594               |
|                    |                  | SUPERFAMILY| SSF53067  | Type III pantothenate kinase | 4             | 119         |              |          |                          |
|                    |                  | SUPERFAMILY| SSF53067  |                                 | 121           | 240         |              |          |                          |
|                    |                  | TIGRFAM  | TIGR00671  | bafl: pantothenate kinase, type III | 5             | 240         | IPR004619    | F        | GO:0004594               |

*aID type abbreviations – F, Family
bInterPro ID – IPR004619: Type III pantothenate kinase
cGO term (Molecular Function) – GO:0004594: pantothenate kinase activity

**Supplementary Table 6** PanK MEME + motif locations

| Mycoplasma species | p-value | Motif locations |
|-------------------|---------|----------------|
|                   |         | Motif 1 | Motif 2 | Motif 3 | Motif 4 |
| M. pulmonis       |         |         |         |         |         |
| M. sturni         |         |         |         |         |         |
| M. synoviae       |         |         |         |         |         |
| M. testudinis      |         |         |         |         |         |
| Query          | Hit type   | ID region start | ID region end | E-Value  | Accession     | Short name | Superfamily | Definition                                                                 |
|----------------|------------|-----------------|--------------|----------|---------------|------------|-------------|-----------------------------------------------------------------------------|
| M. alligatoris | non-specific | 2               | 375          | 6.90e-78 | PRK05579      | PRK05579   | cl27193     | bifunctional phosphopantothenoylcysteine decarboxylase/phosphopantothenate synthase |
| M. alvi        | superfamily | 2               | 375          | 6.90e-78 | cl27193       | DFP superfamily | -          | DNA / pantothenate metabolism flavoprotein                                 |
| M. anatis      | non-specific | 1               | 375          | 5.97e-71 | TIGR00521     | coaBC_dfp  | cl27193     | phosphopantothenoylcysteine decarboxylase / phosphopantothenate--cysteine ligase |
| M. arginini    | specific    | 1               | 375          | 5.33e-61 | COG0452       | CoaBC      | cl27193     | Phosphopantothenoylcysteine synthetase/decarboxylase                        |
| M. buteonis    | non-specific | 1               | 172          | 9.30e-37 | PRK07313      | PRK07313   | cl19190     | phosphopantothenoylcysteine decarboxylase                                  |
| M. columborale | superfamily | 1               | 172          | 9.30e-37 | cl19190       | Flavoprotein superfamily | -          | Flavoprotein                                                               |
| M. crocodyli   | non-specific | 2               | 315          | 8.63e-32 | PRK13982      | PRK13982   | cl27193     | bifunctional SbtC-like/phosphopantothenoylcysteine decarboxylase/phosphopantothenate synthase |
| M. gallinaceum | specific    | 1               | 139          | 1.04e-27 | pfam02441     | Flavoprotein | cl19190     | Flavoprotein                                                               |
| M. iowae       | non-specific | 171             | 332          | 2.78e-25 | pfam04127     | DFP        | cl27193     | DNA / pantothenate metabolism flavoprotein                                 |

**Supplementary Table 7 CoaBC CDD results**
| Organism       | Genus          | Species      | Type       | Accession   | Description                                           |
|---------------|----------------|--------------|------------|-------------|-------------------------------------------------------|
| M. arginini   | non-specific   | 2            | 162        | TIGR02113   | coaC_strep cl19190 phosphopantothenoylcysteine decarboxylase, streptococcal |
|               | non-specific   | 2            | 158        | PLN02496    | PLN02496 cl19190 probable phosphopantothenoylcysteine decarboxylase |
|               | non-specific   | 171          | 372        | PRK09620    | PRK09620 cl27193 hypothetical protein                  |
|               | non-specific   | 172          | 372        | PRK06732    | PRK06732 cl27193 phosphopantothenate–cysteine ligase  |
|               | non-specific   | 172          | 371        | TIGR02114   | coaB_strep cl19190 phosphopantothenate–cysteine ligase, streptococcal |
|               | non-specific   | 71            | 96         | PRK08305    | spoVFB cl19190 dipicolinate synthase subunit B       |
|               | non-specific   | 2            | 373        | PRK05579    | PRK05579 cl27193 bifunctional phosphopantothenoylcysteine decarboxylase/phosphopantothenate synthase |
| specific      | superfamily    | 2            | 373        | cl27193     | DFP superfamily - DNA / pantotenate metabolism flavoprotein |
|               | specific       | 1            | 373        | COG0452     | CoaBC cl27193 Phosphopantothenoylcysteine synthetase/decarboxylase |
|               | non-specific   | 1            | 340        | TIGR00521   | coaBC_dfp cl27193 phosphopantothenoylcysteine decarboxylase / phosphopantothenate–cysteine ligase |
|               | non-specific   | 2            | 340        | PRK13982    | PRK13982 cl27193 bifunctional SbtC-like/phosphopantothenoylcysteine decarboxylase/phosphopantothenate synthase |
|               | non-specific   | 1            | 169        | PRK07313    | PRK07313 cl19190 phosphopantothenoylcysteine decarboxylase |
| specific      | superfamily    | 1            | 169        | Flavoprotein superfamily cl19190 Flavoprotein |
|               | specific       | 1            | 173        | pfam02441   | Flavoprotein cl19190 Flavoprotein                      |
|               | non-specific   | 169          | 340        | pfam04127   | DFP cl27193 DNA / pantotenate metabolism flavoprotein |
|               | non-specific   | 2            | 169        | TIGR02113   | coaC_strep cl19190 phosphopantothenoylcysteine decarboxylase, streptococcal |
|               | non-specific   | 2            | 176        | PLN02496    | PLN02496 cl19190 probable phosphopantothenoylcysteine decarboxylase |
|               | non-specific   | 176          | 368        | TIGR02114   | coaB_strep cl19190 phosphopantothenate–cysteine ligase, streptococcal |
|               | non-specific   | 176          | 342        | PRK09620    | PRK09620 cl27193 hypothetical protein                  |
|               | non-specific   | 176          | 368        | PRK06732    | PRK06732 cl27193 phosphopantothenate–cysteine ligase  |
| M. columborale| non-specific   | 2            | 374        | PRK05579    | PRK05579 cl27193 bifunctional phosphopantothenoylcysteine decarboxylase/phosphopantothenate synthase |
|               | superfamily    | 2            | 374        | cl27193     | DFP superfamily - DNA / pantotenate metabolism flavoprotein |
|               | specific       | 1            | 371        | TIGR00521   | coaB_dfp cl19190 phosphopantothenoylcysteine decarboxylase / phosphopantothenate–cysteine ligase |
| M. columborale| specific       | 1            | 375        | COG0452     | CoaBC cl27193 Phosphopantothenoylcysteine synthetase/decarboxylase |
|        |        |        |        |        |        |        |
|--------|--------|--------|--------|--------|--------|--------|
| non-specific | 2 | 334 | 3.07e-4 | PRK13982 | PRK13982 | cl27193 | bifunctional SbtC-like/phosphopantothenoylcysteine decarboxylase/phosphopantothenate synthase |
| non-specific | 1 | 167 | 1.76e-38 | PRK07313 | PRK07313 | cl19190 | phosphopantothenoylcysteine decarboxylase |
| superfamily | 1 | 167 | 1.76e-38 | cl19190 | Flavoprotein superfamily | - | Flavoprotein |
| specific | 1 | 169 | 1.61e-35 | pfam02441 | Flavoprotein | cl19190 | Flavoprotein |
| non-specific | 171 | 332 | 2.35e-35 | pfam04127 | DFP | cl27193 | DNA / pantothenate metabolism flavoprotein |
| non-specific | 2 | 153 | 3.16e-25 | TIGR02113 | coaC_strep | cl19190 | phosphopantothenoylcysteine decarboxylase, streptococcal |
| non-specific | 2 | 168 | 3.40e-23 | PLN02496 | PLN02496 | cl19190 | probable phosphopantothenoylcysteine decarboxylase |
| non-specific | 172 | 263 | 3.28e-06 | TIGR02114 | coaB_strep | cl27193 | phosphopantothenate–cysteine ligase, streptococcal |
| non-specific | 172 | 263 | 4.86e-06 | PRK06732 | PRK06732 | cl27193 | phosphopantothenate–cysteine ligase |
| non-specific | 1 | 102 | 3.18e-05 | COG0163 | UbiX | cl19190 | 3-polyisoprenyl-4-hydroxybenzoate decarboxylase |
| non-specific | 1 | 102 | 0.000164 | PRK05920 | PRK05920 | cl19190 | aromatic acid decarboxylase |
| non-specific | 2 | 140 | 0.007562 | TIGR00421 | ubiX_pad | cl19190 | polyisoprenyl-4-hydroxybenzoate and phenylacrylic acid decarboxylases |
| non-specific | 1 | 102 | 0.009011 | PRK06029 | PRK06029 | cl19190 | 3-octaprenyl-4-hydroxybenzoate carboxylase |
| non-specific | 2 | 377 | 8.21e-88 | PRK05579 | PRK05579 | cl27193 | bifunctional phosphopantothenoylcysteine decarboxylase/phosphopantothenate synthase |
| superfamily | 2 | 377 | 8.21e-88 | cl27193 | DFP superfamily | - | DNA / pantothenate metabolism flavoprotein |
| non-specific | 1 | 367 | 2.67e-73 | TIGR00521 | coaBC_dfp | cl27193 | phosphopantothenoylcysteine decarboxylase / phosphopantothenate–cysteine ligase |
| specific | 1 | 376 | 7.41e-72 | COG0452 | CoaBC | cl27193 | Phosphopantothenoylcysteine synthetase/decarboxylase |
| non-specific | 2 | 371 | 2.81e-41 | PRK13982 | PRK13982 | cl27193 | bifunctional SbtC-like/phosphopantothenoylcysteine decarboxylase/phosphopantothenate synthase |
| specific | 169 | 332 | 1.02e-37 | pfam04127 | DFP | cl27193 | DNA / pantothenate metabolism flavoprotein |
| non-specific | 1 | 167 | 1.27e-33 | PRK07313 | PRK07313 | cl19190 | phosphopantothenoylcysteine decarboxylase |
| superfamily | 1 | 167 | 1.27e-33 | cl19190 | Flavoprotein superfamily | - | Flavoprotein |
| non-specific | 1 | 168 | 8.96e-31 | pfam02441 | Flavoprotein | cl19190 | Flavoprotein |
| non-specific | 2 | 158 | 4.89e-17 | PLN02496 | PLN02496 | cl19190 | probable phosphopantothenoylcysteine decarboxylase |
|          |     |    |                      |                     |                          |                               |                           |
|----------|-----|----|----------------------|---------------------|--------------------------|--------------------------------|---------------------------|
|          |     |    |                      |                     |                          |                               |                           |
|          |     |    |                      |                     |                          |                               |                           |
| M. gallinaceum | 2  | 167| 7.40e-17             | TIGR02113           | coaC_strep               | cl19190                        | phosphopantothenoylcysteine decarboxylase, streptococcal |
|          |     |    |                      |                     |                          |                               |                           |
|          |     |    |                      |                     |                          |                               |                           |
|          |     |    |                      |                     |                          |                               |                           |
| M. gallinaceum | 169| 374| 3.40e-07             | PRK09620            | PRK09620                 | cl27193                        | hypothetical protein |
|          |     |    |                      |                     |                          |                               |                           |
|          |     |    |                      |                     |                          |                               |                           |
|          |     |    |                      |                     |                          |                               |                           |
| M. gallinaceum | 172| 372| 1.44e-06             | PRK06732            | PRK06732                 | cl27193                        | phosphopantothenate-cysteine ligase |
|          |     |    |                      |                     |                          |                               |                           |
|          |     |    |                      |                     |                          |                               |                           |
|          |     |    |                      |                     |                          |                               |                           |
| M. gallinaceum | 2  | 81 | 0.003177             | pfam02525           | Flavodoxin_2             | cl00438                        | Flavodoxin-like fold |
|          |     |    |                      |                     |                          |                               |                           |
|          |     |    |                      |                     |                          |                               |                           |
|          |     |    |                      |                     |                          |                               |                           |
| M. gallinaceum | 1  | 81 | 0.003177             | c00438              | FMN_red superfamily      | -                              | NADPH-dependent FMN reductase |
|          |     |    |                      |                     |                          |                               |                           |
|          |     |    |                      |                     |                          |                               |                           |
|          |     |    |                      |                     |                          |                               |                           |
| M. gallinaceum | 2  | 339| 2.03e-07             | PRK05579            | PRK05579                 | cl27193                        | bifunctional phosphopantothenoylcysteine decarboxylase/phosphopantothenate synthase |
|          |     |    |                      |                     |                          |                               |                           |
|          |     |    |                      |                     |                          |                               |                           |
| M. gallinaceum | 1  | 340| 1.50e-05             | COG0452             | CoaBC                    | cl27193                        | Phosphopantothenoylcysteine synthetase/decarboxylase |
|          |     |    |                      |                     |                          |                               |                           |
|          |     |    |                      |                     |                          |                               |                           |
| M. gallinaceum | 1  | 378| 1.60e-09             | TIGR00521           | coaBC_dfp                | cl27193                        | phosphopantothenoylcysteine decarboxylase / phosphopantothenate-cysteine ligase |
|          |     |    |                      |                     |                          |                               |                           |
|          |     |    |                      |                     |                          |                               |                           |
|          |     |    |                      |                     |                          |                               |                           |
| M. gallinaceum | 1  | 179| 1.07e-03             | PRK07313            | PRK07313                 | cl19190                        | phosphopantothenoylcysteine decarboxylase |
|          |     |    |                      |                     |                          |                               |                           |
|          |     |    |                      |                     |                          |                               |                           |
|          |     |    |                      |                     |                          |                               |                           |
| M. gallinaceum | 1  | 179| 1.07e-03             | c119190             | Flavoprotein superfamily | -                              | Flavoprotein |
|          |     |    |                      |                     |                          |                               |                           |
|          |     |    |                      |                     |                          |                               |                           |
|          |     |    |                      |                     |                          |                               |                           |
| M. gallinaceum | 2  | 339| 1.22e-03             | PRK13982            | PRK13982                 | cl27193                        | bifunctional SbtC-like/phosphopantothenoylcysteine decarboxylase/phosphopantothenate synthase |
|          |     |    |                      |                     |                          |                               |                           |
|          |     |    |                      |                     |                          |                               |                           |
| M. gallinaceum | 1  | 372| 4.18e-03             | pfam02341           | Flavoprotein             | cl19190                        | Flavoprotein |
|          |     |    |                      |                     |                          |                               |                           |
|          |     |    |                      |                     |                          |                               |                           |
|          |     |    |                      |                     |                          |                               |                           |
| M. gallinaceum | 179| 339| 6.89e-06             | pfam04127           | DFP                      | cl27193                        | DNA / pantoothenate metabolism flavoprotein |
|          |     |    |                      |                     |                          |                               |                           |
|          |     |    |                      |                     |                          |                               |                           |
|          |     |    |                      |                     |                          |                               |                           |
| M. gallinaceum | 2  | 165| 1.12e-01             | PLN02496            | PLN02496                 | cl19190                        | probable phosphopantothenoylcysteine decarboxylase |
|          |     |    |                      |                     |                          |                               |                           |
|          |     |    |                      |                     |                          |                               |                           |
|          |     |    |                      |                     |                          |                               |                           |
| M. gallinaceum | 179| 377| 4.29e-06             | PRK06732            | PRK06732                 | cl27193                        | phosphopantothenate-cysteine ligase |
|          |     |    |                      |                     |                          |                               |                           |
|          |     |    |                      |                     |                          |                               |                           |
|          |     |    |                      |                     |                          |                               |                           |
| M. gallinaceum | 1  | 103| 0.000137             | COG0163             | UbiX                     | cl19190                        | 3-polyprenyl-4-hydroxybenzoate decarboxylase |
|          |     |    |                      |                     |                          |                               |                           |
|          |     |    |                      |                     |                          |                               |                           |
|          |     |    |                      |                     |                          |                               |                           |
| M. gallinaceum | 179| 381| 0.000214             | TIGR02114           | coaC_strep               | cl27193                        | phosphopantothenate-cysteine ligase, streptococcal |
|          |     |    |                      |                     |                          |                               |                           |
|          |     |    |                      |                     |                          |                               |                           |
|          |     |    |                      |                     |                          |                               |                           |
| M. gallinaceum | 77 | 109| 0.000224             | COG1036             | COG1036                  | cl27425                        | Archaeal flavoprotein |
|          |     |    |                      |                     |                          |                               |                           |
|          |     |    |                      |                     |                          |                               |                           |
|          |     |    |                      |                     |                          |                               |                           |
| M. gallinaceum | 77 | 109| 0.000224             | c127425             | COG1036 superfamily      | -                              | Archaeal flavoprotein |
|          |     |    |                      |                     |                          |                               |                           |
|          |     |    |                      |                     |                          |                               |                           |
|          |     |    |                      |                     |                          |                               |                           |
| M. gallinaceum | 179| 356| 0.000777             | PRK09620            | PRK09620                 | cl27193                        | hypothetical protein |
|          |     |    |                      |                     |                          |                               |                           |
|          |     |    |                      |                     |                          |                               |                           |
|          |     |    |                      |                     |                          |                               |                           |
| M. gallinaceum | 76 | 107| 0.001221             | TIGR02700           | flavo_MJ0208             | cl25361                        | archaeoflavoprotein, MJ0208 family |
|          |     |    |                      |                     |                          |                               |                           |
|          |     |    |                      |                     |                          |                               |                           |
|          |     |    |                      |                     |                          |                               |                           |
| M. gallinaceum | 76 | 107| 0.001221             | c125361             | NuoI superfamily         | -                              | Formate hydrogenlyase subunit 6/NADH:ubiquinone oxidoreductase 23 kD subunit (chain I) |
| Non-specific | 77 | 114 | 0.002808 | TIGR02699 | archaeo_AfpA | cl27425 | archaeoflavoprotein AfpA |
|-------------|----|-----|----------|-----------|------------|--------|-------------------------|
| **M. mobile** |   |     |          |           |            |        |                         |
| Non-specific | 1  | 356 | 7.5e-80  | PRK05579  | PRK05579  | cl27193 | bifunctional phosphopantothenoylcysteine decarboxylase/phosphopantothenate synthase |
| Superfamily  | 1  | 356 | 7.5e-80  | cl27193   | DFP superfamily | - | DNA / pantothenate metabolism flavoprotein |
| Non-specific | 2  | 355 | 8.99e-63 | TIGR00521 | coaBC_dfp  | cl27193 | phosphopantothenoylcysteine decarboxylase/ phosphopantothenate--cysteine ligase |
| Specific     | 1  | 356 | 8.69e-61 | COG0452   | CoaBC      | cl27193 | Phosphopantothenoylcysteine synthetase/ decarboxylase |
| Non-specific | 2  | 317 | 1.03e-45 | PRK13982  | PRK13982  | cl27193 | bifunctional SbtC-like/phosphopantothenoylcysteine decarboxylase/ phosphopantothenate synthase |
| Non-specific | 1  | 173 | 1.98e-32 | PRK07313  | PRK07313  | cl19190 | phosphopantothenoylcysteine decarboxylase |
| Superfamily  | 1  | 173 | 1.98e-32 | cl19190   | Flavoprotein superfamily | - | Flavoprotein |
| Specific     | 2  | 164 | 5.41e-32 | pfam02441 | Flavoprotein | cl19190 | Flavoprotein |
| Non-specific | 176| 318 | 2.58e-26 | pfam04127 | DFP        | cl19190 | DNA / pantothenate metabolism flavoprotein |
| Specific     | 177| 356 | 9.90e-10 | TIGR02114 | coaB_strep | cl27193 | phosphopantothenoylcysteine decarboxylase, streptococcal |
| Non-specific | 22 | 115 | 1.38e-05 | TIGR02852 | spore_dpaB | cl19190 | dipicolinic acid synthetase, B subunit |
| Non-specific | 2  | 115 | 0.000155 | PRK08305  | spoVFB     | cl19190 | dipicolinate synthase subunit B |
| Specific     | 70 | 112 | 0.002594 | COG1036   | COG1036   | cl27425 | Archaeal flavoprotein |
| Superfamily  | 70 | 112 | 0.002594 | cl27425   | COG1036 superfamily | - | Archaeal flavoprotein |
| Non-specific | 1  | 95  | 0.008873 | PRK06029  | PRK06029  | cl19190 | 3-octaprenyl-4-hydroxybenzoate carboxy-lyase |
| **M. sturni** |   |     |          |           |            |        |                         |
| Non-specific | 2  | 376 | 1.13e-104 | PRK05579 | PRK05579  | cl27193 | bifunctional phosphopantothenoylcysteine decarboxylase/phosphopantothenate synthase |
| Superfamily  | 2  | 376 | 1.13e-104 | cl27193   | DFP superfamily | - | DNA / pantothenate metabolism flavoprotein |
| Non-specific | 1  | 370 | 7.06e-81 | TIGR00521 | coaBC_dfp  | cl27193 | phosphopantothenoylcysteine decarboxylase / phosphopantothenate--cysteine ligase |
| Specific     | 1  | 357 | 1.29e-74 | COG0452   | CoaBC      | cl27193 | Phosphopantothenoylcysteine synthetase/ decarboxylase |
| Non-specific | 2  | 372 | 2.43e-49 | PRK13982  | PRK13982  | cl27193 | bifunctional ShbC-like/phosphopantothenoylcysteine decarboxylase/ phosphopantothenate synthase |
| non-specific | 1 | 165 | 6.92e-40 | PRK07313 | PRK07313 | cl19190 | phosphopantothenoylcysteine decarboxylase |
| superfamily | 1 | 165 | 6.92e-40 | cl19190 | Flavoprotein superfamily | - | Flavoprotein |
| specific | 1 | 158 | 6.94e-37 | pfam02441 | Flavoprotein | cl19190 | Flavoprotein |
| non-specific | 171 | 346 | 1.82e-36 | pfam04127 | DFP | cl27193 | DNA / pantothenate metabolism flavoprotein |
| non-specific | 2 | 153 | 4.43e-28 | TIGR02113 | coaC_strep | cl19190 | phosphopantothenoylcysteine decarboxylase, streptococcal |
| non-specific | 3 | 161 | 1.51e-22 | PLN02496 | PLN02496 | cl19190 | probable phosphopantothenoylcysteine decarboxylase |
| non-specific | 172 | 373 | 5.67e-09 | PRK06732 | PRK06732 | cl27193 | phosphopantothenate--cysteine ligase |
| non-specific | 171 | 376 | 2.66e-07 | PRK09620 | PRK09620 | cl27193 | hypothetical protein |
| non-specific | 172 | 371 | 1.08e-05 | TIGR02114 | coaB_strep | cl27193 | phosphopantothenate--cysteine ligase, streptococcal |
| non-specific | 17 | 111 | 0.000138 | TIGR02700 | flavo_MJ0208 | cl25361 | archaeoflavoprotein, MJ0208 family |
| superfamily | 17 | 111 | 0.000138 | cl25361 | Nuol superfamily | - | Formate hydrogenlyase subunit 6/NADH:ubiquinone oxidoreductase 23 kD subunit (chain I) |
| non-specific | 71 | 103 | 0.001128 | COG1036 | COG1036 | cl27425 | Archaeal flavoprotein |
| superfamily | 71 | 103 | 0.001128 | cl27425 | COG1036 superfamily | - | Archaeal flavoprotein |
| non-specific | 2 | 373 | 5.66e-80 | PRK05579 | PRK05579 | cl27193 | bifunctional phosphopantothenoylcysteine decarboxylase/phosphopantothenate synthase |
| superfamily | 2 | 373 | 5.66e-80 | cl27193 | DFP superfamily | - | DNA / pantothenate metabolism flavoprotein |
| specific | 1 | 373 | 7.79e-67 | COG0452 | CoaBC | cl27193 | Phosphopantothenoylcysteine synthetase/decarboxylase |
| non-specific | 1 | 340 | 2.68e-66 | TIGR00521 | coaBC_dfp | cl27193 | phosphopantothenoylcysteine decarboxylase / phosphopantothenate--cysteine ligase |
| non-specific | 2 | 340 | 5.08e-41 | PRK13982 | PRK13982 | cl27193 | bifunctional SbtC-like/phosphopantothenoylcysteine decarboxylase/phosphopantothenate synthase |
| non-specific | 1 | 169 | 5.76e-36 | PRK07313 | PRK07313 | cl19190 | phosphopantothenoylcysteine decarboxylase |
| superfamily | 1 | 169 | 5.76e-36 | cl19190 | Flavoprotein superfamily | - | Flavoprotein |
| specific | 1 | 173 | 3.14e-34 | pfam02441 | Flavoprotein | cl19190 | Flavoprotein |
| non-specific | 169 | 340 | 8.87e-30 | pfam04127 | DFP | cl27193 | DNA / pantothenate metabolism flavoprotein |
| non-specific | 2 | 169 | 6.90e-26 | TIGR02113 | coaC_strep | cl19190 | phosphopantothenoylcysteine decarboxylase, streptococcal |
| M. testudinis | non-specific | 2 | 176 | 1.45e-19 | PLN02496 | PLN02496 | cl19190 | probable phosphopantothenoylcysteine decarboxylase |
|--------------|-------------|---|-----|----------|----------|----------|--------|-----------------------------------------------|
| non-specific | 176         | 368 | 2.41e-07 | TIGR02114 | coaB_strep | cl27193 | phosphopantothenate–cysteine ligase, streptococcal |
| non-specific | 176         | 368 | 1.73e-05 | PRK06732 | PRK06732 | cl27193 | phosphopantothenate–cysteine ligase |
| non-specific | 176         | 342 | 6.05e-05 | PRK09620 | PRK09620 | cl27193 | hypothetical protein |
| M. testudinis | non-specific | 17 | 379 | 2.14e-53 | PRK05579 | PRK05579 | cl27193 | bifunctional phosphopantothenoylcysteine decarboxylase/phosphopantothenate synthase |
| superfamily  | 17 | 379 | 2.14e-53 | cl27193 | DFP superfamily | - | DNA / pantothenate metabolism flavoprotein |
| non-specific | 17 | 378 | 2.82e-51 | TIGR00521 | coaBC_dfp | cl27193 | phosphopantothenoylcysteine decarboxylase / phosphopantothenate–cysteine ligase |
| specific     | 17 | 377 | 1.07e-45 | COG0452 | CoaBC | cl27193 | Phosphopantothenoylcysteine synthetase/decarboxylase |
| non-specific | 25 | 379 | 1.75e-33 | PRK13982 | PRK13982 | cl27193 | bifunctional SbtC-like/phosphopantothenoylcysteine decarboxylase/phosphopantothenate synthase |
| non-specific | 15 | 196 | 1.91e-28 | PRK07313 | PRK07313 | cl19190 | phosphopantothenoylcysteine decarboxylase |
| superfamily  | 15 | 196 | 1.91e-28 | cl19190 | Flavoprotein superfamily | - | Flavoprotein |
| specific     | 17 | 162 | 3.39e-22 | pfam02441 | Flavoprotein | cl19190 | Flavoprotein |
| non-specific | 16 | 192 | 7.99e-14 | TIGR02113 | coaC_strep | cl19190 | phosphopantothenoylcysteine decarboxylase, streptococcal |
| non-specific | 18 | 140 | 7.92e-09 | PLN02496 | PLN02496 | cl19190 | probable phosphopantothenoylcysteine decarboxylase |
| non-specific | 196 | 327 | 1.21e-06 | pfam04127 | DFP | cl27193 | DNA / pantothenate metabolism flavoprotein |
| M. testudinis | non-specific | 199 | 377 | 0.000432 | TIGR02114 | coaB_strep | cl27193 | phosphopantothenate–cysteine ligase, streptococcal |
| non-specific | 94 | 161 | 0.001286 | PRK08305 | spoVFB | cl19190 | dipicolinate synthase subunit B |
| non-specific | 200 | 377 | 0.003129 | PRK06732 | PRK06732 | cl27193 | phosphopantothenate–cysteine ligase |
| M. iowae (PPCDC) | non-specific | 3 | 177 | 9.47e-70 | PRK07313 | PRK07313 | cl19190 | phosphopantothenoylcysteine decarboxylase |
| superfamily  | 3 | 177 | 9.47e-70 | cl19190 | Flavoprotein superfamily | - | Flavoprotein |
| non-specific | 1 | 177 | 6.25e-64 | PRK05579 | PRK05579 | cl27193 | bifunctional phosphopantothenoylcysteine decarboxylase/phosphopantothenate synthase |
| superfamily  | 1 | 177 | 6.25e-64 | cl27193 | DFP superfamily | - | DNA / pantothenate metabolism flavoprotein |
| non-specific | 3 | 176 | 3.91e-58 | TIGR02113 | coaC_strep | cl19190 | phosphopantothenoylcysteine decarboxylase, streptococcal |
| specific     | 1 | 177 | 1.86e-53 | COG0452 | CoaBC | cl27193 | Phosphopantothenoylcysteine synthetase/decarboxylase |
| non-specific | 2 | 171 | 1.76e-51 | TIGR00521 | coaBC_dfp | cl27193 | phosphopantothenoylcysteine decarboxylase / phosphopantothenate–cysteine ligase |
| non-specific | 3 | 174 | 2.56e-41 | pfam02441 | Flavoprotein | cl19190 | Flavoprotein |
| non-specific | 3 | 165 | 6.77e-25 | PRK13982 | PRK13982 | cl27193 | bifunctional SbtC-like/phosphopantothenoylcysteine decarboxylase/phosphopantothenate synthase |
| non-specific | 5 | 166 | 6.90e-24 | PLN02496 | PLN02496 | cl19190 | probable phosphopantothenoylcysteine decarboxylase |
| non-specific | 1 | 174 | 1.40e-07 | COG0163 | UbiX | cl19190 | 3-polypropenyl-4-hydroxybenzoate decarboxylase |
| non-specific | 79 | 176 | 3.10e-06 | COG1036 | COG1036 | cl27425 | Archaeal flavoprotein |
| non-specific | 79 | 176 | 3.10e-06 | cl27425 | COG1036 superfamily | - | Archaeal flavoprotein |
| non-specific | 79 | 121 | 2.99e-05 | TIGR02699 | archaeo_AfpA | cl27425 | archaeoflavoprotein AfpA |
| non-specific | 79 | 174 | 3.73e-05 | TIGR00421 | ubiX_pad | cl19190 | polypropenyl P-hydroxybenzoate and phenylacrylic acid decarboxylases |
| non-specific | 2 | 101 | 0.000127 | PRK08305 | spoVFB | cl19190 | dipicolinate synthase subunit B |
| non-specific | 78 | 149 | 0.00026 | PRK06029 | PRK06029 | cl19190 | 3-octaprenyl-4-hydroxybenzoate carboxy-lyase |
| non-specific | 1 | 115 | 0.000576 | PRK05920 | PRK05920 | cl19190 | aromatic acid decarboxylase |
| non-specific | 1 | 235 | 4.40e-46 | PRK06732 | PRK06732 | cl27193 | phosphopantothenate–cysteine ligase |
| superfamily | 1 | 235 | 4.40e-46 | cl27193 | DFP superfamily | - | DNA / pantothenate metabolism flavoprotein |
| non-specific | 2 | 235 | 2.55e-32 | TIGR02114 | coaB_strep | cl27193 | phosphopantothenate–cysteine ligase, streptococcal |
| non-specific | 2 | 233 | 4.06e-16 | PRK09620 | PRK09620 | cl27193 | hypothetical protein |
| non-specific | 2 | 194 | 6.27e-13 | pfam04127 | DFP | cl27193 | DNA / pantothenate metabolism flavoprotein |
| non-specific | 2 | 194 | 9.56e-12 | PRK05579 | PRK05579 | cl27193 | bifunctional phosphopantothenoylcysteine decarboxylase/phosphopantothenate synthase |
| non-specific | 1 | 210 | 5.70e-10 | COG0452 | CoaBC | cl27193 | Phosphopantothenoylcysteine synthetase/decarboxylase |
| non-specific | 2 | 194 | 7.80e-10 | TIGR00521 | coaBC_dfp | cl27193 | phosphopantothenoylcysteine decarboxylase / phosphopantothenate–cysteine ligase |
| non-specific | 1 | 112 | 0.005721 | COG0451 | WcaG | cl25660 | Nucleoside-di-phosphate-sugar epimerase |
| superfamily | 1 | 112 | 0.005721 | cl25660 | Epimerase superfamily | - | NAD dependent epimerase/dehydratase family |

* M. iowae (PPCS)
## Supplementary Table 8 CoaBC InterPro results

| Mycoplasma species | Amino acid region | Database | Database ID | Database signature description | ID region start | ID region end | InterPro ID<sup>b</sup> | ID type<sup>a</sup> | Gene Ontology (GO) term<sup>c</sup> |
|--------------------|-------------------|----------|-------------|-------------------------------|----------------|--------------|-----------------|-------------|--------------------------|
| M. anatis          | 375               | Gene3D   | G3DSA:3.40.50.1950 | 1 | 165 | IPR036551 | H | GO:0003824 |
|                    |                   | Gene3D   | G3DSA:3.40.50.10300 | 166 | 375 | IPR035929 | H |                       |
|                    |                   | PANTHER  | PTHR14359:SF6 | 2 | 334 |          |     |               |
|                    |                   | PANTHER  | PTHR14359 | 2 | 334 |          |     |               |
|                    |                   | Pfam     | PF02441 | Flavoprotein | 1 | 163 | IPR003382 | D | GO:0003824 |
|                    |                   | Pfam     | PF04127 | DNA / pantothenate metabolism flavoprotein | 170 | 335 | IPR007085 | D |                       |
|                    |                   | Phobius   | SIGNAL_PEPTIDE N_REGION | N-terminal region of a signal peptide. | 1 | 2 |          |     |               |
|                    |                   | Phobius   | SIGNAL PEPTIDE H_REGION | Hydrophobic region of a signal peptide. | 3 | 13 |          |     |               |
|                    |                   | Phobius   | SIGNAL PEPTIDE C_REGION | C-terminal region of a signal peptide. | 14 | 18 |          |     |               |
|                    |                   | Phobius   | SIGNAL PEPTIDE | Signal peptide region | 1 | 18 |          |     |               |
|                    |                   | Phobius   | NON_CYTOPLASMIC_D | Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region. | 19 | 375 |          |     |               |
|                    |                   | SUPERFAMILY | SSF52507 | 1 | 165 | IPR036551 | H | GO:0003824 |
|                    |                   | SUPERFAMILY | SSF102645 | 170 | 373 | IPR035929 | H |                       |
|                    |                   | TIGRFAM   | TIGR000521 | coaBC_dfp: phosphopantothenoylcysteine decarboxylase / phosphopantothenate--cysteine ligase | 1 | 371 | IPR005252 | F | GO:0004632; GO:0004635; GO:0010181; GO:0015937; GO:0015941 |
| M. arginini        | 384               | Gene3D   | G3DSA:3.40.50.1950 | 1 | 168 | IPR036551 | H | GO:0003824 |
|                    |                   | Gene3D   | G3DSA:3.40.50.10300 | 169 | 384 | IPR035929 | H |                       |
|                    |                   | PANTHER  | PTHR14359 | 2 | 344 |          |     |               |
|                    |                   | PANTHER  | PTHR14359:SF6 | 2 | 344 |          |     |               |
|                    |                   | Pfam     | PF02441 | Flavoprotein | 1 | 171 | IPR003382 | D | GO:0003824 |
|                    |                   | Pfam     | PF04127 | Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region. | 17 | 384 |          |     |               |
|                    |                   | Phobius   | NON_CYTOPLASMIC_D | Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region. | 17 | 384 |          |     |               |
|                    |                   | Phobius   | SIGNAL PEPTIDE C_REGION | C-terminal region of a signal peptide. | 12 | 16 |          |     |               |
|                    |                   | Phobius   | SIGNAL PEPTIDE | Signal peptide region | 1 | 16 |          |     |               |
|                    |                   | Phobius   | SIGNAL PEPTIDE N_REGION | N-terminal region of a signal peptide. | 1 | 2 |          |     |               |
|                    |                   | Phobius   | SIGNAL PEPTIDE H_REGION | Hydrophobic region of a signal peptide. | 3 | 11 |          |     |               |
|                    |                   | SignalP_EUK | SignalP:noTM | 1 | 17 |          |     |               |
|                    |                   | SUPERFAMILY | SSF102645 | 176 | 381 | IPR035929 | H | GO:0003824 |
|                    |                   | SUPERFAMILY | SSF52507 | 1 | 169 | IPR036551 | H | GO:0003824 |
|                    |                   | TIGRFAM   | TIGR000521 | coaBC_dfp: phosphopantothenoylcysteine decarboxylase / phosphopantothenate--cysteine ligase | 1 | 376 | IPR005252 | F | GO:0004632; GO:0004635; GO:0010181; GO:0015937; GO:0015941 |
| **Mycoplasma species** | **Amino acid region** | **Database** | **Database ID** | **Database signature description** | **ID region start** | **ID region end** | **InterPro ID b** | **ID type b** | **Gene Ontology (GO) term b** |
|-----------------------|-----------------------|--------------|----------------|----------------------------------|--------------------|----------------|------------------|---------------|-----------------------------|
| **M. columborale**    | 377                   | Gene3D       | G3DSA:3.40.50.10300 |  | 165 376 | IPR035929 | H |  |  |
|                       |                       | Gene3D       | G3DSA:3.40.50.1950 |  | 1 164 | IPR036551 | H | GO:0003824 |  |
|                       |                       | PANTHER     | PTHR14359 |  | 2 341 |  |  |  |  |
|                       |                       | PANTHER     | PTHR14359-SF6 |  | 2 341 |  |  |  |  |
|                       |                       | Phobius     | SIGNAL PEPTIDE | DNA / pantothenate metabolism flavoprotein | 171 335 | IPR007085 | D |  |  |
|                       |                       | Phobius     | SIGNAL PEPTIDE_C_REGION | C-terminal region of a signal peptide | 169 336 | IPR007085 | D |  |  |
|                       |                       | Phobius     | SIGNAL PEPTIDE_N_REGION | N-terminal region of a signal peptide | 1 2 |  |  |  |  |
|                       |                       | Phobius     | SIGNAL PEPTIDE_H_REGION | Hydrophobic region of a signal peptide | 3 11 |  |  |  |  |
|                       |                       | Phobius     | NON_CYTOPLASMIC_D | Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region | 17 377 |  |  |  |  |
|                       |                       | SUPERFAMILY | SSF52507 |  | 1 166 | IPR036551 | H | GO:0003824 |  |
|                       |                       | SUPERFAMILY | SSF102645 |  | 170 373 | IPR035929 | H |  |  |
|                       |                       | TIGRFAM     | TIGR00521 | coaBC_dfp: phosphopantothenoylcysteine decarboxylase / phosphopantothenate--cysteine ligase | 1 370 | IPR005252 | F |  |  |
| **M. cricetuli**      | 377                   | Gene3D       | G3DSA:3.40.50.10300 |  | 169 377 | IPR035929 | H |  |  |
|                       |                       | Gene3D       | G3DSA:3.40.50.1950 |  | 1 168 | IPR036551 | H | GO:0003824 |  |
|                       |                       | PANTHER     | PTHR14359 |  | 2 344 |  |  |  |  |
|                       |                       | PANTHER     | PTHR14359-SF6 |  | 2 344 |  |  |  |  |
|                       |                       | Phobius     | SIGNAL PEPTIDE | Flavoprotein | 1 167 | IPR003382 | D | GO:0003824 |  |
|                       |                       | Phobius     | SIGNAL PEPTIDE | DNA / pantothenate metabolism flavoprotein | 169 336 | IPR007085 | D |  |  |
|                       |                       | Phobius     | SIGNAL PEPTIDE | Signal peptide region | 1 16 |  |  |  |  |
|                       |                       | Phobius     | SIGNAL PEPTIDE_C_REGION | C-terminal region of a signal peptide | 12 16 |  |  |  |  |
|                       |                       | Phobius     | SIGNAL PEPTIDE_H_REGION | Hydrophobic region of a signal peptide | 3 11 |  |  |  |  |
|                       |                       | Phobius     | NON_CYTOPLASMIC_D | Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region | 17 377 |  |  |  |  |
|                       |                       | SUPERFAMILY | SSF102645 |  | 169 376 | IPR035929 | H |  |  |
|                       |                       | SUPERFAMILY | SSF52507 |  | 1 167 | IPR036551 | H | GO:0003824 |  |
|                       |                       | TIGRFAM     | TIGR00521 | coaBC_dfp: phosphopantothenoylcysteine decarboxylase / phosphopantothenate--cysteine ligase | 1 371 | IPR005252 | F | GO:0004632; GO:0004633; GO:0010181; GO:0015937; GO:0015941 |  |
| **M. gallinaceum**    | 385                   | Gene3D       | G3DSA:3.40.50.1950 |  | 1 176 | IPR036551 | H | GO:0003824 |  |
|                       |                       | Gene3D       | G3DSA:3.40.50.10300 |  | 177 385 | IPR035929 | H |  |  |
|                       |                       | PANTHER     | PTHR14359 |  | 2 342 |  |  |  |  |
|                       |                       | PANTHER     | PTHR14359-SF6 |  | 2 342 |  |  |  |  |
| Mycoplasma species | Amino acid region | Database | Database ID | Database signature description | ID region start | ID region end | InterPro IDb | ID typec | Gene Ontology (GO) termd |
|-------------------|------------------|----------|------------|--------------------------------|----------------|--------------|-------------|---------|--------------------------|
| M. gallinaceum    | 385              | Pfam     | PF04127    | DNA / pantothenate metabolism flavoprotein | 178            | 348          | IPR007085   | D       |                          |
|                   |                  | Pfam     | PF02441    | Flavoprotein                    | 1              | 173          | IPR003382   | D       | GO:0003824               |
|                   |                  | SUPERFAMILY | SSF52507 |                                | 1              | 173          | IPR036551   | H       | GO:0003824               |
|                   |                  | SUPERFAMILY | SSF102645 |                                | 178            | 382          | IPR035929   | H       |                          |
|                   |                  | TIGRFAM  | TIGR00521  | coaBC_dfp: phosphopantothenoylcysteine decarboxylase / phosphopantothenate--cysteine ligase | 1              | 377          | IPR005252   | F       |                          |
| M. iowae (PPCS)   | 236              | Gene3D   | G3DSA:3.40.50.10300 |                                | 1              | 236          | IPR035929   | H       |                          |
|                   |                  | PANTHER  | PTHR14359-SF22 |                                | 1              | 226          |             |         |                          |
|                   |                  | PANTHER  | PTHR14359   |                                | 1              | 226          |             |         |                          |
|                   |                  | Pfam     | PF04127    | DNA / pantothenate metabolism flavoprotein | 2              | 195          | IPR007085   | D       |                          |
|                   |                  | SUPERFAMILY | SSF102645 |                                | 1              | 232          | IPR035929   | H       |                          |
| M. iowae (PPCDC)  | 178              | Gene3D   | G3DSA:3.40.50.1950 |                                | 1              | 177          | IPR036551   | H       | GO:0003824               |
|                   |                  | PANTHER  | PTHR14359   |                                | 2              | 174          |             |         |                          |
|                   |                  | PANTHER  | PTHR14359-SF6 |                                | 2              | 174          |             |         |                          |
|                   |                  | Pfam     | PF02441    | Flavoprotein                    | 3              | 175          | IPR003382   | D       | GO:0003824               |
|                   |                  | ProSiteProfiles | PS51257 | Prokaryotic membrane lipoprotein lipid attachment site profile. | 1              | 15           |             |         |                          |
|                   |                  | SUPERFAMILY | SSF52507 |                                | 2              | 175          | IPR036551   | H       | GO:0003824               |
|                   |                  | Gene3D   | G3DSA:3.40.50.1950 |                                | 1              | 171          | IPR036551   | H       | GO:0003824               |
|                   |                  | Gene3D   | G3DSA:3.40.50.10300 |                                | 172            | 230          | IPR035929   | H       |                          |
|                   |                  | Gene3D   | G3DSA:3.40.50.10300 |                                | 231            | 360          | IPR035929   | H       |                          |
|                   |                  | PANTHER  | PTHR14359   |                                | 3              | 323          |             |         |                          |
|                   |                  | PANTHER  | PTHR14359-SF6 |                                | 3              | 323          |             |         |                          |
|                   |                  | Pfam     | PF04127    | Flavoprotein                    | 3              | 164          | IPR003382   | D       | GO:0003824               |
|                   |                  | Pfam     | PF04127    | DNA / pantothenate metabolism flavoprotein | 175            | 358          | IPR035929   | H       |                          |
|                   |                  | SUPERFAMILY | SSF102645 |                                | 172            | 358          | IPR035929   | H       |                          |
|                   |                  | SUPERFAMILY | SSF52507 |                                | 2              | 170          | IPR036551   | H       | GO:0003824               |
| M. mobile         | 360              | Gene3D   | G3DSA:3.40.50.1950 |                                | 1              | 165          | IPR036551   | H       | GO:0003824               |
|                   |                  | Gene3D   | G3DSA:3.40.50.10300 |                                | 166            | 376          | IPR035929   | H       |                          |
|                   |                  | PANTHER  | PTHR14359-SF6 |                                | 2              | 334          |             |         |                          |
|                   |                  | PANTHER  | PTHR14359   |                                | 2              | 334          |             |         |                          |
|                   |                  | Pfam     | PF02441    | Flavoprotein                    | 2              | 164          | IPR003382   | D       | GO:0003824               |
|                   |                  | Pfam     | PF04127    | DNA / pantothenate metabolism flavoprotein | 170            | 334          | IPR007085   | D       |                          |
| M. sturni          | 376              | Gene3D   | G3DSA:3.40.50.1950 |                                | 1              | 165          | IPR036551   | H       | GO:0003824               |
|                   |                  | Gene3D   | G3DSA:3.40.50.10300 |                                | 166            | 376          | IPR035929   | H       |                          |
|                   |                  | PANTHER  | PTHR14359-SF6 |                                | 2              | 334          |             |         |                          |
|                   |                  | PANTHER  | PTHR14359   |                                | 2              | 334          |             |         |                          |
|                   |                  | Pfam     | PF02441    | Flavoprotein                    | 2              | 164          | IPR003382   | D       | GO:0003824               |
|                   |                  | Pfam     | PF04127    | DNA / pantothenate metabolism flavoprotein | 170            | 334          | IPR007085   | D       |                          |
|                   |                  | Phobius  | SIGNAL PEPTIDE_N_REGION | N-terminal region of a signal peptide. | 1              | 2           |             |         |                          |
|                   |                  | Phobius  | SIGNAL PEPTIDE_C_REGION | C-terminal region of a signal peptide. | 15             | 18          |             |         |                          |
|                   |                  | Phobius  | SIGNAL PEPTIDE | Signal peptide region | 1              | 18          |             |         |                          |
|                   |                  | Phobius  | NON_CYTOPLASMIC_D | Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region. | 19             | 376         |             |         |                          |
|                   |                  | Phobius  | SIGNAL PEPTIDE_H_REGION | Hydrophobic region of a signal peptide. | 3              | 14          |             |         |                          |
| Mycoplasma species | Amino acid region | Database | Database ID | Database signature description | ID region start | ID region end | InterPro ID\(^{b}\) | ID type\(^{a}\) | Gene Ontology (GO) term\(^{c}\) |
|-------------------|------------------|----------|------------|--------------------------------|----------------|--------------|----------------|-----------|-------------------------------|
| M. sturni         |                 | SUPERFAMILY | SSF102645 |                                | 170            | 375          | IPR035929 | H         |                               |
|                   |                 | SUPERFAMILY | SSF52507  |                                | 1              | 164          | IPR036551 | H         |                               |
|                   | TIGRFAM         | TIGR00521 | coaBC_dfp: phosphopantothenoylcysteine decarboxylase / phosphopantothenate--cysteine ligase | 2              | 370          | IPR005252 | F         |                               |
|                   |                 | Gene3D    | G3DSA.3.40.50.10300 |                                | 169            | 384          | IPR035929 | H         |                               |
|                   |                 | Gene3D    | G3DSA.3.40.50.1950 |                                | 1              | 168          | IPR036551 | H         |                               |
|                   | PANTHER         | PTHR14359 | DNA / pantothenate metabolism flavoprotein | 176            | 342          | IPR007085 | D         |                               |
|                   |                 | Plam      | PF04127   | Flavoprotein                    | 1              | 171          | IPR003382 | D         |                               |
|                   | Phobius         | SIGNAL_PEPTIDE_H_REGION | Hydrophobic region of a signal peptide. | 3              | 11           |                |           |                               |
|                   | Phobius         | SIGNAL_PEPTIDE | Signal peptide region | 1              | 16           |                |           |                               |
|                   | Phobius         | SIGNAL_PEPTIDE_N_REGION | N-terminal region of a signal peptide. | 1              | 2            |                |           |                               |
|                   | Phobius         | NON_CYTOPLASMIC_D | Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region. | 17              | 384          |                |           |                               |
|                   | Phobius         | SIGNAL_PEPTIDE_C_REGION | C-terminal region of a signal peptide. | 12              | 16           |                |           |                               |
|                   | SignalP_EUK     | SignalP-eno1M |                                | 1              | 17           |                |           |                               |
|                   | SUPERFAMILY     | SSF102645 |                                | 176            | 381          | IPR035929 | H         |                               |
|                   | SUPERFAMILY     | SSF52507  |                                | 1              | 169          | IPR036551 | H         |                               |
|                   | TIGRFAM         | TIGR00521 | coaBC_dfp: phosphopantothenoylcysteine decarboxylase / phosphopantothenate--cysteine ligase | 1              | 376          | IPR005252 | F         |                               |
| M. synoviae       |                 | Gene3D    | G3DSA.3.40.50.1950 |                                | 13             | 195          | IPR036551 | H         |                               |
|                   |                 | Gene3D    | G3DSA.3.40.50.10300 |                                | 196            | 246          | IPR035929 | H         |                               |
|                   |                 | Gene3D    | G3DSA.3.40.50.10300 |                                | 247            | 380          | IPR035929 | H         |                               |
|                   | PANTHER         | PTHR14359 |                                | 17              | 242          | IPR003382 | D         |                               |
|                   | Plam            | PF02441   | Flavoprotein                    | 17              | 186          | IPR007085 | D         |                               |
|                   | Plam            | PF04127   | DNA / pantothenate metabolism flavoprotein | 196            | 347          | IPR035929 | H         |                               |
|                   | SUPERFAMILY     | SSF102645 |                                | 17              | 190          | IPR036551 | H         |                               |
|                   | SUPERFAMILY     | SSF52507  |                                | 196            | 379          | IPR035929 | H         |                               |

\(^{a}\)ID type abbreviations – H, Homologous superfamily; F, Family; D, Domain

\(^{b}\)InterPro ID – IPR036551: Flavin prenyltransferase-like; IPR035929: CoaB-like superfamily; IPR005252: Coenzyme A biosynthesis bifunctional protein, CoaBC; IPR003382: Flavoprotein; IPR007085: DNA/pantothenate metabolism flavoprotein, C-terminal

\(^{c}\)GO term (Biological Process) – GO:00015937: Coenzyme A biosynthetic process; GO:0015941: Pantothenate catabolic process

\(^{d}\)GO term (Molecular Function) – GO:0003824: catalytic activity; GO:0004632: Phosphopantothenate--cysteine ligase activity; GO:0004633: Phosphopantothenoylcysteine decarboxylase activity; GO:0010181: FMN binding
**Supplementary Table 9** CoaBC MEME + motif locations

| Mycoplasma species  | p-value     | Motif locations |
|---------------------|-------------|-----------------|
|                     |             | Motif 1 | Motif 2 | Motif 3 | Motif 4 |
| M. anatis           | 2.69e-117   | 61-100  | 134-161 | 171-199 | 212-261 |
| M. arginini         | 1.95e-121   | 66-105  | 138-165 | 175-203 | 216-265 |
| M. columborale      | 6.19e-120   | 61-100  | 134-161 | 171-199 | 212-261 |
| M. cricetuli        | 8.35e-115   | 61-100  | 134-161 | 171-199 | 212-261 |
| M. gallinaceum      | 1.20e-112   | 68-107  | 141-168 | 178-206 | 219-268 |
| M. mobile           | 1.77e-60    | 62-101  | 134-161 | 176-204 | -       |
| M. sturni           | 5.66e-122   | 61-100  | 134-161 | 171-199 | 212-261 |
| M. synoviae         | 3.78e-121   | 66-105  | 138-165 | 175-205 | 216-265 |
| M. testudinis       | 1.42e-56    | 84-123  | 157-184 | 198-226 | -       |
| M. iowae (PPCDC)    | 5.76e-35    | 69-108  | 143-170 | -       | -       |
| M. iowae (PPCS)     | 5.34e-14    | -       | -       | 1-29    | -       |

**Supplementary Table 10** PPAT CDD results

| Query                | Hit type | ID region start | ID region end | E-Value | Accession | Short name     | Superfamily | Definition                                                                 |
|----------------------|----------|-----------------|---------------|---------|-----------|----------------|-------------|-----------------------------------------------------------------------------|
| M. agalactiae        | specific | 1               | 140           | 7.72e-76 | PRK13964  | coaD           | c000015     | phosphopantetheine adenylyltransferase                                       |
|                      | superfamily | 1             | 140           | 7.72e-76 | c00015    | nt_trans superfamily | c000015     | nucleotidyl transferase superfamily                                         |
|                      | non-specific | 1             | 134           | 1.14e-44 | COG00669  | coaD           | c000015     | Phosphopantetheine adenylyltransferase                                      |
| non-specific         | 4         | 133            | 1.13e-40      | cd02163  | PPAT      | c000015        | Phosphopantetheine adenylyltransferase                                    |
| non-specific         | 4         | 133            | 5.88e-39      | TIGR01510| coaD_prev_kdtB | c000015     | Pantetheine-phosphate adenylyltransferase                                  |
| specific             | 1         | 133            | 6.60e-38      | PRK00168  | coaD      | c000015        | Phosphopantetheine adenylyltransferase                                    |
|                      | non-specific | 4             | 60            | 1.67e-07 | TIGR00125  | c000015        | Cytidylyltransferase-like domain                                          |
|                      | 4         | 66             | 1.13e-06      | cd02165  | NMNAT     | c000015        | Nicotinamide/nicotinate mononucleotide adenylyltransferase                 |
|                     | 1         | 51             | 2.22e-06      | PRK00071  | nadD      | c000015        | Nicotinic acid mononucleotide adenylyltransferase                          |
|                     | 1         | 66             | 1.31e-05      | cd28367  | nadD_superfamily | c000015     | Putative nicotinate-nucleotide adenylyltransferase                         |
|                     | 4         | 60             | 2.15e-05      | cd02156  | nt_trans  | c000015        | Nucleotidyl transferase superfamily                                       |
| Query       | Hit type | ID region start | ID region end | E-Value | Accession   | Short name       | Superfamily | Definition                                                                 |
|------------|----------|-----------------|---------------|---------|-------------|-----------------|-------------|---------------------------------------------------------------------------|
| non-specific | 5        | 51              |               | 2.74e-05 | TIGR00482   | TIGR00482       | c000015     | nicotinate (nicotinamide) nucleotide adenylyltransferase                  |
| non-specific | 1        | 87              |               | 4.49e-05 | cd02170     | cytidylyltransferase | c000015    | cytidylyltransferase                                                     |
| non-specific | 1        | 41              |               | 4.94e-05 | COG1057     | NadD            | c000015      | Nicotinic acid mononucleotide adenylyltransferase                        |
| non-specific | 1        | 59              |               | 0.000196 | COG1056     | NadR            | c000015      | Nicotinamide mononucleotide adenylyltransferase                          |
| non-specific | 5        | 73              |               | 0.00042  | cd02167     | NMNAT_NadR      | c000015      | Nicotinamide/nicotinate mononucleotide adenylyltransferase               |
| non-specific | 14       | 39              |               | 0.000487 | pfam02569   | Pantoate_ligase | c000015      | Pantoate-beta-alanine ligase                                            |
| non-specific | 1        | 68              |               | 0.002358 | cd02171     | G3P_Cytidylyltransferase | c000015 | glycerol-3-phosphate cytidylyltransferase                                |
| non-specific | 13       | 39              |               | 0.002895 | PRK00380    | PanC            | c000015      | pantoate-beta-alanine ligase                                             |
| non-specific | 8        | 36              |               | 0.001563 | COG0615     | TagD            | c000015      | Glycerol-3-phosphate cytidylyltransferase, cytidylyltransferase family  |
| non-specific | 5        | 42              |               | 0.00664  | cd02173     | ECT             | c000015      | CTP:phosphoethanolamine cytidylyltransferase (ECT)                       |
| non-specific | 14       | 67              |               | 0.006924 | cd00560     | PanC            | c000015      | Pantoate-beta-alanine ligase                                             |
| non-specific | 4        | 35              |               | 0.00929  | PRK01153    | PRK01153       | c000015      | nicotinamide-nucleotide adenylyltransferase                              |
| non-specific | 14       | 39              |               | 0.009867 | COG0414     | PanR            | c000015      | Pantothenate synthetase                                                  |
| non-specific | 5        | 145             |               | 6.82e-61 | PRK13964    | coaD            | c000015      | phosphopantetheine adenylyltransferase                                   |
| superfamily | 5        | 145             |               | 6.82e-61 | c000015     | nt_trans superfamily | c000015 | nucleotidy transferase superfamily                                       |
| M. alligatoris | 4        | 139             |               | 5.23e-43 | COG0669     | CoaD            | c000015      | Phosphopantetheine adenylyltransferase                                   |
| non-specific | 6        | 138             |               | 3.36e-39 | cd02163     | PPAT            | c000015      | Phosphopantetheine adenylyltransferase                                   |
| non-specific | 5        | 138             |               | 4.23e-37 | PRK00168    | coaD            | c000015      | phosphopantetheine adenylyltransferase                                   |
| non-specific | 6        | 138             |               | 4.91e-36 | TIGR01510   | coaD_prev_kdtB  | c000015      | pantetheine-phosphate adenylyltransferase                               |
| specific    | 8        | 140             |               | 6.16e-19 | plam01467   | CTP_transf like | c000015      | Cytidylyltransferase-like                                                |
| non-specific | 6        | 138             |               | 2.11e-11 | cd02039     | cytidylyltransferase_like | c000015 | Cytidylyltransferase-like domain                                        |
| non-specific | 6        | 65              |               | 1.92e-09 | TIGR00125   | cyt_tran rel    | c000015      | cytidylyltransferase-like domain                                        |
| M. alligatoris | 8        | 138             |               | 3.57e-08 | cd02167     | NMNAT_NadR      | c000015      | Nicotinamide/nicotinate mononucleotide adenylyltransferase               |
| non-specific | 1        | 55              |               | 3.89e-08 | PRK00071    | nadD            | c000015      | nicotinic acid mononucleotide adenylyltransferase                        |
| non-specific | 7        | 145             |               | 1.33e-06 | cd02165     | NMNAT           | c000015      | Nicotinamide/nicotinate mononucleotide adenylyltransferase               |
| non-specific | 2        | 55              |               | 7.19e-06 | COG1057     | NadR            | c000015      | Nicotinic acid mononucleotide adenylyltransferase                        |
| non-specific | 6        | 61              |               | 8.85e-06 | cd02156     | nt_trans        | c000015      | nucleotidy transferase superfamily                                      |
| non-specific | 8        | 74              |               | 1.38e-05 | TIGR00482   | TIGR00482       | c000015      | nicotinate (nicotinamide) nucleotide adenylyltransferase                 |
| non-specific | 4        | 71              |               | 1.89e-05 | PRK07152    | nadD            | c128367      | putative nicotinate-nucleotide adenylyltransferase                      |
| superfamily | 4        | 71              |               | 1.89e-05 | c128367     | nadD_superfamily | -           | putative nicotinate-nucleotide adenylyltransferase                      |
| non-specific | 1        | 139             |               | 1.92e-05 | PRK08099    | PRK08099       | c128365      | bifunctional DNA-binding transcriptional repressor/ NMN adenylyltransferase |
| superfamily | 1        | 139             |               | 1.92e-05 | c128365     | PRK08099_superfamily | -           | bifunctional DNA-binding transcriptional repressor/ NMN adenylyltransferase |
| non-specific | 8        | 138             |               | 2.08e-05 | TIGR01526   | nadR_NMN_Atrans | c128365      | nicotinamide-nucleotide adenylyltransferase                             |
| non-specific | 3        | 76              |               | 4.92e-05 | COG1056     | NadR            | c000015      | Nicotinamide mononucleotide adenylyltransferase                          |
| non-specific | 5        | 35              |               | 0.000102 | PRK00777    | PRK00777       | c000015      | phosphopantetheine adenylyltransferase                                   |
| non-specific | 8        | 45              |               | 0.000144 | cd02174     | CCT             | c000015      | CTP:phosphochoeline cytidylyltransferase                                |
| non-specific | 11       | 44              |               | 0.000385 | TIGR02199   | rfaE.dom II     | c000015      | rfaE: bifunctional protein, domain II                                   |
| non-specific | 5        | 39              |               | 0.000474 | COG0615     | TagD            | c000015      | Glycerol-3-phosphate cytidylyltransferase, cytidylyltransferase family  |
| non-specific | 5        | 39              |               | 0.000767 | cd02170     | cytidylyltransferase | c000015 | cytidylyltransferase                                                    |
| Query | Hit type | ID region start | ID region end | E-Value | Accession | Short name | Superfamily | Definition |
|-------|----------|----------------|--------------|---------|-----------|------------|-------------|------------|
| non-specific | 1 | 36 | 0.001749 | COG1019 | CAB4 | c00015 | Phosphopantetheine adenyltr transferase |
| non-specific | 6 | 45 | 0.002804 | cd02173 | ECT | c00015 | CTP-phosphoethanolamine cytidylyltransferase (ECT) |
| non-specific | 11 | 44 | 0.002804 | COG2870 | RfaE | cl28454 | ADP-heptose synthase, bifunctional sugar kinase/adenyltransferase |
| superfamily | 11 | 44 | 0.002804 | cl28454 | RfaE superfamily | - | ADP-heptose synthase, bifunctional sugar kinase/adenyltransferase |
| non-specific | 7 | 38 | 0.003547 | PRK05379 | PRK05379 | cl28366 | bifunctional nicotinamide mononucleotide adenyltransferase |
| superfamily | 7 | 38 | 0.003547 | cl28366 | PRK05379 superfamily | - | bifunctional nicotinamide mononucleotide adenyltransferase |
| non-specific | 5 | 46 | 0.003932 | cd02171 | G3P_Cytidyltransferase | c00015 | glycerol-3-phosphate cytidylyltransferase |
| non-specific | 11 | 43 | 0.004677 | PRK11316 | PRK11316 | cl28454 | bifunctional heptose 7-phosphate kinase/heptose 1-phosphate adenyltransferase |
| M. alvi | non-specific | 5 | 136 | 1.05e-34 | cd02163 | PPAT | c00015 | Phosphopantetheine adenyltransferase |
| superfamily | 5 | 136 | 1.05e-34 | e00015 | nt_trans superfamily | - | nucleotidyl transferase superfamily |
| non-specific | 3 | 136 | 1.63e-33 | COG0669 | coaD | c00015 | Phosphopantetheine adenyltransferase |
| non-specific | 3 | 136 | 1.11e-31 | PRK00168 | coaD | c00015 | phosphopantetheine adenyltransferase |
| non-specific | 5 | 136 | 1.40e-31 | TIGR01510 | coaD_prev_kdtB | c00015 | pantetheine-phosphate adenyltransferase |
| non-specific | 3 | 147 | 1.40e-27 | PRK13964 | coaD | c00015 | phosphopantetheine adenyltransferase |
| non-specific | 7 | 137 | 4.55e-14 | pfam01467 | CTP transfer like | c00015 | Cytidyltransferase-like |
| non-specific | 5 | 37 | 3.10e-10 | TIGR00125 | cyt_trans_rel | c00015 | cytidyltransferase-like domain |
| non-specific | 1 | 40 | 2.38e-09 | COG1057 | NadD | c00015 | Nicotinic acid mononucleotide adenyltransferase |
| non-specific | 1 | 38 | 4.96e-09 | PRK00071 | nadD | c00015 | nicotinic acid mononucleotide adenyltransferase |
| non-specific | 6 | 37 | 1.43e-07 | cd02166 | NNMAT_Archaean | c00015 | Nicotinamide/nicotinate mononucleotide adenyltransferase |
| non-specific | 1 | 37 | 1.53e-07 | COG1056 | NadR | c00015 | Nicotinamide mononucleotide adenyltransferase |
| M. alvi | non-specific | 1 | 50 | 2.48e-07 | cd02165 | NNMAT | c00015 | Nicotinamide/nicotinate mononucleotide adenyltransferase |
| non-specific | 5 | 37 | 5.59e-07 | PRK01153 | PRK01153 | c00015 | nicotinamide-nucleotide adenyltransferase |
| non-specific | 5 | 37 | 2.28e-07 | PRK07152 | nadD | c00015 | putative nicotinate-nucleotide adenyltransferase |
| superfamily | 3 | 45 | 1.01e-06 | tig05762 | nadD superfamily | - | putative nicotinate-nucleotide adenyltransferase |
| non-specific | 6 | 30 | 3.31e-06 | cd02156 | nt_trans | c00015 | nucleotidyl transferase superfamily |
| non-specific | 5 | 136 | 4.91e-05 | cd02039 | cytidyltransferase | c00015 | Cytidyltransferase-like domain |
| non-specific | 7 | 40 | 0.000267 | TIGR00482 | TIGR00482 | c00015 | nicotinate (nicotinamide) adenyltransferase |
| non-specific | 10 | 38 | 0.000627 | COG0615 | TagD | c00015 | Glycerol-3-phosphate cytidyltransferase, cytidyltransferase family |
| non-specific | 10 | 38 | 0.000673 | cd02170 | cytidyltransferase | c00015 | cytidyltransferase |
| non-specific | 3 | 38 | 0.000929 | TIGR01526 | nadR_NMN_Atrans | c00015 | nicotinamide-nucleotide adenyltransferase |
| superfamily | 3 | 38 | 0.000929 | cl28365 | PRK08099 superfamily | - | bifunctional DNA-binding transcriptional repressor/ NMM adenyltransferase |
| non-specific | 4 | 35 | 0.000937 | PRK06973 | PRK06973 | c00015 | nicotinic acid mononucleotide adenyltransferase |
| non-specific | 6 | 37 | 0.001266 | TIGR01527 | arch_NMN_Atrans | c00015 | nicotinamide-nucleotide adenyltransferase |
| non-specific | 3 | 43 | 0.001379 | cd02172 | RfaE, N | c00015 | N-terminal domain of RfaE |
| non-specific | 4 | 37 | 0.003214 | PTZ00308 | PTZ00308 | c00015 | ethanolamine-phosphate cytidyltransferase |
| superfamily | 4 | 37 | 0.003214 | cl28626 | PNN2406 superfamily | - | ethanolamine-phosphate cytidyltransferase |
| non-specific | 5 | 38 | 0.003822 | cd02167 | NNMAT_NadR | c00015 | Nicotinamide/nicotinate mononucleotide adenyltransferase |
| Query      | Hit type | ID region start | ID region end | E-Value | Accession   | Short name                  | Superfamily                  | Definition                                                                 |
|------------|----------|-----------------|---------------|---------|-------------|-----------------------------|------------------------------|---------------------------------------------------------------------------|
| non-specific | 1       | 44              | 121           | 0.007022 | PRK08099    | PRK08099                    | c128365                     | bifunctional DNA-binding transcriptional repressor/ NMN adenyltransferase  |
| non-specific | 3       | 142             | 5.32e-63      |          | PRK13964    | coaD                         | c00015                      | phosphopantetheine adenyltransferase                                   |
| superfamily | 3       | 142             | 5.32e-63      |          | c00015      | nt_trans superfamily        |                             | nucleotidyl transferase superfamily                                   |
| non-specific | 2       | 136             | 8.28e-44      |          | COG0669     | CoaD                         | c00015                      | Phosphopantetheine adenyltransferase                                  |
| non-specific | 6       | 135             | 1.09e-42      |          | TIGR01510   | coaD_prev_kdB                | c00015                      | pantetheine-phosphate adenyltransferase                               |
| non-specific | 6       | 133             | 4.40e-42      |          | c02163      | PPAT                         | c00015                      | Phosphopantetheine adenyltransferase                                  |
| non-specific | 3       | 133             | 1.05e-39      |          | TIGR00168   | coaD                         | c00015                      | phosphopantetheine adenyltransferase                                  |
| specific   | 7       | 137             | 1.87e-18      |          | Pram01467   | CTP transf like              | c00015                      | Cytidyltransferase-like                                                |
| non-specific | 6       | 47              | 4.37e-10      |          | TIGR000125  | cyt_tran_rel                 | c00015                      | putative nicotinate-nucleotide adenyltransferase                      |
| non-specific | 3       | 68              | 1.64e-07      |          | PRK07152    | nadD                         | c128367                     | putative nicotinate-nucleotide adenyltransferase                      |
| superfamily | 3       | 68              | 1.64e-07      |          | c128367     | nadD superfamily             |                             | nucleotidyl transferase superfamily                                   |
| non-specific | 5       | 135             | 2.38e-07      |          | c02039      | cytidyltransferase_like     | c00015                      | Cytidyltransferase-like domain                                        |
| non-specific | 1       | 57              | 8.37e-07      |          | COG1057     | NadD                         | c00015                      | Nicotinic acid mononucleotide adenyltransferase                        |
| non-specific | 6       | 68              | 1.21e-06      |          | c02165      | NMNAT                        | c00015                      | Nicotinate/nicotinate mononucleotide adenyltransferase                 |
| non-specific | 1       | 53              | 2.42e-06      |          | PRK00071    | nadD                         | c00015                      | Nicotinate/nicotinate mononucleotide adenyltransferase                 |
| non-specific | 1       | 37              | 4.98e-06      |          | COG1056     | NadR                         | c00015                      | Nicotinamide mononucleotide adenyltransferase                          |
| non-specific | 6       | 51              | 4.50e-05      |          | c02156      | nt_trans                     | c00015                      | nucleotidyl transferase superfamily                                  |
| non-specific | 6       | 37              | 4.67e-05      |          | PRK01153    | PRK01153                     | c00015                      | nicotinamide-nucleotide adenyltransferase                             |
| non-specific | 6       | 37              | 0.000133      |          | c02166      | NMNAT_Archaea                | c00015                      | Nicotinamide/nicotinate mononucleotide adenyltransferase               |
| non-specific | 7       | 44              | 0.000544      |          | c02173      | ECI                          | c00015                      | CTP:phosphoethanolamine cytidyltransferase (ECI)                       |
| non-specific | 7       | 46              | 0.000563      |          | TIGR00482   | TIGR00482                    | c00015                      | nicotinate (nicotinamide) nucleotide adenyltransferase                |
| non-specific | 7       | 135             | 0.001898      |          | c02167      | NMNAT_NadR                   | c00015                      | Nicotinamide/nicotinate mononucleotide adenyltransferase               |
| non-specific | 6       | 37              | 0.00322       |          | TIGR01527   | arch_NMN_Atrans             | c00015                      | nicotinamide-nucleotide adenyltransferase                             |
| non-specific | 10      | 88              | 0.003576      |          | COG0615     | TagD                         | c00015                      | Glycerol-3-phosphate cytidyltransferase, cytidyltransferase family    |
| non-specific | 10      | 35              | 0.005471      |          | PRK00777    | PRK00777                     | c00015                      | phosphopantetheine adenyltransferase                                |
| superfamily | 9       | 44              | 0.008923      |          | c128626     | PLN02406 superfamily        |                             | ethanolamine-phosphate cytidyltransferase                             |
| specific   | 4       | 44              | 0.008923      |          | c128626     | PLN02406 superfamily        |                             | ethanolamine-phosphate cytidyltransferase                             |
| superfamily | 1       | 140             | 3.43e-72      |          | PRK13964    | coaD                         | c00015                      | phosphopantetheine adenyltransferase                                |
| superfamily | 1       | 140             | 3.43e-72      |          | c00015      | nt_trans superfamily        |                             | nucleotidyl transferase superfamily                                  |
| non-specific | 1       | 134             | 1.29e-46      |          | COG0669     | CoaD                         | c00015                      | Phosphopantetheine adenyltransferase                                |
| non-specific | 3       | 133             | 5.90e-43      |          | c02163      | PPAT                         | c00015                      | Phosphopantetheine adenyltransferase                                |
| non-specific | 1       | 133             | 4.85e-40      |          | PRK0168     | coaD                         | c00015                      | phosphopantetheine adenyltransferase                                |
| specific   | 3       | 133             | 2.98e-38      |          | TIGR01510   | coaD_prev_kdB                | c00015                      | pantetheine-phosphate adenyltransferase                              |
| specific   | 5       | 133             | 3.14e-21      |          | Pflam01467  | CTP transf like              | c00015                      | Cytidyltransferase-like                                                |
| non-specific | 3       | 35              | 4.10e-12      |          | TIGR00125   | cyt_tran_rel                 | c00015                      | cytidyltransferase-like domain                                       |
| non-specific | 3       | 35              | 2.72e-11      |          | c02039      | cytidyltransferase_like     | c00015                      | cytidyltransferase-like domain                                       |
| non-specific | 1       | 66              | 6.91e-09      |          | COG1057     | NadD                         | c00015                      | Nicotinic acid mononucleotide adenyltransferase                       |
| non-specific | 5       | 133             | 6.44e-08      |          | c02167      | NMNAT_NadR                   | c00015                      | Nicotinamide/nicotinate mononucleotide adenyltransferase               |
| non-specific | 3       | 39              | 7.00e-08      |          | c02156      | nt_trans                     | c00015                      | nucleotidyl transferase superfamily                                  |
| non-specific | 4       | 66              | 7.56e-08      |          | c02165      | NMNAT                        | c00015                      | Nicotinamide/nicotinate mononucleotide adenyltransferase               |
| non-specific | 1       | 41              | 2.06e-07      |          | PRK00071    | nadD                         | c00015                      | nicotinic acid mononucleotide adenyltransferase                       |

**M. anatis**

- **M. anatis**

- **Specific**

- **Superfamily**

- **Non-specific**

**M. arginini**

- **Query**

- **Hit type**

- **ID region start**

- **ID region end**

- **E-Value**

- **Accession**

- **Short name**

- **Superfamily**

- **Definition**
| Query                  | Hit type | ID region start | ID region end | E-Value  | Accession | Short name | Superfamily | Definition                                                                 |
|-----------------------|----------|----------------|--------------|----------|-----------|------------|-------------|-----------------------------------------------------------------------------|
| non-specific          | 1        | 36             |              | 3.33e-07 | cd02170   | cytidylyltransferase |             | cytidylyltransferase                                                        |
| non-specific          | 1        | 85             |              | 4.47e-07 | COG0615   | TagD       |             | Glycerol-3-phosphate cytidylyltransferase, cytidylyltransferase family      |
| non-specific          | 1        | 43             |              | 6.80e-07 | PRK07152  | nadD       |             | putative nicotinate-nucleotide adenylyltransferase                         |
| superfamily           | 1        | 43             |              | 6.80e-07 | c28367    | nadD superfamily |             | putative nicotinate-nucleotide adenylyltransferase                         |
| non-specific          | 5        | 62             |              | 2.09e-06 | TIGR00482 | TIGR00482  |             | nicotinate (nicotinamide) nucleotide adenylyltransferase                   |
| non-specific          | 1        | 35             |              | 2.18e-06 | COG1056   | NadR       |             | Nicotinamide mononucleotide adenylyltransferase                            |
| non-specific          | 1        | 33             |              | 1.71e-06 | PRK00777  | PRK00777   |             | phosphopantetheine adenylyltransferase                                     |
| non-specific          | 1        | 0.000131       |              | 0.000131 | TIGR01526 | nadR_NMN_Atrans | 0.000131 | nicotinamide-nucleotide adenylyltransferase                                |
| superfamily           | 1        | 36             |              | 0.000131 | c28365    | PRK08099   | superfamily | -                                                                           |
| non-specific          | 1        | 36             |              | 0.000394 | cd02171   | G3P        |             | glycerol-3-phosphate cytidylyltransferase                                  |
| non-specific          | 8        | 41             |              | 8.000535 | cd02174   | CCT        |             | CTP:phosphocholine cytidylyltransferase                                    |
| non-specific          | 3        | 35             |              | 0.001099 | cd02166   | NMNAT_Archaean |             | Nicotinamide/nicotinate mononucleotide adenylyltransferase                 |
| non-specific          | 2        | 35             |              | 0.001112 | PRK01153  | PRK01153   |             | nicotinamide-nucleotide adenylyltransferase                                |
| non-specific          | 7        | 41             |              | 0.00136  | PTZ00308  | PTZ00308   |             | ethanolamine-phosphate cytidylyltransferase                               |
| superfamily           | 7        | 41             |              | 0.00136  | c28266    | PLN02406   | superfamily | -                                                                           |
| non-specific          | 8        | 57             |              | 0.002223 | TIGR01518 | g3p_cytidylylms |             | glycerol-3-phosphate cytidylyltransferase                                 |
| non-specific          | 3        | 41             |              | 0.002408 | cd02173   | ECT        |             | CTP:phosphoethanolamine cytidylyltransferase (ECT)                        |
| non-specific          | 8        | 134            |              | 0.008463 | PRK08099  | PRK08099   |             | bifunctional DNA-binding transcriptional repressor/NMN adenylyltransferase |
| non-specific          | 1        | 140            |              | 1.28e-52 | PRK13964  | coaD       |             | phosphopantetheine adenylyltransferase                                    |
| superfamily           | 1        | 140            |              | 1.28e-52 | co00015   | nt_trans superfamily |             | -                                                                           |
| non-specific          | 1        | 134            |              | 1.75e-42 | COG0669   | CoaD       |             | Phosphopantetheine adenylyltransferase                                    |
| non-specific          | 3        | 133            |              | 1.91e-40 | cd02163   | PPAT       |             | Phosphopantetheine adenylyltransferase                                    |
| non-specific          | 1        | 133            |              | 2.71e-39 | PRK00168  | coaD       |             | Phosphopantetheine adenylyltransferase                                    |
| non-specific          | 3        | 133            |              | 6.95e-37 | TIGR01510 | coaD_prev kdtB |             | pantothenic phosphate adenylyltransferase                                |
| specific              | 5        | 135            |              | 7.94e-24 | pflm01467 | CTP transf like |             | CTP:transf like                                                            |
| non-specific          | 5        | 133            |              | 9.44e-14 | cd02167   | NMNAT_NadR |             | Nicotinamide/nicotinate mononucleotide adenylyltransferase                 |
| non-specific          | 3        | 57             |              | 1.21e-12 | TIGR00125 | cyt_tran_rel |             | cytidylyltransferase-like domain                                          |
| non-specific          | 3        | 133            |              | 1.51e-10 | cd02039   | cytidylyltransferase_like |             | Cytidylyltransferase-like domain                                          |
| M. arginini           | non-specific | 1            | 66         | 2.48e-10 | PRK00071  | nadD       |             | nicotinic acid mononucleotide adenylyltransferase                        |
| non-specific          | 1        | 66             |              | 4.65e-10 | COG1057   | NadD       |             | Nicotinic acid mononucleotide adenylyltransferase                        |
| non-specific          | 1        | 133            |              | 7.25e-09 | TIGR01526 | nadR_NMN_Atrans | 0.000131 | nicotinamide-nucleotide adenylyltransferase                                |
| superfamily           | 1        | 133            |              | 7.25e-09 | c28365    | PRK08099   | superfamily | -                                                                           |
| non-specific          | 4        | 66             |              | 9.14e-09 | cd02165   | NMNAT      |             | Nicotinamide/nicotinate mononucleotide adenylyltransferase                 |
| non-specific          | 1        | 35             |              | 3.95e-08 | COG1056   | NadR       |             | Nicotinamide mononucleotide adenylyltransferase                           |
| non-specific          | 5        | 66             |              | 4.77e-08 | TIGR00482 | TIGR00482  |             | nicotinate (nicotinamide) nucleotide adenylyltransferase                  |
| non-specific          | 1        | 66             |              | 7.58e-08 | PRK07152  | nadD       |             | putative nicotinate-nucleotide adenylyltransferase                       |
| superfamily           | 1        | 66             |              | 7.58e-08 | c28367    | nadD superfamily |             | putative nicotinate-nucleotide adenylyltransferase                       |
| non-specific          | 1        | 35             |              | 3.11e-07 | PRK01153  | PRK01153   |             | nicotinate-nucleotide adenylyltransferase                                |
| non-specific          | 3        | 67             |              | 3.94e-07 | cd02166   | NMNAT_Archaean |             | Nicotinamide/nicotinate mononucleotide adenylyltransferase                 |
| Query                  | Hit type | ID region start | ID region end | E-Value  | Accession      | Short name | Superfamily             | Definition                                                                 |
|-----------------------|----------|----------------|---------------|----------|----------------|------------|------------------------|-----------------------------------------------------------------------------|
| non-specific          | 8        | 134            |               | 4.62e-07 | PRK08099       | PRK08099   | c128365                | bifunctional DNA-binding transcriptional repressor/ NMN adenylyltransferase |
| non-specific          | 3        | 77             |               | 2.82e-06 | TIGR01527      | arch_NMN_ATrans       | c00015       | nicotinamide-nucleotide adenylyltransferase |
| non-specific          | 4        | 50             |               | 3.24e-06 | PRK05379       | PRK05379   | c12366                | bifunctional nicotinamide mononucleotide adenylyltransferase               |
| superfamily           | 4        | 50             |               | 3.24e-06 | c128366        | PRK05379 superfamily | -           | -                          |
| non-specific          | 1        | 33             |               | 3.44e-05 | PRK00777       | PRK00777   | c00015                | phosphopentehane adenylyltransferase                                      |
| non-specific          | 1        | 58             |               | 4.60e-05 | COG0615        | TagD       | c00015                | Glycerol-3-phosphate cytidylyltransferase, cytidylyltransferase family     |
| non-specific          | 1        | 56             |               | 4.75e-05 | COG1019        | CAB4       | c00015                | Phosphopentehane adenylyltransferase                                      |
| non-specific          | 4        | 50             |               | 4.99e-05 | c02168         | NMNAT_Nudix | c00015                | Nicotinamide/nicotinate mononucleotide adenylyltransferase                 |
| non-specific          | 7        | 56             |               | 5.04e-05 | c02164         | PPAT_CoAS   | c00015                | phosphopentehane adenylyltransferase                                      |
| non-specific          | 3        | 85             |               | 0.000344 | c02156         | nt_trans    | c00015                | nucleotidyl transferase superfamily                                       |
| non-specific          | 1        | 133            |               | 0.000777 | c02170         | cytidylyltransferase | c00015        | cytidylyltransferase                                                  |
| non-specific          | 5        | 55             |               | 0.001778 | c02174         | CCT        | c00015                | CTP:phosphocholine cytidylyltransferase                                   |
| non-specific          | 1        | 57             |               | 0.00191  | c02171         | G3P_Cytidylyltransferase | c00015 | glycerol-3-phosphate cytidylyltransferase                           |
| non-specific          | 8        | 140            |               | 0.005664 | COG0196        | RibF       | c127514                | FAD synthase                                                            |
| superfamily           | 8        | 140            |               | 0.005664 | c127514        | Flavokinase superfamily | -           | Riboflavin kinase                                                   |
| non-specific          | 8        | 64             |               | 0.007382 | PRK07143       | PRK07143   | c127514                | hypothetical protein                                                     |
| specific              | 1        | 140            | 7.89e-71      | 1.10e-03 | PRK13964       | coaD       | c00015                | phosphopentehane adenylyltransferase                                      |
| superfamily           | 1        | 140            | 7.89e-71      | 1.10e-03 | c00015        | nt_trans superfamily | c00015 | nucleotidyl transferase superfamily                                |
| specific              | 1        | 139            | 1.50e-44      | 1.10e-03 | COG0669        | CoaD       | c00015                | phosphopentehane adenylyltransferase                                      |
| specific              | 4        | 133            | 6.78e-41      | 1.10e-03 | c02163         | PPAT       | c00015                | phosphopentehane adenylyltransferase                                      |
| specific              | 4        | 133            | 3.43e-38      | 1.10e-03 | TIGR01510      | coaD_prev_kdB | c00015 | pentetehane-phosphate adenylyltransferase                           |
| specific              | 1        | 133            | 1.34e-37      | 1.10e-03 | PRK00168       | coaD       | c00015                | phosphopentehane adenylyltransferase                                      |
| specific              | 5        | 135            | 1.14e-19      | 1.10e-03 | pfam01467      | CTP_transf like  | c00015 | CTP: transforam-like                                              |
| specific              | 4        | 63             | 2.65e-11      | 1.10e-03 | TIGR00125      | cyt_trn_rel | c00015 | cytidylyltransferase-like domain                                   |
| specific              | 4        | 133            | 3.31e-11      | 1.10e-03 | c02039         | cytidylyltransferase like | c00015 | Cytidylyltransferase-like domain                                   |
| specific              | 1        | 97             | 6.97e-10      | 1.10e-03 | COG01056       | NadR       | c00015                | Nicotinamide mononucleotide adenylyltransferase                           |
| specific              | 1        | 66             | 1.18e-08      | 1.10e-03 | PRK07152       | nadD       | c128367                | putative nicotinate-nucleotide adenylyltransferase                        |
| superfamily           | 1        | 66             | 1.18e-08      | 1.10e-03 | c128367        | nadD superfamily | -           | putative nicotinate-nucleotide adenylyltransferase                    |
| specific              | 4        | 66             | 6.46e-08      | 1.10e-03 | c02165         | NMNAT      | c00015                | Nicotinamide/nicotinate mononucleotide adenylyltransferase                 |
| specific              | 1        | 60             | 2.23e-07      | 1.10e-03 | COG1057        | NadD       | c00015                | Nicotinic acid mononucleotide adenylyltransferase                         |
| specific              | 1        | 66             | 2.33e-07      | 1.10e-03 | PRK00071       | nadD       | c00015                | nicotinic acid mononucleotide adenylyltransferase                         |
| specific              | 4        | 90             | 1.81e-06      | 1.10e-03 | c02156         | nt_trans    | c00015                | nucleotidyl transferase superfamily                                      |
| specific              | 5        | 60             | 4.47e-06      | 1.10e-03 | TIGR00482      | TIGR00482   | c00015                | nicotinate (nicotinamide) nucleotidyl transferase superfamily              |
| specific              | 13       | 39             | 6.07e-05      | 1.10e-03 | pfam02569      | Pantoate_ligase | c00015 | Pantoate-beta-alanine ligase                                     |
| specific              | 5        | 67             | 6.49e-05      | 1.10e-03 | c02167         | NMNAT_NadR | c00015 | Nicotinamide/nicotinate mononucleotide adenylyltransferase           |
| specific              | 4        | 35             | 0.000109      | 1.10e-03 | PRK01153       | PRK01153   | c00015                | nicotinamide-nucleotide adenylyltransferase                               |
| specific              | 8        | 36             | 0.000227      | 1.10e-03 | c02170         | cytidylyltransferase | c00015 | cytidylyltransferase                                               |
| specific              | 4        | 35             | 0.000243      | 1.10e-03 | c02166         | NMNAT_Archaean | c00015 | Nicotinamide/nicotinate mononucleotide adenylyltransferase          |
| specific              | 3        | 35             | 0.00039       | 1.10e-03 | PRK05379       | PRK05379   | c128366                | bifunctional nicotinamide mononucleotide adenylyltransferase             |
| superfamily           | 3        | 35             | 0.00039       | 1.10e-03 | c128366        | PRK05379 superfamily | -           | bifunctional nicotinamide mononucleotide adenylyltransferase          |

**M. bovigenitalium**

**M. bovis**
| Query | Hit type | ID region start | ID region end | E-Value | Accession | Short name | Superfamily | Definition |
|-------|----------|----------------|---------------|---------|-----------|------------|-------------|------------|
| non-specific | 8 | 43 | 0.000079 | COG0615 | TagD | c00015 | Glycerol-3-phosphate cytidylyltransferase, cytidylyltransferase family |
| non-specific | 8 | 134 | 0.00069 | PRK08099 | PRK08099 | c128365 | bifunctional DNA-binding transcriptional repressor/ NMN adenyltransferase |
| superfamily | 8 | 134 | 0.00069 | c128365 | PRK08099 superfamily | - | bifunctional DNA-binding transcriptional repressor/ NMN adenyltransferase |
| non-specific | 1 | 68 | 0.001024 | c002171 | G3P_Cytidylyltransferase | c00015 | glycerol-3-phosphate cytidylyltransferase |
| non-specific | 4 | 139 | 0.0011 | TIGR01527 | arch_NMN_Atrans | c00015 | nicotinamide-nucleotide adenyltransferase |
| non-specific | 13 | 39 | 0.001386 | COG0414 | PanC | c00015 | Pantothenate synthetase |
| non-specific | 13 | 39 | 0.001429 | PRK00308 | panC | c00015 | Pantothenate–beta-alanine ligase |
| non-specific | 13 | 39 | 0.001477 | c000560 | PanC | c00015 | Pantothenate-beta-alanine ligase |
| M. bovis | non-specific | 1 | 49 | 0.001604 | PRK00777 | PRK00777 | c00015 | phosphopantetheine adenyltransferase |
| non-specific | 8 | 69 | 0.001618 | COG1019 | CAB4 | c00015 | Phosphopantetheine adenyltransferase |
| non-specific | 1 | 133 | 0.001948 | TIGR01526 | nadR_NMN_Atrans | c128365 | nicotinamide-nucleotide adenyltransferase |
| non-specific | 5 | 42 | 0.002332 | c002173 | ECT | c00015 | CTP-phosphoethanolamine cytidylyltransferase (ECT) |
| M. buteonis | non-specific | 5 | 52 | 0.002498 | PRK11316 | PRK11316 | c128454 | bifunctional heptose 7-phosphate kinase/heptose 1-phosphate adenyltransferase |
| superfamily | 8 | 52 | 0.002498 | c128454 | RfaE superfamily | - | ADP-heptose synthase, bifunctional sugar kinase/adenyltransferase |
| non-specific | 13 | 39 | 0.002915 | PLN02660 | PLN02660 | c00015 | pantothene–beta-alanine ligase |
| non-specific | 8 | 68 | 0.004536 | TIGR01518 | g3p_cytidylyltrans | c00015 | glycerol-3-phosphate cytidylyltransferase |
| non-family | 7 | 41 | 0.005859 | PTZ0308 | PTZ0308 | c128266 | ethanamine-phosphoethanolamine cytidylyltransferase |
| superfamily | 7 | 41 | 0.005859 | c128266 | PLN02406 superfamily | - | ethanamine-phosphate cytidylyltransferase |
| non-family | 5 | 145 | 1.43e-47 | PRK13964 | coaD | c00015 | phosphopantetheine adenyltransferase |
| superfamily | 5 | 145 | 1.43e-47 | c100015 | nt trans superfamily | - | nucleotidyl transferase superfamily |
| non-family | 4 | 141 | 4.02e-41 | COG0669 | CoaD | c00015 | Phosphopantetheine adenyltransferase |
| non-family | 7 | 139 | 2.75e-38 | c002163 | PPAT | c00015 | Phosphopantetheine adenyltransferase |
| non-family | 7 | 139 | 7.00e-37 | TIGR01510 | coaD prev_kdB | c00015 | pantetheine-adenyltransferase |
| non-family | 5 | 139 | 1.28e-36 | PRK00168 | coaD | c00015 | phosphopantetheine adenyltransferase |
| specific | 9 | 139 | 8.26e-18 | pfam01467 | CTP transf like | c00015 | Cytidylyltransferase-like |
| non-family | 7 | 48 | 5.44e-08 | TIGR00125 | cyt_trans_rel | c00015 | cytidylyltransferase-like domain |
| non-family | 3 | 51 | 1.76e-07 | COG1057 | NadD | c00015 | Nicotinic acid mononucleotide adenyltransferase |
| non-family | 4 | 52 | 1.23e-06 | PRK00071 | nadD | c00015 | nicotinic acid mononucleotide adenyltransferase |
| non-family | 7 | 139 | 2.50e-06 | c002156 | cytidylyltransferase like | c00015 | Cytidylyltransferase-like domain |
| non-family | 5 | 70 | 4.51e-06 | PRK07152 | nadD | c128367 | putative nicotinate-nucleotide adenyltransferase |
| superfamily | 5 | 70 | 4.51e-06 | c128367 | nadD superfamily | - | putative nicotinate-nucleotide adenyltransferase |
| non-family | 7 | 43 | 2.45e-05 | c002165 | NMMAT | c00015 | Nicotinamide/nicotinate mononucleotide adenyltransferase |
| non-family | 9 | 47 | 0.000078 | TIGR00482 | TIGR00482 | c00015 | nicotinate (nicotinamide) nucleotide adenyltransferase |
| non-family | 5 | 39 | 0.000485 | COG1056 | NadR | c00015 | Nicotinamide mononucleotide adenyltransferase |
| non-family | 8 | 124 | 0.001859 | c002156 | nt trans | c00015 | Nucleotidyl transferase superfamily |
| non-family | 8 | 39 | 0.001777 | c002166 | NMMAT_Archaeb | c00015 | Nicotinamide/nicotinate mononucleotide adenyltransferase |
| non-family | 5 | 40 | 0.002714 | PRK00777 | PRK00777 | c00015 | phosphopantetheine adenyltransferase |
| non-family | 8 | 39 | 0.007417 | PRK01153 | PRK01153 | c00015 | phosphopantetheine adenyltransferase |
| Query | Hit type | ID region start | ID region end | E-Value | Accession | Short name | Superfamily | Definition |
|-------|----------|----------------|---------------|---------|-----------|------------|-------------|------------|
| non-specific | 1 | 140 | 6.19e-55 | PRK13964 | coaD | c00015 | phosphopantetheine adenylyltransferase |
| superfamily | 1 | 140 | 6.19e-55 | c100015 | nt trans superfamily | c00015 | nucleotidyl transferase superfamily |
| non-specific | 1 | 134 | 1.63e-42 | COG0669 | coaD | c00015 | phosphopantetheine adenylyltransferase |
| non-specific | 3 | 133 | 3.31e-37 | PRK00168 | coaD | c00015 | phosphopantetheine adenylyltransferase |
| non-specific | 3 | 133 | 7.92e-37 | cd02163 | PPAT | c00015 | phosphopantetheine adenylyltransferase |
| non-specific | 5 | 135 | 1.65e-20 | pfam01467 | CTP trans' like | c00015 | CTPyltransferase-like |
| superfamily | 3 | 56 | 2.09e-10 | TIGR00125 | cyt tran rel | c00015 | cytidylyltransferase-like |
| non-specific | 1 | 66 | 5.55e-10 | PRK00071 | nadD | c00015 | nicotinic acid mononucleotide adenylyltransferase |
| non-specific | 1 | 66 | 3.72e-09 | COG1057 | NadD | c00015 | nicotinic acid mononucleotide adenylyltransferase |
| non-specific | 4 | 66 | 5.98e-09 | cd02165 | NMNAT | c00015 | nicotinamide/nicotinate mononucleotide adenylyltransferase |
| non-specific | 3 | 133 | 1.16e-08 | cd02039 | cytidylyltransferase like | c00015 | cytidylyltransferase-like |
| non-specific | 5 | 66 | 4.47e-07 | TIGR00482 | TIGR00482 | c00015 | nicotinate (nicotinamide) nucleotide adenylyltransferase |
| non-specific | 4 | 58 | 8.49e-07 | PRK05379 | PRK05379 | c128366 | bifunctional nicotinamide mononucleotide adenylyltransferase |
| superfamily | 1 | 66 | 1.60e-06 | COG1056 | NadR | c00015 | nicotinamide mononucleotide adenylyltransferase |
| specific | 4 | 65 | 1.77e-06 | cd02168 | NMNAT Napid | c00015 | nicotinamide/nicotinate mononucleotide adenylyltransferase |
| specific | 5 | 133 | 1.90e-06 | cd02167 | NMNAT Napid | c00015 | nicotinamide/nicotinate mononucleotide adenylyltransferase |
| non-specific | 1 | 71 | 1.05e-05 | PRK07152 | nadD | c128367 | putative nicotinate-nucleotide adenylyltransferase |
| superfamily | 1 | 71 | 1.05e-05 | cd02837 | nadD superfamily | - | putative nicotinate-nucleotide adenylyltransferase |
| non-specific | 3 | 35 | 6.25e-05 | PRK07077 | PRK07077 | c00015 | phosphopantetheine adenylyltransferase |
| specific | 1 | 133 | 0.000161 | TIGR01526 | nadR NMN Atrans | c128365 | nicotinamide-nucleotide adenylyltransferase |
| superfamily | 1 | 133 | 0.000161 | cd028365 | PRK08099 superfamily | - | bifunctional DNA-binding transcriptional repressor/ NMN adenylyltransferase |
| specific | 3 | 35 | 0.000733 | cd02166 | NMNAT Archaea | c00015 | nicotinamide/nicotinate mononucleotide adenylyltransferase |
| specific | 2 | 35 | 0.000152 | PRK01153 | PRK01153 | c00015 | nicotinamide-nucleotide adenylyltransferase |
| non-specific | 3 | 46 | 0.002521 | TIGR01327 | arch NMN Atrans | c00015 | nicotinamide-nucleotide adenylyltransferase |
| non-specific | 3 | 56 | 0.000504 | cd02156 | nt trans | c00015 | nucleotidyl transferase superfamily |
| non-specific | 1 | 36 | 0.006027 | cd02171 | G3P Cytidylyltransferase | c00015 | glycerol-1-phosphate cytidylyltransferase |
| non-specific | 5 | 139 | 6.25e-44 | PRK13964 | coaD | c00015 | phosphopantetheine adenylyltransferase |
| superfamily | 5 | 139 | 6.25e-44 | cd00015 | nt trans superfamily | - | nucleotidyl transferase superfamily |
| specific | 5 | 138 | 6.62e-40 | COG0669 | coaD | c00015 | phosphopantetheine adenylyltransferase |
| non-specific | 6 | 138 | 1.24e-39 | cd02163 | PPAT | c00015 | phosphopantetheine adenylyltransferase |
| specific | 6 | 138 | 7.44e-38 | PRK00168 | coaD | c00015 | phosphopantetheine adenylyltransferase |
| specific | 8 | 138 | 1.27e-19 | pfam01467 | CTP trans' like | c00015 | CTPyltransferase-like |
| specific | 6 | 136 | 4.07e-11 | cd02039 | cytidylyltransferase like | c00015 | CTPyltransferase-like |
| non-specific | 6 | 51 | 2.76e-10 | TIGR00125 | cyt tran rel | c00015 | cytidylyltransferase-like |
| specific | 6 | 51 | 2.44e-08 | COG1056 | NadR | c00015 | nicotinamide mononucleotide adenylyltransferase |
| non-specific | 6 | 38 | 9.48e-08 | cd02166 | NMNAT Archaea | c00015 | nicotinamide/nicotinate mononucleotide adenylyltransferase |
| specific | 5 | 40 | 2.80e-07 | PRK01153 | PRK01153 | c00015 | nicotinamide-nucleotide adenylyltransferase |
| specific | 7 | 58 | 3.06e-07 | cd02165 | NMNAT | c00015 | nicotinamide/nicotinate mononucleotide adenylyltransferase |
| non-specific | 1 | 49 | 7.06e-06 | PRK00071 | nadD | c00015 | nicotinamide mononucleotide adenylyltransferase |
| Query       | Hit type          | ID  | ID     | E-Value | Accession       | Short name          | Superfamily                                      | Definition                                                                 |
|------------|-------------------|-----|--------|---------|-----------------|--------------------|-------------------------------------------------|--------------------------------------------------------------------------------|
| M. capricolum | non-specific | 6   | 38     | 7.70e-06 | TIGR01527       | arch_NM_Atrans     | c00015                                        | nicotinamide-nucleotide adenylyltransferase                           |
| M. capricolum | non-specific | 6   | 58     | 3.07e-05 | cd02156         | nt_trans           | c00015                                        | nucleotidyl transferase superfamily                               |
| M. capricolum | non-specific | 5   | 68     | 4.43e-05 | COG1057         | NadD               | c00015                                        | Nicotinic acid mononucleotide adenylyltransferase                     |
| M. capricolum | non-specific | 5   | 68     | 0.000197 | PRK07152        | nadD               | c128367                                       | putative nicotinate-nucleotide adenylyltransferase                   |
| M. capricolum | superfamily     | 5   | 68     | 0.000197 | c128367         | nadD superfamily   | -                                             | putative nicotinate-nucleotide adenylyltransferase                   |
| M. capricolum | non-specific | 7   | 47     | 0.000295 | PRK05379        | PRK05379           | c128366                                       | bifunctional nicotinamide mononucleotide adenylyltransferase         |
| M. capricolum | superfamily     | 7   | 47     | 0.000295 | c128366         | PRK05379 superfamily | -                                             | bifunctional nicotinamide mononucleotide adenylyltransferase         |
| M. capricolum | non-specific | 1   | 57     | 0.001443 | COG1019         | CAB4               | c00015                                        | Phosphopantetheine adenylyltransferase                              |
| M. capricolum | non-specific | 11  | 36     | 0.002717 | PRK00777        | PRK00777           | c00015                                        | Phosphopantetheine adenylyltransferase                              |
| M. capricolum | non-specific | 7   | 47     | 0.003878 | cd02168         | NMNAT Nudix        | c00015                                        | Nicotinamide/nicotinate mononucleotide adenylyltransferase           |
| M. capricolum | non-specific | 6   | 47     | 0.006711 | cd02173         | ECT                | c00015                                        | CTP:phosphoethanolamine cytidylyltransferase (ECT)                   |
| M. capricolum | non-specific | 21  | 62     | 0.008447 | PT00272         | PT00272            | c127733                                       | heat shock protein 83 kDa (Hsp83)                                   |
| M. capricolum | superfamily     | 21  | 62     | 0.008447 | c127733         | HSP90 superfamily  | -                                             | Hsp90 protein                                                       |
| M. capricolum | specific       | 1   | 140    | 2.82e-73 | PRK13964        | coaD               | c00015                                        | phosphopantetheine adenylyltransferase                              |
| M. capricolum | superfamily     | 1   | 140    | 2.82e-73 | e00015          | nt_trans superfamily| -                                             | nucleotidyl transferase superfamily                                |
| M. capricolum | specific       | 3   | 140    | 1.76e-64 | TIGR01510       | coaD-prev kdhA     | c00015                                        | pantetheine-phosphate adenylyltransferase                           |
| M. capricolum | non-specific   | 1   | 139    | 2.40e-45 | COG00669        | CoaD               | c00015                                        | phosphopantetheine adenylyltransferase                              |
| M. capricolum | non-specific   | 1   | 135    | 3.82e-44 | PRK00168        | coaD               | c00015                                        | phosphopantetheine adenylyltransferase                              |
| M. capricolum | non-specific   | 3   | 139    | 1.89e-43 | cd02163         | PPAT               | c00015                                        | phosphopantetheine adenylyltransferase                              |
| M. capricolum | specific       | 5   | 135    | 5.20e-20 | pfasl04167      | CTP_transf_like    | c00015                                        | Cytidylyltransferase-like                                          |
| M. capricolum | non-specific   | 3   | 63     | 8.10e-14 | TIGR00125       | cyt_transfrel      | c00015                                        | cytidylyltransferase-like domain                                   |
| M. capricolum | specific       | 3   | 134    | 2.99e-11 | cd02039         | cytidylyltransferase_like | c00015                                     | Cytidylyltransferase-like domain                                   |
| M. capricolum | non-specific   | 1   | 77     | 2.61e-10 | PRK07152        | nadD               | c128367                                       | putative nicotinate-nucleotide adenylyltransferase                   |
| M. capricolum | superfamily     | 1   | 77     | 2.61e-10 | c128367         | nadD superfamily   | -                                             | putative nicotinate-nucleotide adenylyltransferase                   |
| M. capricolum | non-specific   | 1   | 66     | 1.68e-08 | COG1057         | NadD               | c00015                                        | Nicotinic acid mononucleotide adenylyltransferase                    |
| M. capricolum | non-specific   | 3   | 77     | 1.43e-07 | cd02165         | NMNAT              | c00015                                        | Nicotinamide/nicotinate mononucleotide adenylyltransferase           |
| M. capricolum | non-specific   | 1   | 46     | 2.31e-07 | COG1056         | NadR               | c00015                                        | Nicotinamide mononucleotide adenylyltransferase                      |
| M. capricolum | non-specific   | 1   | 136    | 2.56e-07 | PRK00777        | PRK00777           | c00015                                        | phosphopantetheine adenylyltransferase                              |
| M. capricolum | non-specific   | 1   | 66     | 3.85e-07 | PRK0071        | nadD               | c00015                                        | nicotinic acid mononucleotide adenylyltransferase                    |
| M. capricolum | non-specific   | 1   | 136    | 6.19e-06 | COG1019         | CAB4               | c00015                                        | Phosphopantetheine adenylyltransferase                              |
| M. capricolum | non-specific   | 1   | 71     | 1.09e-05 | TIGR01526       | nadR_NM_Atrans     | c128365                                       | nicotinamide-nucleotide adenylyltransferase                         |
| M. capricolum | superfamily     | 1   | 71     | 1.09e-05 | c128365         | PRK08099 superfamily | -                                             | bifunctional DNA-binding transcriptional repressor/ NMN adenylyltransferase |
| M. capricolum | non-specific   | 3   | 134    | 1.30e-05 | cd02167         | NMNAT_NadR         | c00015                                        | Nicotinamide/nicotinate mononucleotide adenylyltransferase           |
| M. capricolum | non-specific   | 4   | 130    | 4.30e-05 | cd02156         | nt_trans           | c00015                                        | nucleotidyl transferase superfamily                                |
| M. capricolum | non-specific   | 4   | 35     | 7.26e-05 | cd02166         | NMNAT_Archea       | c00015                                        | Nicotinamide/nicotinate mononucleotide adenylyltransferase           |
| M. capricolum | non-specific   | 4   | 68     | 0.00016 | TIGR01527       | arch_NM_Atrans     | c00015                                        | nicotinamide-nucleotide adenylyltransferase                         |
| M. capricolum | non-specific   | 4   | 35     | 0.000417 | PRK01153        | PRK01153           | c00015                                        | nicotinamide-nucleotide adenylyltransferase                         |
| M. capricolum | non-specific   | 3   | 35     | 0.000499 | PRK05379        | PRK05379           | c128366                                       | bifunctional nicotinamide mononucleotide adenylyltransferase        |
| M. capricolum | superfamily     | 3   | 35     | 0.000499 | c128366         | PRK05379 superfamily | -                                             | bifunctional nicotinamide mononucleotide adenylyltransferase        |
| M. capricolum | non-specific   | 5   | 60     | 0.002833 | TIGR00482       | TIGR00482          | c00015                                        | nicotinate (nicotinamide) nucleotide adenylyltransferase            |
| M. capricolum | non-specific   | 1   | 36     | 0.003701 | cd02171         | G3P_Cytidylyltransferase | c00015                                     | glycerol-3-phosphate cytidylyltransferase                          |
| M. capricolum | non-specific   | 8   | 57     | 0.004943 | cd02170         | cytidylyltransferase | c00015                                        | cytidylyltransferase                                               |
| Query       | Hit type | ID region start | ID region end | E-Value     | Accession | Short name | Superfamily                     | Definition                                                                 |
|-------------|----------|-----------------|---------------|-------------|-----------|------------|---------------------------------|----------------------------------------------------------------------------|
| M. columbinum | non-specific | 1 | 76 | 0.004984 | PRK08887 |            | c00015 | nicotinic acid mononucleotide adenylyltransferase |
|             | non-specific | 8 | 145 | 7.72e-33 | PRK13964 |            | c00015 | phosphopantetheine adenylyltransferase |
|             | superfamily | 8 | 145 | 7.72e-53 | c00015 |            | c00015 | nucleotidytransferase superfamily |
|             | non-specific | 6 | 140 | 4.38e-34 | COG0669  |            | c00015 | Phosphopantetheine adenylyltransferase |
|             | non-specific | 9 | 137 | 1.17e-42  | cd02163  |            | c00015 | Phosphopantetheine adenylyltransferase |
|             | non-specific | 9 | 139 | 1.11e-40  | TIGR01510 |            | c00015 | pantetheine-phosphate adenylyltransferase |
|             | non-specific | 11 | 141 | 2.23e-16  | pfam1467 |            | c00015 | Cytidylyltransferase-like |
|             | non-specific | 9 | 69 | 3.49e-10  | TIGR00125 |            | c00015 | cytidylyltransferase-like domain |
|             | non-specific | 9 | 139 | 2.01e-08  | cd02039  | cytidylyltransferase-like | c00015 | Cytidylyltransferase-like domain |
|             | non-specific | 10 | 72 | 1.02e-06  | cd02165  | NNMAT      | c00015 | Nicotinamide/nicotinate mononucleotide adenylyltransferase |
|             | non-specific | 8 | 41 | 1.43e-05  | PRK01153 |            | c00015 | nicotinamide-nucleotide adenylyltransferase |
|             | non-specific | 9 | 64 | 2.26e-05  | cd02156  |            | c00015 | nucleotidytransferase superfamily |
|             | non-specific | 9 | 41 | 6.88e-05  | cd02166  | NNMAT_Archaearna | c00015 | Nicotinamide/nicotinate mononucleotide adenylyltransferase |
|             | non-specific | 8 | 72 | 8.18e-05  | COG1057  | NadD       | c00015 | Nicotinic acid mononucleotide adenylyltransferase |
|             | non-specific | 8 | 41 | 9.27e-05  | COG1056  | NadR       | c00015 | Nicotinamide mononucleotide adenylyltransferase |
|             | superfamily | 10 | 57 | 0.000585 | PRK05379 |            | c00015 | bifunctional nicotinamide mononucleotide adenylyltransferase |
|             | superfamily | 10 | 57 | 0.000585 | c28366  | PRK05379 superfamily | c00015 | bifunctional nicotinamide mononucleotide adenylyltransferase |
|             | non-specific | 7 | 48 | 0.000824 | PRK00071 | nadD       | c00015 | nicotinic acid mononucleotide adenylyltransferase |
| M. collis   | non-specific | 7 | 77 | 0.001049 | cd02170  |            | c00015 | cytidylyltransferase |
|             | non-specific | 11 | 139 | 0.001357 | cd02167  | NNMAT_NadR | c00015 | Nicotinamide/nicotinate mononucleotide adenylyltransferase |
|             | superfamily | 8 | 72 | 0.001399 | PRK07152 | nadD superfamily | c00015 | putative nicotinate-nucleotide adenylyltransferase |
|             | superfamily | 8 | 72 | 0.001399 | PRK07152 | nadD superfamily | c00015 | putative nicotinate-nucleotide adenylyltransferase |
|             | superfamily | 11 | 45 | 0.00196  | TIGR00482 |            | c00015 | nicotinate (nicotinamide) nucleotide adenylyltransferase |
|             | superfamily | 13 | 57 | 0.002052 | cd02173  | ECT        | c00015 | CTP-phosphoehanolamine cytidylyltransferase (ECT) |
| M. collis   | non-specific | 18 | 73 | 0.004238 | smart00764 |            | c00015 | Citrate lyase C-terminal domain |
|             | non-specific | 20 | 55 | 0.004977 | COG0414  | PnC        | c00015 | Pantetheinase synthetase |
|             | non-specific | 18 | 73 | 0.005843 | cd02169  |            | c00015 | Citrate lyase ligase |
|             | superfamily | 14 | 49 | 0.007424 | cd02174  |            | c00015 | CTP-phosphocholine cytidylyltransferase |
|             | superfamily | 2 | 141 | 2.76e-62 | PRK13964 | coaD       | c00015 | phosphopantetheine adenylyltransferase |
| M. columbinum | superfamily | 2 | 141 | 2.76e-62 | c00015 |            | c00015 | nucleotidytransferase superfamily |
|             | non-specific | 1 | 141 | 4.83e-44 | COG0669  |            | c00015 | Phosphopantetheine adenylyltransferase |
|             | non-specific | 4 | 135 | 3.24e-38 | cd02163  |            | c00015 | Phosphopantetheine adenylyltransferase |
|             | non-specific | 4 | 135 | 1.49e-37 | TIGR01510 |            | c00015 | pantetheine-phosphate adenylyltransferase |
|             | superfamily | 2 | 135 | 4.49e-36 | PRK00168 |            | c00015 | phosphopantetheine adenylyltransferase |
|             | superfamily | 6 | 137 | 6.97e-19 | pfam1467 |            | c00015 | Cytidylyltransferase-like |
|             | superfamily | 4 | 135 | 8.19e-11 | cd02039  |            | c00015 | Cytidylyltransferase-like domain |
|             | superfamily | 4 | 44 | 1.63e-10 | TIGR00125 |            | c00015 | cytidylyltransferase-like domain |
| M. columbinum | non-specific | 1 | 59 | 2.73e-10 | COG1057  | NadD       | c00015 | Nicotinic acid mononucleotide adenylyltransferase |
|             | non-specific | 1 | 68 | 4.32e-10 | PRK00071 |            | c00015 | nicotinic acid mononucleotide adenylyltransferase |
|             | non-specific | 4 | 42 | 7.86e-08 | cd02163  | NNMAT      | c00015 | Nicotinamide/nicotinate mononucleotide adenylyltransferase |
|             | non-specific | 1 | 36 | 1.62e-06 | COG1056  | NadR       | c00015 | Nicotinamide mononucleotide adenylyltransferase |
|             | non-specific | 2 | 49 | 3.02e-06 | PRK07152 |            | c00015 | putative nicotinate-nucleotide adenylyltransferase |
| Query     | Hit type  | ID region start | ID region end | E-Value | Accession | Short name | Superfamily                                                                 | Definition                                                                 |
|-----------|-----------|-----------------|---------------|---------|-----------|------------|--------------------------------------------------------------------------------|----------------------------------------------------------------------------|
| superfamily | 2        | 49              |               | 3.02e-06| c128367   | nadD       | superfamily                                                      | putative nicotinate-nucleotide adenylyltransferase                         |
| non-specific | 4       | 36              | 6.72e-06      | PRK05379 | c128366   | PRK05379   | superfamily                                                      | bifunctional nicotinamide mononucleotide adenylyltransferase             |
| superfamily | 4        | 36              | 14e-05        | c128366   | PRK05379   | superfamily                                                      | bifunctional nicotinamide mononucleotide adenylyltransferase             |
| non-specific | 6       | 61              | 14e-05        | TIGR00482| c128366   | TIGR00482  | superfamily                                                      | nicotinate (nicotinamide) nucleotide adenylyltransferase                 |
| non-specific | 5       | 54              | 144e-05       | cd02166  | NMNAT_Archaearubescens | c000015 | Nicotinamide/nicotinate mononucleotide adenylyltransferase         |                                                                            |
| non-specific | 4        | 37              | 0000128       | PRK08887 | c000015   | PRK08887   | superfamily                                                      | nicotinate/nicotinate mononucleotide adenylyltransferase                 |
| non-specific | 5        | 65              | 0000329       | TIGR01526| c000015   | TIGR01526  | superfamily                                                      | nicotinate-nucleotide adenylyltransferase                                |
| superfamily | 2        | 37              | 0000329       | c128365   | PRK080999 | PRK080999  | superfamily                                                      | bifunctional DNA-binding transcriptional repressor/ NMN adenylyltransferase |
| non-specific | 5        | 36              | 0000493       | PRK01153 | c000015   | PRK01153   | superfamily                                                      | nicotinamide-nucleotide adenylyltransferase                              |
| non-specific | 1        | 37              | 00119         | cd02170  | c000015   | cd02170    | superfamily                                                      | cytidylyltransferase                                                     |
| non-specific | 15       | 40              | 0001861       | cd00560  | c000015   | cd00560    | superfamily                                                      | Pantoate-beta-alanine ligsan                                             |
| non-specific | 5        | 64              | 8160-05      | TIGR01527| c000015   | TIGR01527  | superfamily                                                      | nicotinamide-nucleotide adenylyltransferase                              |
| non-specific | 1        | 38              | 0000128       | PRK08887 | c000015   | PRK08887   | superfamily                                                      | nicotinate acid mononucleotide adenylyltransferase                       |
| non-specific | 5        | 65              | 0000329       | TIGR01526| c000015   | TIGR01526  | superfamily                                                      | nicotinate acid mononucleotide adenylyltransferase                       |
| superfamily | 2        | 37              | 0000329       | c128365   | PRK080999 | PRK080999  | superfamily                                                      | bifunctional DNA-binding transcriptional repressor/ NMN adenylyltransferase |
| non-specific | 5        | 36              | 0000493       | PRK01153 | c000015   | PRK01153   | superfamily                                                      | nicotinamide-nucleotide adenylyltransferase                              |
| non-specific | 1        | 37              | 00119         | cd02170  | c000015   | cd02170    | superfamily                                                      | cytidylyltransferase                                                     |
| non-specific | 15       | 40              | 0001861       | cd00560  | c000015   | cd00560    | superfamily                                                      | Pantoate-beta-alanine ligsan                                             |
| non-specific | 5        | 64              | 8160-05      | TIGR01527| c000015   | TIGR01527  | superfamily                                                      | nicotinamide-nucleotide adenylyltransferase                              |
| non-specific | 1        | 38              | 0000128       | PRK08887 | c000015   | PRK08887   | superfamily                                                      | nicotinate acid mononucleotide adenylyltransferase                       |
| superfamily | 2        | 37              | 0000329       | c128365   | PRK080999 | PRK080999  | superfamily                                                      | bifunctional DNA-binding transcriptional repressor/ NMN adenylyltransferase |
| non-specific | 5        | 36              | 0000493       | PRK01153 | c000015   | PRK01153   | superfamily                                                      | nicotinamide-nucleotide adenylyltransferase                              |
| non-specific | 1        | 37              | 00119         | cd02170  | c000015   | cd02170    | superfamily                                                      | cytidylyltransferase                                                     |
| non-specific | 15       | 40              | 0001861       | cd00560  | c000015   | cd00560    | superfamily                                                      | Pantoate-beta-alanine ligsan                                             |
| non-specific | 5        | 64              | 8160-05      | TIGR01527| c000015   | TIGR01527  | superfamily                                                      | nicotinamide-nucleotide adenylyltransferase                              |
| non-specific | 1        | 38              | 0000128       | PRK08887 | c000015   | PRK08887   | superfamily                                                      | nicotinate acid mononucleotide adenylyltransferase                       |
| superfamily | 2        | 37              | 0000329       | c128365   | PRK080999 | PRK080999  | superfamily                                                      | bifunctional DNA-binding transcriptional repressor/ NMN adenylyltransferase |
| non-specific | 5        | 36              | 0000493       | PRK01153 | c000015   | PRK01153   | superfamily                                                      | nicotinamide-nucleotide adenylyltransferase                              |
| non-specific | 1        | 37              | 00119         | cd02170  | c000015   | cd02170    | superfamily                                                      | cytidylyltransferase                                                     |
| non-specific | 15       | 40              | 0001861       | cd00560  | c000015   | cd00560    | superfamily                                                      | Pantoate-beta-alanine ligsan                                             |
| non-specific | 5        | 64              | 8160-05      | TIGR01527| c000015   | TIGR01527  | superfamily                                                      | nicotinamide-nucleotide adenylyltransferase                              |
| non-specific | 1        | 38              | 0000128       | PRK08887 | c000015   | PRK08887   | superfamily                                                      | nicotinate acid mononucleotide adenylyltransferase                       |
| superfamily | 2        | 37              | 0000329       | c128365   | PRK080999 | PRK080999  | superfamily                                                      | bifunctional DNA-binding transcriptional repressor/ NMN adenylyltransferase |
| non-specific | 5        | 36              | 0000493       | PRK01153 | c000015   | PRK01153   | superfamily                                                      | nicotinamide-nucleotide adenylyltransferase                              |
| non-specific | 1        | 37              | 00119         | cd02170  | c000015   | cd02170    | superfamily                                                      | cytidylyltransferase                                                     |
| non-specific | 15       | 40              | 0001861       | cd00560  | c000015   | cd00560    | superfamily                                                      | Pantoate-beta-alanine ligsan                                             |
| non-specific | 5        | 64              | 8160-05      | TIGR01527| c000015   | TIGR01527  | superfamily                                                      | nicotinamide-nucleotide adenylyltransferase                              |
| non-specific | 1        | 38              | 0000128       | PRK08887 | c000015   | PRK08887   | superfamily                                                      | nicotinate acid mononucleotide adenylyltransferase                       |
| M. columbarale | 40 | 38              | 00123         | PRK00777 | c000015   | PRK00777   | superfamily                                                      | phosphopantetheine adenylyltransferase                                  |

- **M. columbarale**
- **M. columbinum**
| Query | Hit type | ID | ID region start | ID region end | E-Value | Accession | Short name | Superfamily | Definition |
|-------|----------|----|-----------------|---------------|---------|-----------|------------|-------------|------------|
| non-specific | 1 | 135 | 0.0000343 | cd02167 | NNMAT_NadR | c000015 | Nicotinamide/nicotinate mononucleotide adenylyltransferase |
| non-specific | 4 | 0.001285 | TIGR01526 | nadR_NMN_Atrans | c28365 | nicotinamide-nucleotide adenyltransferase |
| superfamily | 4 | 0.001285 | c28365 | PRK08099 superfamily | - | - |
| non-specific | 1 | 135 | 0.001697 | TIGR00482 | TIGR00482 | c000015 | nicotinamide/nicotinate mononucleotide adenylyltransferase |
| non-specific | 1 | 0.031386 | PRK05379 | PRK05379 | c28366 | nicotinamide-nucleotide adenyltransferase |
| superfamily | 1 | 0.031386 | c28366 | PRK05379 superfamily | - | - |
| non-specific | 10 | 0.03564 | cd02164 | PPAT_CoAS | c000015 | phosphopantetheine adenyltransferase |
| non-specific | 5 | 0.066841 | PRK01170 | PRK01170 | c000866 | phosphopantetheine adenyltransferase |
| superfamily | 5 | 0.066841 | c000866 | NTPase_I-T superfamily | - | - |
| non-specific | 6 | 0.008472 | cd02166 | NNMAT_Archaea | c000015 | Nicotinamide/nicotinate mononucleotide adenylyltransferase |
| specific | 10 | 138 | 0.008472 | COG0069 | CoaD | c000015 | phosphopantetheine adenyltransferase |
| superfamily | 10 | 0.008472 | cd02166 | PRK013964 | PRK013964 | - | - |
| non-specific | 10 | 148 | 0.008472 | PRK013964 | PRK013964 | - | - |
| non-specific | 13 | 140 | 0.008472 | cd02164 | PRK01135 | PRK01135 | - | - |
| non-specific | 13 | 140 | 0.008472 | cd02164 | PRK01135 | PRK01135 | - | - |
| superfamily | 13 | 0.008472 | cd02164 | PRK01135 | PRK01135 | - | - |
| non-specific | 13 | 140 | 0.008472 | cd02164 | PRK01135 | PRK01135 | - | - |
| non-specific | 10 | 148 | 0.008472 | cd02164 | PRK01135 | PRK01135 | - | - |
| superfamily | 10 | 0.008472 | cd02164 | PRK01135 | PRK01135 | - | - |
| non-specific | 13 | 140 | 0.008472 | cd02164 | PRK01135 | PRK01135 | - | - |
| non-specific | 13 | 140 | 0.008472 | cd02164 | PRK01135 | PRK01135 | - | - |
| superfamily | 13 | 0.008472 | cd02164 | PRK01135 | PRK01135 | - | - |

**M. conjunctivae**

- **Query**: non-specific, specific, superfamily
- **E-Value**: 0.000015, 0.000015, 0.000015
- **Accession**: COG1056, COG1056, COG1056
- **Short name**: NadR, NadR, NadR
- **Superfamily**: -

**Definition**: Nicotinamide mononucleotide adenylyltransferase.
| Query | Hit type | ID region start | ID region end | E-Value | Accession | Short name | Superfamily | Definition |
|-------|----------|----------------|--------------|---------|-----------|------------|-------------|------------|
| non-specific | 10 | 45 | | 0.002877 | cd02171 | G3P Cytidylyltransferase | cd00015 | glycerol-3-phosphate cytidylyltransferase |
| non-specific | 22 | 48 | | 0.003383 | PRK00380 | panC | cd00015 | pantoate-beta-alanine ligase |
| non-specific | 25 | 80 | | 0.00385 | smart00754 | Citrate ly lig | cd00015 | Citrate lyase ligase C-terminal domain |
| non-specific | 22 | 48 | | 0.004388 | cd00560 | PanC | cd00015 | Pantoate-beta-alanine ligase |
| non-specific | 17 | 51 | | 0.004435 | TIGR02199 | rfaE_dom II | cd00015 | rfaE bifunctional protein, domain II |
| non-specific | 25 | 80 | | 0.005019 | cd02169 | Citrate lyase ligase | cd00015 | Citrate lyase ligase |
| M. conjunctivae | | | | | | | | |
| non-specific | 13 | 44 | | 0.006585 | cd02168 | NMNAT Nudix | cd00015 | Nicotinamide/nicotinate mononucleotide adenyltransferase |
| non-specific | 17 | 96 | | 0.007066 | PRK05627 | PRK05827 | cl27514 | bifunctional riboflavin kinase/FMN adenyltransferase |
| superfamily | 17 | 96 | | 0.007066 | cd17514 | Flavokinase superfamily | - | Riboflavin kinase |
| non-specific | 2 | 50 | | 0.009592 | PRK08099 | PRK08099 | cl28365 | bifunctional DNA-binding transcriptional repressor/ NMN adenyltransferase |
| non-specific | 3 | 142 | | 2.92e-62 | PRK13964 | coaD | cd00015 | phosphopantetheine adenyltransferase |
| superfamily | 3 | 142 | | 2.92e-62 | e100015 | nt_trans superfamily | - | nucleotidyl transferase superfamily |
| non-specific | 4 | 136 | | 8.86e-48 | COG0669 | coaD | cd00015 | Phosphopantetheine adenyltransferase |
| non-specific | 5 | 135 | | 1.57e-44 | cd02165 | PPAT | cd00015 | Phosphopantetheine adenyltransferase |
| non-specific | 5 | 135 | | 9.74e-44 | TIGR01510 | coaD prev_kdB | cd00015 | pantetheine-phosphate adenyltransferase |
| non-specific | 4 | 135 | | 1.86e-43 | PRK00168 | coaD | cd00015 | phosphopantetheine adenyltransferase |
| specific | 7 | 137 | | 1.52e-21 | pfam01467 | CTP transf like | cd00015 | Cytidylyltransferase-like |
| non-specific | 5 | 65 | | 1.46e-11 | TIGR00125 | cyt_trans like | cd00015 | cytidylyltransferase-like domain |
| non-specific | 1 | 68 | | 1.52e-11 | PRK00071 | nadD | cd00015 | nicotinic acid mononucleotide adenyltransferase |
| non-specific | 5 | 68 | | 1.17e-10 | cd02165 | NMNAT | cd00015 | Nicotinamide/nicotinate mononucleotide adenyltransferase |
| non-specific | 1 | 57 | | 7.02e-09 | COG1057 | NadD | cd00015 | Nicotinic acid adenyltransferase |
| non-specific | 4 | 68 | | 2.03e-08 | PRK07152 | nadD | cd00015 | nicotinamide-nucleotide adenyltransferase |
| superfamily | 4 | 68 | | 2.03e-08 | cl28367 | nadD superfamily | - | putative nicotinate-nucleotide adenyltransferase |
| non-specific | 5 | 135 | | 4.94e-08 | PRK00203 | cytidylyltransferase_like | cd00015 | Cytidylyltransferase-like domain |
| M. cricetuli | | | | | | | | |
| non-specific | 1 | 37 | | 3.32e-07 | COG1056 | NadR | cd00015 | Nicotinamide mononucleotide adenyltransferase |
| non-specific | 6 | 48 | | 1.27e-06 | cd02156 | nt_trans | cd00015 | nucleotidyl transferase superfamily |
| non-specific | 5 | 135 | | 2.47e-06 | cd02167 | NMNAT NadR | cd00015 | Nicotinamide/nicotinate mononucleotide adenyltransferase |
| non-specific | 1 | 136 | | 1.48e-05 | PRK08099 | PRK08099 | cl28365 | bifunctional DNA-binding transcriptional repressor/ NMN adenyltransferase |
| superfamily | 1 | 136 | | 1.48e-05 | cl28365 | PRK08099 superfamily | - | bifunctional DNA-binding transcriptional repressor/ NMN adenyltransferase |
| non-specific | 7 | 57 | | 1.51e-05 | TIGR00482 | TIGR00482 | cd00015 | nicotinate (nicotinamide) nucleotide adenyltransferase |
| non-specific | 4 | 44 | | 2.42e-05 | PTZ00308 | PTZ00308 | cl28365 | ethanolamine-phosphate cytidylyltransferase |
| superfamily | 4 | 44 | | 2.42e-05 | cl28626 | PLN02406 superfamily | - | ethanolamine-phosphate cytidylyltransferase |
| non-specific | 10 | 38 | | 0.000143 | COG0615 | TagD | cd00015 | Glycerol-3-phosphate cytidylyltransferase, cytidylyltransferase family |
| non-specific | 10 | 38 | | 0.000178 | cd02170 | cytidylyltransferase | cd00015 | cytidylyltransferase |
| non-specific | 6 | 37 | | 0.000211 | PRK01153 | PRK01153 | cd00015 | nicotinamide-nucleotide adenyltransferase |
| non-specific | 10 | 35 | | 0.00061 | PRK00777 | PRK00777 | cd00015 | phosphopantetheine adenyltransferase |
| non-specific | 7 | 43 | | 0.000627 | cd02173 | ECT | cd00015 | CTP:phosphoethanolamine cytidylyltransferase (ECT) |
| non-specific | 6 | 37 | | 0.000779 | cd02166 | NMNAT Archaea | cd00015 | Nicotinamide/nicotinate mononucleotide adenyltransferase |
| non-specific | 4 | 74 | | 0.001273 | TIGR01526 | nadR_NMNAtrans | cl28365 | nicotinamide-nucleotide adenyltransferase |
| Query | Hit type | ID region start | ID region end | E-Value | Accession | Short name | Superfamily | Definition |
|-------|----------|-----------------|---------------|---------|-----------|------------|-------------|------------|
| non-specific | 4 | 38 | 0.005008 | cd02171 | G3P Cytidyltransferase | c00015 | Phosphopantetheine adenyltransferase |
| non-specific | 4 | 43 | 0.005313 | TIGR02199 | rraf, dom I | c00015 | Phosphopantetheine adenyltransferase |
| superfamily | 1 | 37 | 0.008315 | PRK05379 | bifunctional nicotinamide mononucleotide adenyltransferase |
| non-specific | 10 | 37 | 0.007769 | COG1019 | CAB4 | c00015 | Phosphopantetheine adenyltransferase |
| specific | 5 | 146 | 5.89e-66 | PRK13964 | coaD | c00015 | Phosphopantetheine adenyltransferase |
| superfamily | 5 | 146 | 5.89e-66 | e00015 | nt trans superfamily | - | - |
| non-specific | 6 | 140 | 1.71e-39 | COG0669 | coaD | c00015 | Phosphopantetheine adenyltransferase |
| non-specific | 7 | 137 | 2.40e-34 | e02163 | PPAT | c00015 | Phosphopantetheine adenyltransferase |
| non-specific | 7 | 146 | 2.85e-34 | TIGR01510 | coaD prev_polyB | c00015 | Pantetheine-phosphate adenyltransferase |
| non-specific | 6 | 137 | 8.79e-31 | PRK00168 | coaD | c00015 | Phosphopantetheine adenyltransferase |
| specific | 7 | 141 | 8.01e-14 | pfam01467 | CTP trans' like | c00015 | Cytidyltransferase-like |
| non-specific | 7 | 58 | 5.67e-06 | TIGR00125 | cyt tran-rel | c00015 | Cytidyltransferase-like domain |
| non-specific | 7 | 139 | 0.000547 | e02039 | cytidyltransferase like | c00015 | Cytidyltransferase-like domain |
| non-specific | 8 | 71 | 0.008926 | e02165 | NNMAT | c00015 | Nicotinamide/nicotinate mononucleotide adenyltransferase |
| non-specific | 3 | 142 | 8.93e-66 | PRK13964 | coaD | c00015 | Phosphopantetheine adenyltransferase |
| superfamily | 3 | 142 | 8.93e-66 | e00015 | nt trans superfamily | - | - |
| non-specific | 3 | 136 | 1.15e-51 | COG0669 | coaD | c00015 | Phosphopantetheine adenyltransferase |
| non-specific | 5 | 142 | 3.50e-47 | TIGR01510 | coaD prev_polyB | c00015 | Pantetheine-phosphate adenyltransferase |
| non-specific | 5 | 135 | 1.94e-46 | e02163 | PPAT | c00015 | Phosphopantetheine adenyltransferase |
| non-specific | 3 | 135 | 3.41e-46 | PRK00168 | coaD | c00015 | Phosphopantetheine adenyltransferase |
| specific | 7 | 135 | 1.99e-24 | pfam01467 | CTP trans' like | c00015 | Cytidyltransferase-like |
| non-specific | 5 | 65 | 5.00e-14 | TIGR00125 | cyt tran-rel | c00015 | Cytidyltransferase-like domain |
| non-specific | 5 | 135 | 6.32e-14 | e02039 | cytidyltransferase like | c00015 | Cytidyltransferase-like domain |
| non-specific | 6 | 17 | 1.77e-10 | COG1056 | NadR | c00015 | Nicotinamide mononucleotide adenyltransferase |
| specific | 7 | 57 | 6.34e-09 | PRK00071 | nadD | c00015 | nicotinic acid mononucleotide adenyltransferase |
| non-specific | 6 | 135 | 1.07e-08 | e02166 | NNMAT Archaea | c00015 | Nicotinamide/nicotinate mononucleotide adenyltransferase |
| non-specific | 1 | 57 | 3.39e-08 | COG1057 | NadD | c00015 | Nicotinamide mononucleotide adenyltransferase |
| non-specific | 6 | 70 | 1.08e-07 | TIGR01527 | arch NMN Ars | c00015 | Nicotinamide-mononucleotide adenyltransferase |
| non-specific | 6 | 37 | 1.65e-07 | PRK01153 | PRK01153 | c00015 | Nicotinamide-mononucleotide adenyltransferase |
| non-specific | 5 | 135 | 3.51e-07 | e02167 | NNMAT NadR | c00015 | Nicotinamide/nicotinate mononucleotide adenyltransferase |
| non-specific | 5 | 44 | 8.59e-07 | e02165 | NMMAT | c00015 | Nicotinamide/nicotinate mononucleotide adenyltransferase |
| non-specific | 3 | 69 | 1.08e-06 | PRK07152 | nadD | c028367 | Putative nicotinamide-nucleotide adenyltransferase |
| superfamily | 3 | 69 | 1.08e-06 | e28367 | nadD superfamily | c028367 | Putative nicotinamide-nucleotide adenyltransferase |
| non-particular | 7 | 54 | 1.57e-06 | TIGR00482 | TIGR00482 | c00015 | Nicotinamide/nicotinate adenyltransferase |
| non-specific | 3 | 71 | 3.90e-24 | COG1019 | CAB4 | c00015 | Phosphopantetheine adenyltransferase |
| non-specific | 1 | 136 | 3.35e-05 | PRK08099 | PRK08099 | c28365 | Bifunctional DNA-binding transcriptional repressor/ NMN adenyltransferase |
| superfamily | 1 | 136 | 3.35e-05 | e28365 | PRK08099 superfamily | - | - |
| non-specific | 5 | 41 | 3.99e-05 | e02156 | nt trans | c00015 | Nucleotidyl transferase superfamily |
| non-specific | 3 | 65 | 6.86e-05 | PRK00777 | PRK00777 | c00015 | Phosphopantetheine adenyltransferase |
| non-specific | 1 | 37 | 0.00119 | PRK05379 | PRK05379 | c28366 | Bifunctional nicotinamide mononucleotide adenyltransferase |
| Query                     | Hit type       | ID  | ID  | E-Value | Accession          | Short name          | Superfamily                     | Definition                                                                 |
|--------------------------|----------------|-----|-----|---------|--------------------|---------------------|--------------------------------|--------------------------------------------------------------------------------|
| superfamily              | non-specific   | 3   | 38  | 0.009316 | TIGR01526         | nadR_NMN_Atrans     | c28365                        | nicotinamide-nucleotide adenyltransferase                                   |
|                          | non-specific   | 4   | 44  | 0.000666 | c02173            | CCT                 | c00015                        | CTP:phosphoethanolamine cytidylyltransferase (ECT)                          |
|                          | non-specific   | 10  | 57  | 0.000689 | c02174            | CCT                 | c00015                        | CTP:phosphocholine cytidylyltransferase                                    |
|                          | non-specific   | 3   | 38  | 0.000828 | c02170            | cytidylyltransferase | c00015                        | cytidylyltransferase                                                        |
|                          | non-specific   | 2   | 45  | 0.001162 | COG0615           | TagD                | c00015                        | Glycerol-3-phosphate cytidylyltransferase, cytidylyltransferase family       |
|                          | non-specific   | 3   | 43  | 0.001447 | c02172            | RfE_N               | c00015                        | N-terminal domain of RfE                                                    |
|                          | non-specific   | 5   | 27  | 0.002937 | c02168            | NMNAT_Nudix         | c00015                        | Nicotinamide/nicotinate mononucleotide adenyltransferase                    |
|                          | non-specific   | 4   | 56  | 0.002975 | PTZ00308         | PTZ00308            | c283626                       | ethanolamine-phosphate cytidylyltransferase                                 |
| superfamily              | non-specific   | 4   | 56  | 0.002975 | c128626        | PLN02406 superfamily | c00015                        | ethanolamine-phosphate cytidylyltransferase                                 |
|                          | non-specific   | 10  | 88  | 0.005345 | PRK07143          | PRK07143            | c27514                        | hypothetical protein                                                        |
|                          | superfamily    | 10  | 88  | 0.005345 | c27514            | Flavokinase superfamily | -                            | Riboflavin kinase                                                           |
|                          | non-specific   | 16  | 48  | 0.006602 | pfam02569         | Pantoate_beta-alanine_ligase | c00015                        | Pantoate-beta-alanine ligase                                                |
|                          | non-specific   | 5   | 41  | 0.008476 | c02064            | FAD_synthase_N      | c00015                        | FAD synthetase, N-terminal domain of the bifunctional enzyme                |
|                          | non-specific   | 2   | 136 | 6.63e-51 | PRK13964          | coaD                 | c00015                        | phosphopantetheine adenyltransferase                                       |
| superfamily              | non-specific   | 2   | 136 | 6.63e-51 | c00015            | nt_trans superfamily | c00015                        | nucleotidyl transferase superfamily                                        |
|                          | non-specific   | 1   | 133 | 4.17e-41 | COG00609          | CoaD                | c00015                        | Phosphopantetheine adenyltransferase                                       |
|                          | non-specific   | 5   | 133 | 2.40e-39 | TIGR01510         | coaD_prev_kdB       | c00015                        | pantetheine-phosphate adenyltransferase                                    |
|                          | non-specific   | 5   | 131 | 4.17e-38 | c02163            | PPAT                | c00015                        | Phosphopantetheine adenyltransferase                                       |
|                          | non-specific   | 5   | 131 | 0.97e-34 | PRK00168          | coaD                 | c00015                        | phosphopantetheine adenyltransferase                                       |
|                          | specific       | 6   | 135 | 1.82e-19 | pfam01467         | CTP_transf_like     | c00015                        | Cytidyltransferase-like                                                     |
|                          | non-specific   | 5   | 48  | 5.61e+10 | TIGR00125         | cyt_trans_rel       | c00015                        | cytidylyltransferase-like domain                                            |
|                          | non-specific   | 1   | 76  | 3.69e-07 | COG1057           | NadD                | c00015                        | Nicotinic acid mononucleotide adenyltransferase                             |
|                          | non-specific   | 5   | 134 | 3.99e-07 | c02039            | cytidylyltransferase_like | c00015                        | Cytidylyltransferase-like domain                                            |
|                          | non-specific   | 5   | 76  | 5.29e-07 | c02165            | NNMAT               | c00015                        | Nicotinamide/nicotinate mononucleotide adenyltransferase                    |
|                          | non-specific   | 5   | 62  | 1.01e+06 | c02166            | NNMAT_Archaea       | c00015                        | Nicotinamide/nicotinate mononucleotide adenyltransferase                    |
|                          | non-specific   | 1   | 76  | 3.92e-06 | PRK00071          | nadD                | c00015                        | nicotinic acid mononucleotide adenyltransferase                             |
|                          | non-specific   | 1   | 46  | 1.13e-05 | COG01056          | NADP                | c00015                        | Nicotinamide mononucleotide adenyltransferase                               |
|                          | non-specific   | 5   | 36  | 1.17e-05 | PRK05379          | PRK05379            | c28366                        | bifunctional nicotinamide mononucleotide adenyltransferase                 |
| superfamily              | non-specific   | 5   | 36  | 1.17e-05 | c128663           | PRK05379 superfamily | c00015                        | bifunctional nicotinamide mononucleotide adenyltransferase                 |
|                          | non-specific   | 6   | 76  | 2.15e-05 | TIGR00482         | TIGR00482           | c00015                        | nicotinate (nicotinamide) nucleotide adenyltransferase                      |
|                          | non-specific   | 5   | 46  | 2.27e-05 | TIGR01153         | PRK01153            | c00015                        | nicotinamide-nucleotide adenyltransferase                                  |
|                          | non-specific   | 9   | 48  | 1.00e-04 | c02174            | CCT                 | c00015                        | CTP:phosphocholine cytidylyltransferase                                    |
|                          | non-specific   | 5   | 68  | 0.009101 | TIGR01527         | arch_NMN_Atrans     | c00015                        | nicotinamide-nucleotide adenyltransferase                                  |
|                          | non-specific   | 5   | 66  | 0.000241 | PRK07152          | nadD                | c28367                        | putative nicotinate-nucleotide adenyltransferase                           |
| superfamily              | non-specific   | 5   | 66  | 0.000241 | c128367           | nadD superfamily     | c00015                        | putative nicotinate-nucleotide adenyltransferase                           |
|                          | non-specific   | 36  | 0.000349 | c02168            | NNMAT_Nudix        | c00015                        | Nicotinamide/nicotinate mononucleotide adenyltransferase                    |
|                          | non-specific   | 1   | 37  | 0.001005 | PRK08887          | PRK08887            | c00015                        | nicotinic acid mononucleotide adenyltransferase                             |
|                          | non-specific   | 5   | 40  | 0.002275 | c02156            | nt_trans            | c00015                        | nucleotidyl transferase superfamily                                        |
|                          | non-specific   | 9   | 86  | 0.006609 | COG0615           | TagD                | c00015                        | Glycerol-3-phosphate cytidylyltransferase, cytidylyltransferase family       |
|                          | non-specific   | 3   | 141 | 7.03e-63 | PRK13964          | coaD                | c00015                        | phosphopantetheine adenyltransferase                                       |
| Query         | Hit type | ID region start | ID region end | E-Value  | Accession | Short name | Superfamily                        | Definition                                                                 |
|--------------|----------|----------------|--------------|----------|-----------|------------|------------------------------------|---------------------------------------------------------------------------|
| superfamily  | 3        | 141            |              |  7.03e-63| c00015    | nt_trans   | superfamily                       | nucleotidyl transferase superfamily                                      |
| non-specific | 1        | 140            | 8.44e-50     |        | COG0669   | CoaD       | c00015                            | Phosphopantetheine adenyllytransferase                                   |
| non-specific | 4        | 134            | 3.86e-47     |        | c02163    | PPA        | c00015                            | Phosphopantetheine adenyllytransferase                                   |
| non-specific | 3        | 134            | 3.77e-46     |        | PRK00168  | coaD       | c00015                            | Phosphopantetheine adenyllytransferase                                   |
| non-specific | 4        | 134            | 2.60e-42     |        | TIGR01510 | coaD_prev_kdtB| c00015                        | pantetheine-phosphate adenyllytransferase                               |
| specific     | 6        | 136            | 5.06e-23     |        | pfam01467 | CTP_transf_like |                    | Cytidylyltransferase-like                                                |
| non-specific | 4        | 56             | 2.61e-14     |        | TIGR00125 | cyt_tran_rel |                    | cytidylyltransferase-like-domain                                         |
| non-specific | 1        | 68             | 4.23e-12     |        | COG1057   | NadD       | c00015                            | Nicotinic acid mononucleotide adenyllytransferase                        |
| non-specific | 4        | 134            | 6.66e-12     |        | c02039    | cytidylyltransferase_like |                    | Cytidylyltransferase-like domain                                         |
| specific     | 6        | 136            | 5.06e-23     |        | pfam01467 | CTP_transf_like | c00015                        | Cytidylyltransferase-like                                                |
| non-specific | 5        | 67             | 8.01e-11     |        | c02165    | NMNAT      | c00015                            | Nicotinamide/nicotinate mononucleotide adenyllytransferase               |
| non-specific | 3        | 36             | 5.60e-09     |        | COG1056   | NadR       | c00015                            | Nicotinamide mononucleotide adenyllytransferase                          |
| non-specific | 9        | 134            | 1.07e-08     |        | c02167    | NMNAT_NadR| c00015                            | Nicotinamide/nicotinate mononucleotide adenyllytransferase               |
| non-specific | 6        | 61             | 2.32e-08     |        | TIGR00482 | TIGR00482  | c00015                            | nicotinate (nicotinamide) nucleotide adenyllytransferase                 |
| non-specific | 3        | 36             | 4.28e-08     |        | PRK01153  | PRK01153   | c00015                            | nicotinamide-nucleotide adenyllytransferase                             |
| non-specific | 4        | 63             | 6.34e-08     |        | c02166    | NMNAT_Archaea| c00015                        | Nicotinamide/nicotinate mononucleotide adenyllytransferase               |
| non-specific | 5        | 67             | 9.89e-08     |        | c02156    | nt_trans   | c00015                            | nucleotidyl transferase superfamily                                     |
| superfamily  | 3        | 61             | 2.69e-07     |        | c128367   | nadD       | c128367                          | putative nicotinate-nucleotide adenyllytransferase                     |
| non-specific | 4        | 67             | 2.77e-07     |        | TIGR01527 | arch_NMN_Archaea| c00015                        | putative nicotinate-nucleotide adenyllytransferase                     |
| non-specific | 5        | 61             | 8.30e-06     |        | PRK05379  | PRK05379   | c128366                          | bifunctional nicotinamide mononucleotide adenyllytransferase            |
| superfamily  | 5        | 61             | 8.30e-06     |        | c128366   | PRK05379   | superfamily                       | bifunctional nicotinamide mononucleotide adenyllytransferase            |
| superfamily  | 9        | 73             | 2.49e-05     |        | TIGR01526 | nadB_NMN_Archaea| c128365                        | nicotinamide-nucleotide adenyllytransferase                             |
| superfamily  | 9        | 73             | 2.49e-05     |        | c12835   | PRK08099   | superfamily                       | bifunctional DNA-binding transcriptional repressor/ NMN adenyllytransferase |
| non-specific | 9        | 56             | 3.99e-05     |        | COG0615   | TagD       | c00015                            | Glycerol-3-phosphate cytidylyltransferase, cytidylyltransferase family   |
| non-specific | 9        | 37             | 4.05e-05     |        | c02170    | cytidylyltransferase |        | cytidylyltransferase              |
| non-specific | 5        | 78             | 9.88e-05     |        | c02168    | NMNAT_NadX | c00015                          | Nicotinamide/nicotinate mononucleotide adenyllytransferase               |
| non-specific | 3        | 42             | 0.000254     |        | TIGR02199 | rfaE_dom_HI| c00015                          | rfaE: bifunctional protein, domain H                                   |
| non-specific | 9        | 56             | 0.000745     |        | c02174    | CTA       | c00015                            | CTP:phosphocholine cytidylyltransferase                                 |
| M. fermentans| 9        | 15             | 0.000758     |        | pfam02569 | Pantoate_ligase |        | Pantoate-beta-alanine ligase     |
| non-specific | 9        | 57             | 0.000849     |        | TIGR01518 | ghp_cytidylytrans| c00015                        | glycerol-3-phosphate cytidylyltransferase                               |
| non-specific | 8        | 55             | 0.000992     |        | PTZ0308   | PTZ0308    | c128626                          | ethanolamine-phosphate cytidylyltransferase                             |
| non-specific | 8        | 55             | 0.000992     |        | c128626   | PPL02406_superfamily |        | ethanolamine-phosphate cytidylyltransferase                             |
| non-specific | 3        | 64             | 0.001208     |        | c02171    | G3P_Cytidylyltransferase |        | glycerol-3-phosphate cytidylyltransferase                               |
| non-specific | 9        | 42             | 0.002815     |        | COG2870   | RfaE      | c128454                          | ADP-heptose synthase, bifunctional sugar kinase/adenyllytransferase    |
| superfamily  | 9        | 42             | 0.002815     |        | c128454   | RfaE_superfamily |        | ADP-heptose synthase, bifunctional sugar kinase/adenyllytransferase    |
| non-specific | 9        | 135            | 0.00309      |        | PRK08099  | PRK08099  | c128365                          | bifunctional DNA-binding transcriptional repressor/ NMN adenyllytransferase |
| non-specific | 3        | 69             | 0.00316      |        | PRK00777  | PRK00777  | c00015                            | phosphopantetheine adenyllytransferase                                 |
| Query         | Hit type | ID region start | ID region end | E-Value  | Accession      | Short name      | Superfamily                              | Definition                                                                 |
|--------------|----------|----------------|---------------|----------|----------------|----------------|------------------------------------------|---------------------------------------------------------------------------|
| M. gallinaceum | non-specific | 9              | 36            | 0.005021 | PRK11316       | PRK11316       | c128454                                  | bifunctional heptose-7-phosphate kinase/heptose-1-phosphate adenylytransferase |
| M. gallinaceum | non-specific | 8              | 34            | 0.0007501| cd02173        | ECT            | c00015                                   | CTP-phosphoethanolamine cytidylyltransferase (ECT)                         |
| M. gallinaceum | non-specific | 5              | 143           | 9.54e-64  | PRK13964       | coAD           | c00015                                   | phosphopanteine adenyllytransferase                                        |
| M. gallinaceum | superfamily | 5              | 143           | 9.54e-64  | c00015         | nt_trans superfamily | -                                       | nucleotidyl transferase superfamily                                    |
| M. gallinaceum | non-specific | 3              | 145           | 1.96e-45  | COG0669        | CoaD           | c00015                                   | Phosphopanteine adenyllytransferase                                      |
| M. gallinaceum | non-specific | 6              | 145           | 1.02e-41  | TIGR01510      | coAD_prev_kdtB | c00015                                   | pantethene-phosphate adenyllytransferase                                |
| M. gallinaceum | non-specific | 5              | 145           | 9.37e-39  | PRK00168       | coAD           | c00015                                   | phosphopanteine adenyllytransferase                                      |
| M. gallinaceum | non-specific | 6              | 136           | 1.86e-38  | cd02163        | PPAT           | c00015                                   | Phosphopanteine adenyllytransferase                                      |
| M. gallinaceum | specific  | 8              | 138           | 1.46e-19  | pfam01467      | CTP_transf_like | c00015                                   | Cytidylyltransferase-like                                                 |
| M. gallinaceum | non-specific | 6              | 136           | 2.50e-11  | cd02039        | cytidylyltransferase_like                | c00015                                   | Cytidylyltransferase-like domain                                         |
| M. gallinaceum | non-specific | 6              | 38            | 2.53e-09  | TIGR00125      | cytidylyltransferase_like               | c00015                                   | cytidylyltransferase-like domain                                         |
| M. gallinaceum | non-specific | 7              | 69            | 3.46e-08  | cd02165        | NMNAT          | c00015                                   | Nicotinamide/nicotinate mononucleotide adenyllytransferase                |
| M. gallinaceum | non-specific | 5              | 69            | 9.23e-08  | PRK00071       | nadD           | c00015                                   | nicotinic acid mononucleotide adenyllytransferase                         |
| M. gallinaceum | non-specific | 6              | 95            | 4.66e-06  | cd02156        | nt_trans       | c00015                                   | nucleotidyl transferase superfamily                                     |
| M. gallinaceum | non-specific | 8              | 69            | 7.41e-06  | TIGR00482      | TIGR00482      | c00015                                   | nicotinate (nicotinamide) nucleotide adenyllytransferase                  |
| M. gallinaceum | non-specific | 5              | 64            | 1.59e-05  | COG1057        | NadD           | c00015                                   | Nicotinic acid mononucleotide adenyllytransferase                         |
| M. gallinaceum | non-specific | 8              | 48            | 7.01e-05  | cd02167        | NMNAT          | c00015                                   | Nicotinamide/nicotinate mononucleotide adenyllytransferase                |
| M. gallinaceum | non-specific | 8              | 44            | 0.00012   | cd02174        | CCT            | c00015                                   | CTP:phosphocholine cytidylyltransferase                                  |
| M. gallinaceum | non-specific | 5              | 39            | 0.000131  | cd02170        | cytidylyltransferase                      | c00015                                   | cytidylyltransferase                                                     |
| M. gallinaceum | non-specific | 5              | 38            | 0.000193  | COG1056        | NadR           | c00015                                   | Nicotinamide mononucleotide adenyllytransferase                           |
| M. gallinaceum | non-specific | 4              | 144           | 0.000122  | cd02173        | ECT            | c00015                                   | CTP:phosphoethanolamine cytidylyltransferase (ECT)                       |
| M. gallinaceum | non-specific | 3              | 144           | 0.000461  | PTZ0308        | PTZ0308        | c128626                                  | ethanolamine-phosphate cytidylyltransferase                              |
| M. gallinaceum | superfamily | 3              | 44            | 0.000461  | c128626        | PLN02406 superfamily | -                                       | ethanolamine-phosphate cytidylyltransferase                              |
| M. gallinaceum | non-specific | 5              | 69            | 0.000576  | PRK07152       | nadD           | c128367                                  | putative nicotinate-nucleotide adenyllytransferase                       |
| M. gallinaceum | non-specific | 5              | 69            | 0.000576  | c128367       | nadD superfamily | -                                       | putative nicotinate-nucleotide adenyllytransferase                       |
| M. gallinaceum | non-specific | 5              | 139           | 0.000995  | PRK00777       | PRK00777       | c00015                                   | phosphopanteine adenyllytransferase                                     |
| M. gallinaceum | non-specific | 5              | 39            | 0.001682  | cd02171        | G3P_Cytedlyltransferase                  | c00015                                   | Glycerol-3-phosphate cytidylyltransferase                                |
| M. gallinaceum | non-specific | 5              | 39            | 0.002016  | COG0615        | TagD           | c00015                                   | Glycerol-3-phosphate cytidylyltransferase family                         |
| M. gallinaceum | non-specific | 8              | 48            | 0.002371  | TIGR01526      | nadR_NMN_Atrans | c128365                                  | nicotinamide-nucleotide adenyllytransferase                             |
| M. gallinaceum | superfamily | 8              | 48            | 0.002371  | c128365        | PRK08099 superfamily | -                                       | bifunctional DNA-binding transcriptional repressor/ NMN adenyllytransferase |
| M. gallinarum | non-specific | 1              | 66            | 0.006453  | COG1019        | CAB4           | c00015                                   | Phosphopanteine adenyllytransferase                                     |
| M. gallinarum | non-specific | 2              | 141           | 9.93e-64  | PRK13964       | coAD           | c00015                                   | phosphopanteine adenyllytransferase                                     |
| M. gallinarum | non-specific | 2              | 141           | 9.93e-64  | c00015         | nt_trans superfamily | -                                       | nucleotidyl transferase superfamily                                    |
| M. gallinarum | non-specific | 1              | 140           | 1.36e-47  | COG0669        | CoaD           | c00015                                   | Phosphopanteine adenyllytransferase                                     |
| M. gallinarum | non-specific | 4              | 141           | 3.25e-44  | TIGR01510      | coAD_prev_kdtB | c00015                                   | pantethene-phosphate adenyllytransferase                                |
| M. gallinarum | non-specific | 3              | 132           | 8.06e-42  | PRK00168       | coAD           | c00015                                   | phosphopanteine adenyllytransferase                                     |
| M. gallinarum | non-specific | 4              | 132           | 9.66e-42  | cd02163        | PPAT           | c00015                                   | Phosphopanteine adenyllytransferase                                     |
| M. gallinarum | specific  | 6              | 132           | 1.87e-20  | pfam01467      | CTP_transf_like | c00015                                   | Cytidylyltransferase-like                                                |
| M. gallinarum | non-specific | 4              | 64            | 8.98e-14  | TIGR00125      | cyt_trans_rel | c00015                                   | Cytidylyltransferase-like domain                                        |
| M. gallinarum | non-specific | 3              | 67            | 3.27e-11  | PRK07152       | nadD           | c128367                                  | putative nicotinate-nucleotide adenyllytransferase                       |
| Query         | Hit type | ID region start | ID region end | E-Value   | Accession     | Short name       | Superfamily                                      | Definition                                      |
|--------------|----------|----------------|---------------|-----------|---------------|-----------------|------------------------------------------------|------------------------------------------------|
| superfamily  | 3        | 67             |               | 3.27e-11  | cl28367       | nadD superfamily | -                                              | putative nicotinate-nucleotide adenylytransferase |
| non-specific | 1        | 56             |               | 2.69e-10  | COG1057       | NaD             | c000015            | Nicotinic acid mononucleotide adenylytransferase |
| non-specific | 1        | 36             |               | 2.25e-09  | COG1056       | NadR            | c000015            | Nicotinamide mononucleotide adenylytransferase   |
| non-specific | 4        | 134            |               | 3.06e-09  | cl02039       | cytidylytransferase_like | c000015        | Cytidyltransferase-like domain                   |
| non-specific | 4        | 67             |               | 3.78e-09  | cl02165       | NMNAT           | c000015            | Nicotinamide/nicotinate mononucleotide adenylytransferase |
| non-specific | 1        | 53             |               | 1.54e-18  | prk00071      | nadD            | c000015            | nicotinic acid mononucleotide adenylytransferase |
| non-specific | 5        | 56             |               | 6.30e-08  | prk05379      | prk05379        | c028366            | bifunctional nicotinamide mononucleotide adenylytransferase |
| superfamily  | 5        | 56             |               | 6.30e-08  | cl28366       | prk05379 superfamily | c028366        | bifunctional nicotinamide mononucleotide adenylytransferase |
| non-specific | 6        | 56             |               | 6.96e-08  | tigr00482     | tigr00482       | c000015            | nicotinate (nicotinamide) nucleotide adenylytransferase |
| non-specific | 5        | 56             |               | 8.94e-07  | prk01153      | prk01153        | c000015            | nicotinamide-nucleotide adenylytransferase       |
| non-specific | 4        | 91             |               | 9.39e-07  | cl02156       | nt_trans        | c000015            | nucleotidyl transferase superfamily             |
| non-specific | 5        | 36             |               | 1.10e-06  | cl02166       | nmnat Archaea   | c000015            | Nicotinamide/nicotinate mononucleotide adenylytransferase |
| non-specific | 1        | 57             |               | 3.21e-06  | cl02170       | cytidylytransferase | c000015        | cytidyltransferase                              |
| non-specific | 2        | 84             |               | 4.94e-06  | tigr02199     | rfaE dom II     | c000015            | rfaE: bifunctional protein, domain II            |
| non-specific | 4        | 60             |               | 5.26e-06  | cl02168       | nmnat Nudix     | c000015            | Nicotinamide/nicotinate mononucleotide adenylytransferase |
| non-specific | 1        | 72             |               | 1.88e-05  | cog0615       | tagD            | c000015            | Glycerol-3-phosphate cytidyltransferase, cytidyltransferase family |
| non-specific | 4        | 43             |               | 2.66e-05  | cl02167       | nmnat NadR      | c000015            | Nicotinamide/nicotinate mononucleotide adenylytransferase |
| non-specific | 5        | 67             |               | 3.72e-05  | tigr01527     | arch NMN Attrans | c000015          | nicotinamide-nucleotide adenylytransferase       |
| non-specific | 1        | 43             |               | 5.45e-05  | prk08099      | prk08099        | c028365            | bifunctional DNA-binding transcriptional repressor/ NMN adenylytransferase |
| superfamily  | 1        | 43             |               | 5.45e-05  | cl28365       | prk08099 superfamily | -             | bifunctional DNA-binding transcriptional repressor/ NMN adenylytransferase |
| non-specific | 2        | 37             |               | 7.50e-05  | cl02171       | g3p Cytidylyltransferase | c000015        | glycerol-3-phosphate cytidyltransferase         |
| non-specific | 3        | 37             |               | 8.20e-05  | tigr01526     | nadR NMN Attrans | c028365            | nicotinamide-nucleotide adenylytransferase       |
| non-specific | 2        | 36             |               | 0.000151  | pto0308       | pto0308         | cl28626            | ethanolamine-phosphate cytidyltransferase       |
| superfamily  | 2        | 36             |               | 0.000151  | cl28626       | cl28626 superfamily | cl28626 | ethanolamine-phosphate cytidyltransferase       |
| superfamily  | 3        | 36             |               | 0.00023   | prk01170      | prk01170        | c000866            | phosphopantetheine adenylytransferase           |
| superfamily  | 3        | 36             |               | 0.00023   | cl00866       | ntpase 1-f superfamily | c000015        | Protein of unknown function DUF84                |
| non-specific | 14       | 40             |               | 0.000247  | pfla02569     | pantoate ligase  | c000015            | Pantoate-beta-alanine ligase                    |
| non-specific | 1        | 34             |               | 0.000283  | prk00777      | prk00777        | c000015            | phosphopantetheine adenylytransferase           |
| non-specific | 2        | 36             |               | 0.000525  | prk11316      | prk11316        | c028454            | bifunctional heptose 7-phosphate kinase/heptose 1-phosphate adenylytransferase |
| superfamily  | 2        | 36             |               | 0.000525  | cl28454       | rfaE superfamily | -                   | ADP-heptose synthase, bifunctional sugar kinase/adenylytransferase |
| non-specific | 4        | 40             |               | 0.000654  | pfla06574     | fad syn         | c000015            | FAD synthetase                                 |
| non-specific | 9        | 64             |               | 0.000754  | cog1019       | cab4            | c000015            | Phosphopantetheine adenylytransferase           |
| non-specific | 4        | 40             |               | 0.000868  | prk05627      | prk05627        | cl27514            | bifunctional riboflavin kinase/FMN adenylytransferase |
| superfamily  | 4        | 40             |               | 0.000868  | cl27514       | cl27514 superfamily | c000015        | Riboflavin kinase                               |
| non-specific | 6        | 34             |               | 0.000934  | cl02173       | ecf              | c000015            | CTP-phosphoethanolamine cytidyltransferase (ECT) |
| non-specific | 4        | 40             |               | 0.001299  | cl02064       | fad synthetase N | c000015            | FAD synthetase, N-terminal domain of the bifunctional enzyme |
| non-specific | 9        | 42             |               | 0.001831  | cog2870       | rfaE             | cl28454            | ADP-heptose synthase, bifunctional sugar kinase/adenylytransferase |

**M. gallinarum**
| Query | Hit type | ID region start | ID region end | E-Value | Accession | Short name | Superfamily | Definition |
|-------|-----------|----------------|---------------|---------|-----------|------------|-------------|------------|
| non-specific | 2 | 79 | | 0.003548 | PRK07143 | PRK07143 | c127514 | hypothetical protein |
| non-specific | 9 | 56 | | 0.003727 | c02174 | CCT | c00015 | CTP:phosphocholine cytidylyltransferase |
| non-specific | 9 | 64 | | 0.003467 | c02164 | PPAT_CoAS | c00015 | phosphopantetheine adenyllyltransferase |
| non-specific | 9 | 54 | | 0.006477 | TIGR01518 | g3p_cytidyllrans | c00015 | glycerol-3-phosphate cytidylyltransferase |
| non-specific | 2 | 42 | | 0.009744 | c02172 | RfA_EN | c00015 | N-terminal domain of RfA |
| non-specific | 2 | 141 | | 1.65e-35 | PRK13964 | cosD | c00015 | phosphopantetheine adenyllyltransferase |
| superfamily | 2 | 141 | | 1.65e-55 | c100015 | nt_trans superfamily | - | nucleotidyl transferase superfamily |
| non-specific | 1 | 139 | | 3.83e-41 | COG0669 | CoAD | c00015 | Phosphopantetheine adenyllyltransferase |
| non-specific | 2 | 132 | | 9.44e-39 | PRK00168 | cosD | c00015 | phosphopantetheine adenyllyltransferase |
| superfamily | 4 | 132 | | 2.28e-38 | c02163 | PPAT | c00015 | phosphopantetheine adenyllyltransferase |
| non-specific | 4 | 136 | | 7.71e-33 | TIGR01510 | cosD_prev_kdtB | c00015 | pantetheine-phosphate adenyllyltransferase |
| specific | 6 | 141 | | 3.41e-17 | pmam01467 | CTP_transf_like | c00015 | Cytidylyltransferase-like |
| non-specific | 1 | 67 | | 7.16e-12 | COG1057 | NadD | c00015 | Nicotinic acid mononucleotide adenyllyltransferase |
| non-specific | 4 | 64 | | 1.05e-11 | TIGR00125 | cyt_tran_rel | c00015 | cytidylyltransferase-like domain |
| non-specific | 1 | 135 | | 1.44e-11 | PRK08099 | PRK08099 | c128365 | bifunctional DNA-binding transcriptional repressor/NMN adenyllyltransferase |
| superfamily | 1 | 135 | | 1.44e-11 | c128365 | PRK08099 superfamily | - | bifunctional DNA-binding transcriptional repressor/NMN adenyllyltransferase |
| non-specific | 1 | 67 | | 4.81e-11 | PRK00071 | nadD | c00015 | nicotinic acid mononucleotide adenyllyltransferase |
| non-specific | 4 | 134 | | 2.44e-10 | c02167 | NNMAT_NadR | c00015 | Nicotinamide/nicotinate mononucleotide adenyllyltransferase |
| non-specific | 2 | 67 | | 4.93e-10 | PRK07152 | nadD | c128367 | putative nicotinate-nucleotide adenyllyltransferase |
| superfamily | 2 | 67 | | 4.93e-10 | c128367 | nadD superfamily | - | putative nicotinate-nucleotide adenyllyltransferase |
| non-specific | 4 | 134 | | 2.26e-09 | c02039 | cytidylyltransferase_like | c00015 | Cytidylyltransferase-like domain |
| non-specific | 6 | 67 | | 2.80e-09 | TIGR00482 | TIGR00482 | c00015 | nicotinate (nicotinamide) nucleotide adenyllyltransferase |
| non-specific | 1 | 63 | | 7.47e-09 | COG1056 | NadR | c00015 | Nicotinamide mononucleotide adenyllyltransferase |
| non-specific | 4 | 67 | | 8.32e-09 | c02165 | NNMAT | c00015 | Nicotinamide/nicotinate mononucleotide adenyllyltransferase |
| non-specific | 2 | 36 | | 3.02e-06 | TIGR01526 | nadR_NMN_Atrans | c128365 | nicotinamide-nucleotide adenyllyltransferase |
| non-specific | 5 | 63 | | 3.59e-06 | PRK01153 | PRK01153 | c00015 | nicotinamide-nucleotide adenyllyltransferase |
| non-specific | 6 | 91 | | 1.26e-06 | c02156 | nt_trans | c00015 | nucleotidyld transferase superfamily |
| non-specific | 5 | 63 | | 1.28e-05 | c02166 | NNMAT_Archaea | c00015 | Nicotinamide/nicotinate mononucleotide adenyllyltransferase |
| non-specific | 4 | 36 | | 0.000109 | PRK05379 | PRK05379 | c128366 | bifunctional nicotinamide mononucleotide adenyllyltransferase |
| superfamily | 4 | 36 | | 0.000109 | c128366 | PRK05379 superfamily | - | bifunctional nicotinamide mononucleotide adenyllyltransferase |
| non-specific | 9 | 37 | | 0.000179 | PRK00777 | PRK00777 | c00015 | phosphopantetheine adenyllyltransferase |
| non-specific | 1 | 37 | | 0.000229 | c02170 | cytidylyltransferase | c00015 | cytidylyltransferase |
| non-specific | 5 | 61 | | 0.000865 | TIGR01527 | arch_NMN_Atrans | c00015 | nicotinamide-nucleotide adenyllyltransferase |
| non-specific | 3 | 30 | | 0.001251 | PRK06973 | PRK06973 | c00015 | nicotinic acid mononucleotide adenyllyltransferase |
| non-specific | 9 | 40 | | 0.001232 | pmam06574 | FAD_syn | c00015 | FAD synthetase |
| non-specific | 9 | 37 | | 0.000356 | COG1019 | CAB4 | c00015 | Phosphopantetheine adenyllyltransferase |
| non-specific | 9 | 40 | | 0.000369 | PRK05627 | PRK05627 | c127514 | bifunctional riboflavin kinase/FMN adenyllyltransferase |
| superfamily | 9 | 40 | | 0.000369 | c127514 | Flavokinas superfamily | - | Riboflavin kinase |
| non-specific | 3 | 42 | | 0.000460 | PTZ00308 | PTZ00308 | c128626 | ethanolamine-phosphate cytidylyltransferase |
| superfamily | 3 | 42 | | 0.000460 | c128626 | PLN02406 superfamily | - | ethanolamine-phosphate cytidylyltransferase |
| non-specific | 1 | 37 | | 0.000466 | c02171 | G3P_Cytidylltransferase | c00015 | glycerol-3-phosphate cytidylyltransferase |
| Query | Hit type | ID start | ID end | E-Value | Accession | Short name | Superfamily | Definition |
|-------|----------|----------|--------|---------|-----------|------------|-------------|------------|
| M. leachii | non-specific | 1 | 36 | 0.0004933 | COG0615 | TagD | c00015 | Glycerol-3-phosphate cytidylyltransferase, cytidylyltransferase family |
| | non-specific | 2 | 40 | 0.0006074 | PLN02660 | PLN02660 | c00015 | pantoate-beta-alanine ligase |
| | specific | 8 | 141 | 5.58e-31 | PRK13964 | coaD | c00015 | phosphopantetheine adenyltransferase |
| | superfamily | 8 | 141 | 5.58e-31 | c00015 | nt_trans superfamily | - | nucleotidyl transferase superfamily |
| | non-specific | 8 | 136 | 1.04e-28 | COG0669 | CoaD | c00015 | Phosphopantetheine adenyltransferase |
| | non-specific | 8 | 140 | 9.33e-27 | TIGR01510 | coaD_prev_kdtB | c00015 | pantetheine-phosphate adenyltransferase |
| | non-specific | 8 | 136 | 7.25e-26 | c02163 | PPAT | c00015 | Phosphopantetheine adenyltransferase |
| | non-specific | 8 | 136 | 1.01e-23 | PRK00168 | coaD | c00015 | phosphopantetheine adenyltransferase |
| | non-specific | 9 | 138 | 2.07e-07 | pfam01467 | CTP_transf_like | c00015 | Cytidyltransferase-like |
| | non-specific | 8 | 93 | 0.001153 | c02156 | nt_trans | c00015 | nucleotidyl transferase superfamily |
| | non-specific | 8 | 64 | 0.001154 | TIGR00125 | cyt_tran_rel | c00015 | cytidyltransferase-like domain |
| | specific | 8 | 136 | 0.001185 | c02039 | cytidyltransferase like | c00015 | Cytidyltransferase-like domain |
| | superfamily | 1 | 140 | 3.91e-73 | PRK13964 | coaD | c00015 | phosphopantetheine adenyltransferase |
| | non-specific | 3 | 140 | 4.52e-64 | TIGR01510 | coaD_prev_kdtB | c00015 | pantetheine-phosphate adenyltransferase |
| | non-specific | 1 | 139 | 8.52e-46 | COG0669 | CoaD | c00015 | Phosphopantetheine adenyltransferase |
| | non-specific | 1 | 135 | 4.75e-44 | PRK00168 | coaD | c00015 | phosphopantetheine adenyltransferase |
| | specific | 3 | 139 | 1.50e-43 | c02163 | PPAT | c00015 | Phosphopantetheine adenyltransferase |
| | specific | 5 | 135 | 8.49e-21 | pfam01467 | CTP_transf_like | c00015 | Cytidyltransferase-like |
| | non-specific | 4 | 63 | 1.33e-13 | TIGR00125 | cyt_tran_rel | c00015 | cytidyltransferase-like domain |
| | non-specific | 4 | 134 | 6.52e-12 | c02039 | cytidyltransferase_like | c00015 | Cytidyltransferase-like domain |
| | non-specific | 1 | 77 | 1.09e-09 | PRK01752 | nadD | c28367 | putative nicotinate-nucleotide adenyltransferase |
| | superfamily | 1 | 77 | 1.09e-09 | c28367 | nadD superfamily | - | putative nicotinate-nucleotide adenyltransferase |
| | specific | 1 | 66 | 1.65e-07 | COG1057 | NadD | c00015 | Nicotinic acid mononucleotide adenyltransferase |
| | non-specific | 3 | 77 | 4.15e-07 | c02165 | NMNAT | c00015 | Nicotinamide/nicotinate mononucleotide adenyltransferase |
| | specific | 1 | 136 | 5.19e-07 | PRK00777 | PRK00777 | c00015 | phosphopantetheine adenyltransferase |
| | specific | 1 | 46 | 1.35e-06 | COG1056 | NadR | c00015 | Nicotinamide mononucleotide adenyltransferase |
| | specific | 1 | 66 | 1.57e-06 | PRK00771 | nadD | c00015 | nicotinic acid mononucleotide adenyltransferase |
| | specific | 1 | 136 | 6.25e-06 | COG1019 | CAB4 | c00015 | Phosphopantetheine adenyltransferase |
| | non-specific | 3 | 130 | 8.03e-06 | c02156 | nt_trans | c00015 | nucleotidyl transferase superfamily |
| | non-specific | 3 | 134 | 2.76e-05 | c02167 | NMNAT_NadR | c00015 | Nicotinamide/nicotinate mononucleotide adenyltransferase |
| | non-specific | 4 | 68 | 4.23e-05 | c02166 | NMNAT_Archaea | c00015 | Nicotinamide/nicotinate mononucleotide adenyltransferase |
| | specific | 1 | 71 | 7.22e-05 | TIGR01526 | nadR_NMN_Atrans | c28365 | nicotinamide-nucleotide adenyltransferase |
| | superfamily | 1 | 71 | 7.22e-05 | c28365 | PRK08099 superfamily | - | bifunctional DNA-binding transcriptional repressor: NMN adenyltransferase |
| | non-specific | 4 | 68 | 0.00016 | TIGR01527 | arch_NMN_Atrans | c00015 | nicotinamide-nucleotide adenyltransferase |
| | non-specific | 4 | 35 | 0.000363 | PRK01153 | PRK01153 | c00015 | nicotinamide-nucleotide adenyltransferase |
| | non-specific | 4 | 35 | 0.00079 | PRK05379 | PRK05379 | c28366 | bifunctional nicotinamide mononucleotide adenyltransferase |
| | specific | 5 | 66 | 0.001253 | TIGR00482 | TIGR00482 | c00015 | nicotinate (nicotinamide) nucleotide adenyltransferase |
| | specific | 1 | 89 | 0.00256 | c02170 | cytidyltransferase | c00015 | cytidyltransferase |
| | non-specific | 1 | 36 | 0.002969 | c02171 | G3P_Cytidyltransferase | c00015 | glycerol-3-phosphate cytidyltransferase |
| Query          | Hit type      | ID region start | ID region end | E-Value | Accession | Short name | Superfamily | Definition                                      |
|---------------|---------------|-----------------|---------------|---------|-----------|------------|-------------|------------------------------------------------|
| *M. leonicaptivi* | non-specific 2 | 134             | 1.38e-46      | COG0669 | CoaD      | c00015     | Phosphopantetheine adenylyltransferase        |
|                | superfamily   2 | 134             | 1.38e-46      | c00015  | nt trans superfamily | c00015   | nucleotidyl transferase superfamily         |
|                | non-specific 5 | 134             | 7.67e-46      | c02163  | PPAT      | c00015     | Phosphopantetheine adenylyltransferase       |
|                | non-specific 3 | 134             | 3.09e-44      | PRK0168 | coaD      | c00015     | Phosphopantetheine adenylyltransferase       |
|                | non-specific 3 | 137             | 4.65e-42      | PRK13964| coaD      | c00015     | Phosphopantetheine adenylyltransferase       |
|                | non-specific 5 | 134             | 2.30e-41      | TIGR01510| coaD prev_kdtB | c00015   | pantetheine-phosphate adenylyltransferase   |
|                | specific      8 | 136             | 9.01e-24      | pfam01467| CTP transf_like | c00015  | Cytidyltransferase-like                     |
|                | non-specific 5 | 135             | 1.45e-12      | c02039  | cytidylyltransferase_like | c00015  | Cytidyltransferase-like domain             |
|                | non-specific 5 | 48              | 1.59e-11      | TIGR00125| cytidylyltransferase_like | c00015  | Cytidyltransferase-like domain             |
|                | non-specific 1 | 46              | 2.03e-10      | PRK00071| nadD      | c00015     | nicotinic acid mononucleotide adenyltransferase |
|                | non-specific 1 | 48              | 5.65e-09      | COG1057 | NadD      | c00015     | Nicotinic acid mononucleotide adenyltransferase |
|                | non-specific 6 | 48              | 9.93e-08      | PRK01153| PRK01153  | c00015     | nicotinamide-nucleotide adenyltransferase   |
|                | non-specific 1 | 48              | 2.84e-07      | COG1056 | NadR      | c00015     | Nicotinamide mononucleotide adenyltransferase |
|                | non-specific 6 | 48              | 5.20e-07      | c02166  | NMNAT_Ar  | c00015     | Nicotinamide/nicotinate mononucleotide adenyltransferase |
|                | non-specific 1 | 86              | 8.65e-07      | COG0615 | TagD      | c00015     | Glycero-3-phosphate cytidylyltransferase, cytidylyltransferase family |
|                | non-specific 5 | 46              | 1.25e-06      | c02165  | NMNAT      | c00015     | Nicotinamide/nicotinate mononucleotide adenyltransferase |
|                | superfamily   10 | 137             | 1.71e-08      | COG1019 | CAB4      | c00015     | Phosphopantetheine adenylyltransferase       |
|                | specific      4 | 48              | 5.31e-06      | PRK05379| PRK05379  | c28366     | bifunctional nicotinamide monomucleotide adenyltransferase |
|                | superfamily   4 | 48              | 5.31e-06      | c28366  | PRK05379 superfamily | -       | bifunctional nicotinamide monomucleotide adenyltransferase |
|                | non-specific 3 | 88              | 1.99e-05      | PRK07132| nadD      | c28367     | putative nicotinate-nucleotide adenyltransferase |
|                | superfamily   3 | 88              | 1.99e-05      | c28367  | nadD superfamily | c28367  | putative nicotinate-nucleotide adenyltransferase |
|                | non-specific 5 | 48              | 2.27e-05      | c02168  | NMNAT      | c00015     | Nicotinamide/nicotinate mononucleotide adenyltransferase |
|                | non-specific 1 | 38              | 3.74e-05      | c02170  | cytidylyltransferase | c00015  | cytidylyltransferase                       |
|                | non-specific 10 | 137             | 5.81e-05      | PRK00777| PRK00777  | c00015     | phosphopantetheine adenylyltransferase       |
|                | non-specific 8 | 49              | 6.14e-05      | TIGR00482| TIGR00482 | c00015     | nicotinate (nicotinamide) nucleotide adenyltransferase |
|                | non-specific 6 | 132             | 9.09e-05      | c02136  | nt trans superfamily | c00015  | nucleotidyl transferase superfamily        |
|                | non-specific 8 | 69              | 0.00066       | TIGR01527| arch NMN_Atrans | c00015  | nicotinamide-nucleotide adenyltransferase   |
|                | non-specific 1 | 135             | 0.00071       | PRK08099| PRK08099  | c28365     | bifunctional DNA-binding transcriptional repressor/ NMN adenyltransferase |
|                | superfamily   1 | 135             | 0.00071       | c28365  | PRK08099 superfamily | -       | bifunctional DNA-binding transcriptional repressor/ NMN adenyltransferase |
|                | non-specific 10 | 137             | 0.001165      | PRK01170| PRK01170  | c000868    | phosphopantetheine adenylyltransferase       |
|                | superfamily   10 | 137             | 0.001165      | c000866 | NTase I superfamily | c000868  | phosphopantetheine adenylyltransferase       |
|                | non-specific 3 | 57              | 0.001427      | TIGR01526| nadR NMN_Atrans | c28365  | nicotinamide-nucleotide adenyltransferase   |
|                | non-specific 12 | 38              | 0.005519      | pfam05636| HIGH_NTase1 | c27012   | HIGH Nucleotidyl Transferase                |
|                | superfamily   12 | 38              | 0.005519      | c27012  | HIGH_NTase1 superfamily | -       | HIGH Nucleotidyl Transferase                |
|                | non-specific 2 | 37              | 0.006823      | c02173  | ECT       | c00015     | CTP:phosphoethanolamine cytidylyltransferase (ECT) |
|                | non-specific 7 | 135             | 0.006888      | c02164  | PPAT CoAS | c00015     | phosphopantetheine adenylyltransferase       |
|                | non-specific 2 | 80              | 0.007169      | c02169  | Citrate lyase_hgase | c00015  | Citrate lyase hgase                         |
|                | non-specific 10 | 38              | 0.008445      | c09236  | NMNAT Eucarya | c00015  | Nicotinamide/nicotinate mononucleotide adenyltransferase |
| *M. lipofaciens* | non-specific 1 | 140             | 9.74e-63      | PRK13964| coaD      | c00015     | phosphopantetheine adenylyltransferase       |
|                | superfamily   1 | 140             | 9.74e-63      | c00015  | nt trans superfamily | -       | nucleotidyl transferase superfamily        |
| Query    | Hit type | ID region start | ID region end | E-Value | Accession | Short name | Superfamily | Definition                                                                 |
|----------|----------|-----------------|---------------|---------|-----------|------------|-------------|---------------------------------------------------------------------------|
| non-specific | 1        | 134             | 4.02e-43      | COG0669 | CoA    | c00015     | Phosphopantetheine adenlytransferase                                      |
| non-specific | 3        | 133             | 1.48e-38      | cd02163 | PPAT    | c00015     | Phosphopantetheine adenlytransferase                                      |
| non-specific | 3        | 133             | 1.16e-37      | TIGR01530| coaD    | c00015     | pantetheine-phosphate adenlytransferase                                  |
| non-specific | 1        | 133             | 2.28e-37      | PRK00168| coaD    | c00015     | phosphopantetheine adenlytransferase                                    |
| non-specific | 5        | 135             | 1.17e-15      | pfam01467| CTP_transf_like | c00015  | Cytidylyltransferase-like                                               |
| non-specific | 3        | 63              | 6.62e-12      | TIGR00125| cyt_trans_rel | c00015 | cytidylyltransferase-like domain                                        |
| non-specific | 1        | 66              | 1.19e-09      | COG1057 | NadD    | c00015     | Nicotinic acid mononucleotide adenlytransferase                          |
| non-specific | 3        | 133             | 4.38e-08      | cd02039 | cytidylyltransferase_like | c00015 | Cytidylyltransferase-like domain                                        |
| non-specific | 3        | 90              | 7.99e-08      | cd02156 | nt_trans | c00015     | nucleotidyl transferase superfamily                                     |
| non-specific | 5        | 133             | 1.98e-07      | cd02167 | NMNAT    | c00015     | Nicotinamide/nicotinate mononucleotide adenlytransferase                 |
| non-specific | 4        | 66              | 2.34e-07      | cd02165 | NMNAT    | c00015     | Nicotinamide/nicotinate mononucleotide adenlytransferase                 |
| non-specific | 1        | 66              | 1.08e-06      | PRK07152 | nadD    | c00015     | putative nicotinate-nucleotide adenlytransferase                        |
| superfamily  | 1        | 66              | 1.08e-06      | cl28367 | nadD    | c00015     | putative nicotinate-nucleotide adenlytransferase                        |
| non-specific | 1        | 35              | 1.39e-06      | COG1056 | NadR    | c00015     | Nicotinamide mononucleotide adenlytransferase                           |
| non-specific | 1        | 133             | 1.77e-05      | cd02170 | cytidylyltransferase | c00015 | Cytidylyltransferase                                                    |
| non-specific | 1        | 66              | 2.74e-05      | PRK00071 | nadD    | c00015     | nicotinic acid mononucleotide adenlytransferase                         |
| non-specific | 5        | 52              | 3.21e-05      | TIGR00482| TIGR00482 | c00015     | nicotinate (nicotinamide) nucleotide adenlytransferase                  |
| non-specific | 1        | 43              | 8.20e-05      | COG0615 | TagD    | c00015     | Glycerol-3-phosphate cytidylyltransferase, cytidylyltransferase family  |
| non-specific | 13       | 39              | 9.35e-05      | pfam02369| Pantoate | c00015     | Pantoate-beta-alanine ligase                                           |
| non-specific | 1        | 133             | 0.000121      | TIGR01526| nadR_NM_1trans | c00015 | nicotinamide-nucleotide adenlytransferase                               |
| superfamily  | 1        | 133             | 0.000121      | cl28365 | PRK08099 superfamily | - | bifunctional DNA-binding transcriptional repressor: NMN adenlytransferase |
| non-specific | 2        | 35              | 0.000121      | PRK01153 | PRK01153 | c00015     | nicotinamide-nucleotide adenlytransferase                               |
| non-specific | 1        | 72              | 0.000135      | cd02171 | G3P_Cytdylyltransferase | c00015 | glycerol-3-phosphate cytidylyltransferase                              |
| non-specific | 34       | 94              | 0.000149      | PRK10422 | PRK10422 | c00015     | lipopolysaccharide core biosynthesis protein                            |
| superfamily  | 34       | 94              | 0.000149      | c00015 | Glycosyltransferase_GB_type superfamily | - | Glycosyltransferases catalyze the transfer of sugar moieties from activated donor molecules to specific acceptor molecules, forming glycosidic bonds. |
| non-specific | 5        | 61              | 0.000181      | PLN02388 | PLN02388 | c00015     | Phosphopantetheine adenlytransferase                                   |
| non-specific | 3        | 35              | 0.000184      | cd02166 | NMNAT_Archaea | c00015 | Nicotinamide/nicotinate mononucleotide adenlytransferase               |
| non-specific | 1        | 63              | 0.000198      | PRK00777 | PRK00777 | c00015     | phosphopantetheine adenlytransferase                                    |
| non-specific | 4        | 35              | 0.000222      | PRK05379 | PRK05379 | c00015     | phosphopantetheine adenlytransferase                                    |
| superfamily  | 4        | 35              | 0.000222      | PRK05379 | PRK05379 | c00015     | phosphopantetheine adenlytransferase                                   |
| non-specific | 3        | 46              | 0.000235      | TIGR01527| arch_NM_1trans | c00015 | nicotinamide-nucleotide adenlytransferase                               |
| non-specific | 1        | 69              | 0.000255      | COG1019 | CAB4    | c00015     | Phosphopantetheine adenlytransferase                                   |
| non-specific | 7        | 67              | 0.001261      | cd02164 | PPAT_CoAS | c00015 | phosphopantetheine adenlytransferase                                   |
| non-specific | 13       | 80              | 0.001583      | PLN02660 | PLN02660 | c00015     | pantoate--beta-alanine ligase                                          |
| non-specific | 13       | 39              | 0.002191      | COG0414 | PanC | c00015     | Panthothenate synthetase                                               |
| non-specific | 5        | 72              | 0.002316      | TIGR01518 | g3p_cytidhms | c00015 | glycerol-3-phosphate cytidylyltransferase                              |
| superfamily  | 13       | 39              | 0.003169      | cd00560 | PanC | c00015     | Pantoate-beta-alanine ligase                                           |
| non-specific | 13       | 39              | 0.005229      | PRK00380 | PanC | c00015     | Pantoate-beta-alanine ligase                                           |

**M. lipofaciens**

| non-specific | 9        | 96              | 1.63e-14      | PRK13964 | coaD | c00015 | phosphopantetheine adenlytransferase                                   |

**M. mobile**
| Query          | Hit type | ID region start | ID region end | E-Value  | Accession | Short name | Superfamily                                      | Definition                                                                 |
|---------------|----------|----------------|--------------|----------|-----------|-----------|-------------------------------------------------|---------------------------------------------------------------------------|
| superfamily   | 9        | 96             | 1.63e-14     | c00015   | nt_trans superfamily |           | nucleotidyl transferase superfamily            |                                                                           |
| non-specific  | 11       | 96             | 8.75e-14     | TIGR01510| coaD prev kdB | c00015   | pantetheine-phosphate adenyltransferase        |                                                                           |
| non-specific  | 8        | 1.02e-12       | COG0669      | 8        | coaD      | c00015   | Phosphopantetheine adenyltransferase           |                                                                           |
| non-specific  | 11       | 96             | 3.11e-12     | cd02163  | PPAT      | c00015   | Phosphopantetheine adenyltransferase           |                                                                           |
| non-specific  | 8        | 1.73e-11       | PRK00168     | 8        | coaD      | c00015   | Phosphopantetheine adenyltransferase           |                                                                           |
| non-specific  | 11       | 58             | 2.49e-05     | TIGR00125| cyt_tran_re | c00015  | cytidylytransferase-like domain               |                                                                           |
| non-specific  | 1        | 140            | 2.91e-62     | PRK13964 | coaD      | c00015   | Phosphopantetheine adenyltransferase           |                                                                           |
| superfamily   | 1        | 140            | 2.91e-62     | c00015   | nt_trans superfamily |           | nucleotidyl transferase superfamily           |                                                                           |
| non-specific  | 1        | 140            | 3.14e-45     | COG0669  | CoaD      | c00015   | Phosphopantetheine adenyltransferase           |                                                                           |
| non-specific  | 3        | 131            | 5.35e-42     | cd02163  | PPAT      | c00015   | Phosphopantetheine adenyltransferase           |                                                                           |
| non-specific  | 1        | 131            | 2.39e-40     | PRK00168 | coaD      | c00015   | Phosphopantetheine adenyltransferase           |                                                                           |
| non-specific  | 3        | 133            | 2.95e-38     | TIGR01510| coaD prev kdB | c00015  | pantetheine-phosphate adenyltransferase        |                                                                           |
| specific      | 5        | 135            | 8.78e-22     | pfam01467| CTP transf-like | c00015 | Cytidylytransferase-like                       |                                                                           |
| non-specific  | 3        | 63             | 7.16e-12     | TIGR00125| cyt_tran_re | c00015  | cytidylytransferase-like domain               |                                                                           |
| non-specific  | 3        | 135            | 1.09e-09     | cd02039  | cytidylytransferase like | c00015  | Cytidylytransferase-like domain               |                                                                           |
| non-specific  | 1        | 44             | 7.06e-07     | PRK0071  | nadD      | c00015   | putative nicotinate-nucleotide adenyltransferase|                                                                           |
| non-specific  | 3        | 90             | 1.32e-06     | cd02156  | nt_trans superfamily | c00015 | nucleotidyl transferase superfamily           |                                                                           |
| specific      | 1        | 40             | 1.97e-06     | COG1056  | NadR      | c00015   | Nicotinamide mononucleotide adenyltransferase  |                                                                           |
| non-specific  | 4        | 66             | 2.69e-06     | COG1057  | NadD      | c00015   | Nicotinamide mononucleotide adenyltransferase  |                                                                           |
| non-specific  | 4        | 66             | 4.66e-06     | cd02165  | NMNAT     | c00015   | Nicotinamide/nicotinate mononucleotide adenyltransferase |                                                                           |
| superfamily   | 1        | 66             | 8.56e-06     | PRK07152 | nadD      | c128367  | putative nicotinate-nucleotide adenyltransferase|                                                                           |
| non-specific  | 1        | 44             | 7.06e-06     | cd0367   | nadD superfamily | c128367 | putative nicotinate-nucleotide adenyltransferase|                                                                           |
| non-specific  | 3        | 35             | 1.19e-05     | PRK01153 | PRK01153  | c00015   | nicotinamide-nucleotide adenyltransferase       |                                                                           |
| non-specific  | 3        | 35             | 2.27e-05     | cd02166  | NMNAT_Archea | c00015 | Nicotinamide/nicotinate mononucleotide adenyltransferase |                                                                           |
| non-specific  | 5        | 66             | 5.12e-05     | TIGR00482| TIGR00482 | c00015   | nicotinate (nicotinamide) nucleotide adenyltransferase |                                                                           |
| specific      | 7        | 41             | 0.000146     | cd02173  | ECT      | c00015   | CTP:phosphoethanolamine cytidylytransferase (ECT) |                                                                           |
| non-specific  | 1        | 36             | 0.000285     | PRK00777 | PRK00777 | c00015   | phoshopantetheine adenyltransferase            |                                                                           |
| non-specific  | 4        | 35             | 0.000284     | PRK05379 | PRK05379  | c128366  | bifunctional nicotinamide mononucleotide adenyltransferase |                                                                           |
| non-specific  | 4        | 35             | 0.000284     | PRK05379 | PRK05379  | c128366  | bifunctional nicotinamide mononucleotide adenyltransferase |                                                                           |
| non-specific  | 12       | 67             | 0.000349     | smart00764| Citrate ly lig | c00015 | Citrate lyase ligase C-terminal domain       |                                                                           |
| non-specific  | 12       | 66             | 0.000385     | pfam05281| Citrate ly lig | c00015 | Citrate lyase C-terminal domain               |                                                                           |
| non-specific  | 8        | 44             | 0.000398     | TIGR02199| rfaD_dom II | c00015  | rfaD: bifunctional protein, domain II          |                                                                           |
| non-specific  | 1        | 85             | 0.000414     | COG0615  | TagD      | c00015   | Glycerol-3-phosphate cytidylytransferase, cytidylytransferase family |                                                                           |
| specific      | 12       | 71             | 0.000594     | cd02169  | Citrate ly ligase | c00015 | Citrate lyase ligase                          |                                                                           |
| non-specific  | 1        | 57             | 0.001273     | cd02170  | citidylytransferase | c00015 | cytidylytransferase                          |                                                                           |
| non-specific  | 8        | 41             | 0.001836     | cd02174  | CCK       | c00015   | CTP:phoshocoline cytidylytransferase           |                                                                           |
| non-specific  | 7        | 41             | 0.001934     | PTZ00308 | PTZ00308  | c128366  | ethanolamine-phosphate cytidylytransferase     |                                                                           |
| superfamily   | 7        | 41             | 0.001934     | cd02626  | PLN02406 superfamily | - | ethanolamine-phosphate cytidylytransferase |                                                                           |
| non-specific  | 8        | 133            | 0.002042     | COG2870  | RfaE      | c128454  | ADP-heptose synthase, bifunctional sugar kinase/adenylytransferase |                                                                           |
| superfamily   | 8        | 133            | 0.002042     | c128454  | RfaE superfamily | - | ADP-heptose synthase, bifunctional sugar kinase/adenylytransferase |                                                                           |

**M. molare**
| Query | Hit type | ID region start | ID region end | E-Value | Accession | Short name | Superfamily | Definition |
|---|---|---|---|---|---|---|---|---|
| | non-specific | 11 | 64 | 0.002251 | COG3053 | CitC | cI28578 | Citrate lyase synthetase [Energy production and conversion] |
| M. mycoides subsp. capri | superfamily | 11 | 64 | 0.002251 | cI28578 | CitC superfamily | cI28578 | Citrate lyase synthetase [Energy production and conversion] |
| | non-specific | 1 | 55 | 0.005139 | c02171 | G3P_Cytidylyltransferase | c00015 | glycerol-3-phosphate cytidylyltransferase |
| | specific | 1 | 140 | 2.94e-71 | PRK13964 | coaD | c00015 | phosphopantetheine adenyllytransferase |
| | superfamily | 1 | 140 | 2.94e-71 | c00015 | nt_trans superfamily | - | nucleotidyl transferase superfamily |
| | non-specific | 3 | 140 | 1.91e-62 | TIGR01510 | coaD_prev_kdtB | c00015 | pantetheine-phosphate adenyllytransferase |
| | non-specific | 1 | 139 | 1.17e-45 | COG0669 | CoaD | c00015 | phosphopantetheine adenyllytransferase |
| | non-specific | 1 | 135 | 6.52e-44 | PRK01068 | coaD | c00015 | phosphopantetheine adenyllytransferase |
| | non-specific | 3 | 139 | 1.02e-42 | c02163 | PPAT | c00015 | phosphopantetheine adenyllytransferase |
| | specific | 5 | 135 | 7.19e-20 | pfam01467 | CTP_transf_like | c00015 | Cytidyltransferase-like |
| | non-specific | 3 | 63 | 2.98e-13 | TIGR00125 | cYt_tran_rel | c00015 | cytidyltransferase-like domain |
| | non-specific | 3 | 134 | 8.76e-12 | c02039 | cytidyltransferase | c00015 | Cytidyltransferase-like domain |
| | non-specific | 1 | 77 | 6.01e-10 | PRK07152 | nadD | cI28367 | putative nicotinate-nucleotide adenyllytransferase |
| M. mycoides subsp. capri | superfamily | 1 | 77 | 6.01e-10 | cI28367 | nadD superfamily | - | putative nicotinate-nucleotide adenyllytransferase |
| | non-specific | 1 | 66 | 1.52e-08 | COG1057 | NadD | c00015 | Nicotinic acid mononucleotide adenyllytransferase |
| | non-specific | 1 | 136 | 4.04e-08 | PRK00777 | PRK00777 | c00015 | phosphopantetheine adenyllytransferase |
| | non-specific | 3 | 77 | 1.56e-07 | c02165 | NMMAT | c00015 | Nicotinamide/nicotinate mononucleotide adenyllytransferase |
| | non-specific | 1 | 44 | 2.58e-07 | COG1056 | NadR | c00015 | Nicotinamide mononucleotide adenyllytransferase |
| | non-specific | 1 | 136 | 6.67e-07 | COG1019 | CAB4 | c00015 | Phosphopantetheine adenyllytransferase |
| | non-specific | 1 | 66 | 1.60e-06 | PRK0071 | nadD | c00015 | Nicotinic acid mononucleotide adenyllytransferase |
| | non-specific | 1 | 71 | 3.91e-05 | TIGR01526 | nadR_NMN_Atrans | cI28365 | nicotinamide-nucleotide adenyllytransferase |
| | superfamily | 1 | 71 | 3.91e-05 | cI28365 | PRK08099 superfamily | - | bifunctional DNA-binding transcriptional repressor/ NMN adenyllytransferase |
| | non-specific | 4 | 61 | 5.48e-05 | c02166 | NMMAT_Archeae | c00015 | Nicotinamide/nicotinate mononucleotide adenyllytransferase |
| | non-specific | 3 | 134 | 6.30e-05 | c02167 | NMMAT_NadR | c00015 | Nicotinamide/nicotinate mononucleotide adenyllytransferase |
| | non-specific | 4 | 130 | 6.91e-05 | c02156 | nt_trans | c00015 | nucleotidyl transferase superfamily |
| | non-specific | 4 | 68 | 7.26e-05 | TIGR01527 | arch_NMN_Atrans | c00015 | nicotinamide-nucleotide adenyllytransferase |
| | non-specific | 3 | 35 | 0.00049 | PRK05379 | PRK05379 | cI28366 | bifunctional nicotinamide mononucleotide adenyllytransferase |
| M. mycoides subsp. capri | superfamily | 3 | 35 | 0.00049 | cI28366 | PRK05379 superfamily | - | bifunctional nicotinamide mononucleotide adenyllytransferase |
| | non-specific | 4 | 35 | 0.000534 | PRK01153 | PRK01153 | c00015 | nicotinamide-nucleotide adenyllytransferase |
| | non-specific | 1 | 76 | 0.000596 | PRK08887 | PRK08887 | c00015 | nicotinic acid mononucleotide adenyllytransferase |
| | non-specific | 8 | 89 | 0.001492 | c02170 | cytidylyltransferase | c00015 | cytidylyltransferase |
| | non-specific | 2 | 67 | 0.001944 | PRK01170 | PRK01170 | c00015 | phosphopantetheine adenyllytransferase |
| | superfamily | 2 | 67 | 0.001944 | c00866 | NTBse F-T superfamily | c00015 | Protein of unknown function DUF84 |
| | non-specific | 8 | 133 | 0.002054 | c02164 | PPAT_CoAS | c00015 | phosphopantetheine adenyllytransferase |
| | non-specific | 1 | 36 | 0.003852 | c02171 | G3P_Cytidylyltransferase | c00015 | glycerol-3-phosphate cytidylyltransferase |
| | non-specific | 5 | 36 | 0.003895 | TIGR00482 | TIGR00482 | c00015 | nicotinate (nicotinamide) nucleotide adenyllytransferase |
| | specific | 1 | 139 | 1.19e-45 | COG0669 | CoaD | c00015 | phosphopantetheine adenyllytransferase |
| M. mycoides subsp. mycoides | superfamily | 1 | 145 | 4.77e-72 | PRK13964 | coaD | c00015 | phosphopantetheine adenyllytransferase |
| | non-specific | 1 | 140 | 4.77e-72 | c00015 | nt_trans superfamily | - | nucleotidyl transferase superfamily |
| | non-specific | 3 | 140 | 8.20e-62 | TIGR01510 | coaD_prev_kdtB | c00015 | pantetheine-phosphate adenyllytransferase |
| | non-specific | 1 | 139 | 1.19e-45 | COG0669 | CoaD | c00015 | phosphopantetheine adenyllytransferase |
| | non-specific | 1 | 135 | 3.07e-43 | PRK00168 | coaD | c00015 | phosphopantetheine adenyllytransferase |
| Query      | Hit type | ID region start | ID region end | E-Value | Accession | Short name | Superfamily | Definition                                                                 |
|------------|----------|-----------------|---------------|---------|-----------|------------|-------------|---------------------------------------------------------------------------|
| non-specific | 3        | 139             | 1.96e-42      | c02163  | PPAT      | c00015     | Phosphopantetheine adenyltransferase                                       |
| specific    | 5        | 135             | 1.38e-20      | pfam01467| CTP transf like | c00015     | Cytidylyltransferase-like                                                 |
| non-specific | 4        | 63              | 8.39e-13      | TIGR00125| cyt tran rel | c00015     | Cytidylyltransferase-like domain                                          |
| non-specific | 4        | 134             | 2.80e-12      | c02039  | cytidylyltransferase-like | c00015     | Cytidylyltransferase-like domain                                          |
| non-specific | 1        | 124             | 2.63e-10      | PRK07152| nadD      | c28367     | putative nicotinate-nucleotide adenyltransferase                          |
| non-specific | 1        | 124             | 2.63e-10      | c28367  | nadD superfamily | -         | putative nicotinate-nucleotide adenyltransferase                          |
| non-specific | 1        | 66              | 7.45e-08      | COG1057 | NaD       | c00015     | Nicotinic acid mononucleotide adenyltransferase                           |
| non-specific | 1        | 66              | 1.14e-06      | PRK00071| NaD       | c00015     | nicotinic acid mononucleotide adenyltransferase                           |
| non-specific | 3        | 77              | 3.95e-06      | c02165  | NMNAT     | c00015     | Nicotinamid/nicotinate mononucleotide adenyltransferase                   |
| non-specific | 3        | 134             | 4.26e-06      | c02167  | NadR      | c00015     | Nicotinamide/nicotinate mononucleotide adenyltransferase                 |
| non-specific | 1        | 136             | 8.25e-06      | PRK00777| PRK00777  | c00015     | phosphopantetheine adenyltransferase                                     |
| non-specific | 1        | 35              | 1.04e-05      | COG1056 | NaD       | c00015     | Nicotinamide mononucleotide adenyltransferase                             |
| non-specific | 3        | 130             | 1.73e-05      | c02156  | nt trans  | c00015     | nucleotidyl transferase superfamily                                     |
| non-specific | 1        | 71              | 0.000106      | TIGR01526| nadR_NMN_Atrans | c28367     | nicotinamide-nucleotide adenyltransferase                                |
| superfamily | 1        | 71              | 0.000106      | c28365  | PRK08099 superfamily | -         | bifunctional DNA-binding transcriptional repressor/ NMN adenyltransferase |
| non-specific | 5        | 119             | 0.000126      | TIGR00482| TIGR00482 | c00015     | nicotinate (nicotinamide) nucleotide adenyltransferase                   |
| non-specific | 4        | 35              | 0.000356      | PRK01153| PRK01153  | c00015     | nicotinamide-nucleotide adenyltransferase                                |
| non-specific | 1        | 136             | 0.000358      | COG1019 | CAB4      | c00015     | Phosphopantetheine adenyltransferase                                     |
| non-specific | 4        | 35              | 0.000496      | c02166  | NMNAT_Archaea | c00015     | Nicotinamide/nicotinate mononucleotide adenyltransferase                 |
| non-specific | 4        | 35              | 0.000519      | PRK05379| PRK05379  | c28366     | bifunctional nicotinamide mononucleotide adenyltransferase              |
| superfamily | 4        | 35              | 0.000519      | c28366  | PRK05379 superfamily | -         | bifunctional nicotinamide mononucleotide adenyltransferase              |
| non-specific | 1        | 36              | 0.002311      | c02171  | G3P Cytidylyltransferase | c00015     | glycerol-3-phosphate cytidylyltransferase                               |
| non-specific | 1        | 36              | 0.003558      | c02170  | cytidylyltransferase | c00015     | cytidylyltransferase                                                     |
| non-specific | 10       | 35              | 0.006714      | pfam05636| HIGH_NTase1 | c27012     | HIGH Nucleotidyl Transferase                                             |
| superfamily | 10       | 35              | 0.006714      | c27012  | HIGH_NTase1 superfamily | -         | HIGH Nucleotidyl Transferase                                             |
| non-specific | 4        | 68              | 0.007739      | TIGR01527| arch_NMN_Atrans | c00015     | nicotinamide-nucleotide adenyltransferase                                |
| non-specific | 10       | 35              | 0.007951      | PRK13670| PRK13670  | c27012     | hypothetical protein                                                      |
| non-specific | 1        | 141             | 1.49e-55      | PRK13670| coaD      | c00015     | phosphopantetheine adenyltransferase                                     |
| superfamily | 1        | 141             | 1.49e-55      | c00015  | nt_trans superfamily | -         | nucleotidyl transferase superfamily                                     |
| non-specific | 1        | 135             | 7.10e-39      | COG0669 | CoaD      | c00015     | Phosphopantetheine adenyltransferase                                     |
| non-specific | 3        | 134             | 7.30e-35      | TIGR01510| coaD_prev_kdtB | c00015     | pantetheine-phosphate adenyltransferase                                 |
| non-specific | 3        | 132             | 3.82e-34      | c02163  | PPAT      | c00015     | Phosphopantetheine adenyltransferase                                     |
| non-specific | 1        | 132             | 2.96e-32      | PRK00168| coaD      | c00015     | phosphopantetheine adenyltransferase                                     |
| non-specific | 5        | 136             | 2.16e-15      | pfam01467| CTP transf like | c00015     | Cytidylyltransferase-like                                                |
| non-specific | 3        | 51              | 2.96e-10      | TIGR00125| cyt tran rel | c00015     | Cytidylyltransferase-like domain                                         |
| non-specific | 1        | 43              | 7.33e-09      | COG1057 | NaD       | c00015     | Nicotinic acid mononucleotide adenyltransferase                          |
| non-specific | 1        | 67              | 2.07e-08      | PRK07152| nadD      | c28367     | putative nicotinate-nucleotide adenyltransferase                          |
| superfamily | 1        | 67              | 2.07e-08      | c28367  | nadD superfamily | -         | putative nicotinate-nucleotide adenyltransferase                          |
| non-specific | 5        | 67              | 3.93e-08      | TIGR00482| TIGR00482  | c00015     | nicotinamide (nicotinamide) nucleotide adenyltransferase                |
| non-specific | 5        | 134             | 2.86e-07      | c02167  | NMNAT NaD | c00015     | Nicotinamide/nicotinate mononucleotide adenyltransferase                 |
| non-specific | 4        | 67              | 4.08e-07      | NMNAT_Archaea | c00015     | Nicotinamide/nicotinate mononucleotide adenyltransferase                 |
| non-specific | 1        | 35              | 3.27e-06      | COG1056 | NaD       | c00015     | Nicotinamide mononucleotide adenyltransferase                            |
| Query | Hit type | ID region start | ID region end | E-Value | Accession | Short name | Superfamily | Definition |
|-------|---------|----------------|--------------|---------|-----------|------------|-------------|------------|
| non-specific | 1 | 44 | 4.3e-06 | PRK00071 | nadD | c000015 | nicotinic acid mononucleotide adenylyltransferase |
| non-specific | 3 | 134 | 5.17e-06 | cd02039 | cytidylyltransferase_like | c000015 | Cytidylyltransferase-like domain |
| non-specific | 3 | 39 | 5.97e-06 | cd02156 | nt_trans | c000015 | nucleotidyl transferase superfamily |
| non-specific | 1 | 61 | 6.36e-06 | cd02171 | G3P_Cytidylyltransferase | c000015 | glycero-3-phosphate cytidylyltransferase |
| non-specific | 1 | 88 | 2.33e-05 | cd02170 | cytidylyltransferase | c000015 | cytidylyltransferase |
| non-specific | 1 | 36 | 3.02e-05 | COG0615 | TagD | c000015 | Glycerol-3-phosphate cytidylyltransferase, cytidylyltransferase family |
| non-specific | 1 | 33 | 0.000173 | PRK00777 | PRK00777 | c000015 | phosphopantetheine adenylyltransferase |
| non-specific | 1 | 37 | 0.000471 | TIGR01526 | nadR_NMN_Atrans | c28365 | nicotinamide-nucleotide adenylyltransferase |
| superfamily | 1 | 37 | 0.000471 | c128365 | PRK08099 superfamily | - | bifunctional DNA-binding transcriptional repressor/ NMN adenylyltransferase |
| non-specific | 5 | 61 | 0.001081 | TIGR01518 | ghp_cytidylts | c000015 | glycero-3-phosphate cytidylyltransferase |
| non-specific | 14 | 42 | 0.001136 | pfam02569 | Pantoate_ligase | c000015 | Pantoate-beta-alanine ligase |
| non-specific | 2 | 29 | 0.001861 | PRK01153 | PRK01153 | c000015 | nicotinamide-nucleotide adenylyltransferase |
| non-specific | 8 | 50 | 0.002073 | TIGR02199 | rfaE_dom II | c000015 | rfaE: bifunctional protein, domain II |
| non-specific | 4 | 35 | 0.00227 | PRK05379 | PRK05379 | c28366 | bifunctional nicotinamide mononucleotide adenylyltransferase |
| superfamily | 4 | 35 | 0.00227 | c128366 | PRK05379 superfamily | - | bifunctional nicotinamide mononucleotide adenylyltransferase |
| non-specific | 1 | 42 | 0.002519 | PRK08099 | PRK08099 | c28365 | bifunctional DNA-binding transcriptional repressor/ NMN adenylyltransferase |
| M. opalescens | non-specific | 3 | 35 | 0.004583 | cd02166 | NMMAT_Archaea | c000015 | Nicotinamide/nicotinate mononucleotide adenylyltransferase |
| non-specific | 10 | 136 | 8.33e-36 | TIGR01510 | coaD_prev_kdB | c000015 | pantetheine-phosphate adenylyltransferase |
| non-specific | 10 | 136 | 8.33e-36 | c000015 | nt_trans superfamily | - | nucleotidyl transferase superfamily |
| non-specific | 6 | 135 | 1.92e-31 | PRK00168 | coaD | c000015 | phosphopantetheine adenylyltransferase |
| non-specific | 7 | 135 | 1.88e-30 | COG0669 | CoaD | c000015 | Phosphopantetheine adenylyltransferase |
| non-specific | 11 | 136 | 4.53e-29 | cd02163 | PPAT | c000015 | Phosphopantetheine adenylyltransferase |
| non-specific | 7 | 146 | 3.67e-25 | PRK13964 | coaD | c000015 | phosphopantetheine adenylyltransferase |
| non-specific | 11 | 139 | 2.00e-11 | pfam01467 | CTP_transf_like | c000015 | Cytidylyltransferase-like |
| non-specific | 14 | 140 | 2.37e-08 | cd02170 | cytidylyltransferase | c000015 | cytidylyltransferase |
| non-specific | 11 | 42 | 3.71e-08 | TIGR00125 | cyt_trans | c000015 | cytidylyltransferase-like domain |
| M. penetrans | non-specific | 14 | 140 | 1.07e-06 | COG0615 | TagD | c000015 | Glycerol-3-phosphate cytidylyltransferase, cytidylyltransferase family |
| non-specific | 10 | 141 | 4.00e-06 | cd02039 | cytidylyltransferase_like | c000015 | Cytidylyltransferase-like domain |
| non-specific | 5 | 41 | 1.80e-05 | COG1056 | NadR | c000015 | Nicotinamide mononucleotide adenylyltransferase |
| non-specific | 11 | 95 | 3.02e-05 | cd02156 | nt_trans | c000015 | nucleotidyl transferase superfamily |
| non-specific | 14 | 76 | 4.52e-05 | PRK00777 | PRK00777 | c000015 | phosphopantetheine adenylyltransferase |
| non-specific | 14 | 89 | 0.000143 | COG1019 | CAB4 | c000015 | Phosphopantetheine adenylyltransferase |
| non-specific | 8 | 93 | 0.000157 | cd02171 | G3P_Cytidylyltransferase | c000015 | glycero-3-phosphate cytidylyltransferase |
| non-specific | 12 | 41 | 0.001478 | cd02166 | NMMAT_Archaea | c000015 | Nicotinamide/nicotinate mononucleotide adenylyltransferase |
| non-specific | 9 | 41 | 0.00178 | PRK05379 | PRK05379 | c28366 | bifunctional nicotinamide mononucleotide adenylyltransferase |
| superfamily | 9 | 41 | 0.00178 | c128366 | PRK05379 superfamily | - | bifunctional nicotinamide mononucleotide adenylyltransferase |
| non-specific | 6 | 73 | 0.003098 | PRK00771 | nadD | c000015 | nicotinic acid mononucleotide adenylyltransferase |
| non-specific | 14 | 45 | 0.004532 | cd02174 | CCT | c000015 | CTP:phosphocholine cytidylyltransferase |
| non-specific | 10 | 93 | 0.004773 | cd02165 | NMMAT | c000015 | Nicotinamide/nicotinate mononucleotide adenylyltransferase |
| Query          | Hit type                | ID region start | ID region end | E-Value | Accession       | Short name                  | Superfamily                                                                 | Definition                                                                 |
|---------------|-------------------------|-----------------|---------------|---------|-----------------|-----------------------------|-------------------------------------------------------------------------------|------------------------------------------------------------------------------|
|              | non-specific            | 2               | 83            | 0.005485| PRK07143        | PRK07143                    | c27314                                                                      | hypothetical protein                                                          |
| superfamily   | non-specific            | 13              | 50            | 0.005531| c02173          | Flavokinase superfamily     | c27314                                                                      | Riboflavin kinase                                                            |
|              | non-specific            | 6               | 68            | 0.005561| COG1057         | ECT                         | c00015                                                                      | CTP-phosphothanolamine cytidylyltransferase (ECT)                             |
|              | non-specific            | 11              | 41            | 0.006622| PRK01153        | PRK01153                    | c00015                                                                      | Nicotinamide-nucleotide cytidylyltransferase                                 |
|              | non-specific            | 14              | 93            | 0.006986| TIGR01518       | g3p_cytidyltns              | c00015                                                                      | glycerol-3-phosphate cytidylyltransferase                                   |
|              | non-specific            | 5               | 136           | 6.06e-34 | c02163          | PPAT                        | c00015                                                                      | Phosphopantetheine adenyltransferase                                         |
| superfamily   | non-specific            | 5               | 136           | 6.06e-34 | c00015          | nt_trans superfamily        | c00015                                                                      | nucleotidyl transferase superfamily                                         |
|              | non-specific            | 3               | 136           | 1.16e-33 | COG0669         | CoaD                        | c00015                                                                      | Phosphopantetheine adenyltransferase                                         |
|              | non-specific            | 5               | 136           | 6.94e-30 | TIGR01510       | coaD_prev_kdtB              | c00015                                                                      | Pantetheine-phosphate adenyltransferase                                     |
|              | non-specific            | 3               | 136           | 2.01e-29 | PRK00168        | coaD                        | c00015                                                                      | Phosphopantetheine adenyltransferase                                         |
|              | non-specific            | 3               | 148           | 1.60e-27 | PRK13964        | coaD                        | c00015                                                                      | Phosphopantetheine adenyltransferase                                         |
|              | non-specific            | 7               | 137           | 1.78e-09 | pfam01467       | CTP_transf_like             | c00015                                                                      | Cytidylyltransferase-like                                                   |
| superfamily   | non-specific            | 5               | 136           | 1.17e-05 | c02039          | cytidylyltransferase_like   | c00015                                                                      | Cytidylyltransferase-like domain                                             |
|              | non-specific            | 1               | 139           | 0.003566| COG1057         | NadD                        | c00015                                                                      | Nicotinic acid mononucleotide adenyltransferase                             |
| specific      | superfamily            | 1               | 140           | 4.60e-68 | PRK13964        | coaD                        | c00015                                                                      | Phosphopantetheine adenyltransferase                                         |
|              | non-specific            | 3               | 133           | 4.10e-40 | c02163          | PPAT                        | c00015                                                                      | Phosphopantetheine adenyltransferase                                         |
|              | non-specific            | 3               | 133           | 1.77e-39 | TIGR01510       | coaD_prev_kdtB              | c00015                                                                      | Pantetheine-phosphate adenyltransferase                                     |
|              | non-specific            | 1               | 133           | 6.88e-39 | PRK00168        | coaD                        | c00015                                                                      | Phosphopantetheine adenyltransferase                                         |
| specific      | superfamily            | 5               | 135           | 2.92e-19 | pfam01467       | CTP_transf_like             | c00015                                                                      | Cytidylyltransferase-like                                                   |
|              | non-specific            | 3               | 63            | 1.25e-11 | TIGR00125       | cyt_tran_rel                | c00015                                                                      | Cytidylyltransferase-like domain                                             |
|              | non-specific            | 4               | 66            | 5.00e-10 | c02165          | NMMAT                       | c00015                                                                      | Nicotinamide/nicotinate mononucleotide adenyltransferase                    |
|              | non-specific            | 1               | 66            | 2.27e-09 | PRK07152        | nadD                        | c28367                                                                      | putative nicotinate-nucleotide adenyltransferase                            |
| superfamily   | non-specific            | 1               | 66            | 2.27e-09 | c28367          | nadD superfamily            | c00015                                                                      | putative nicotinate-nucleotide adenyltransferase                            |
|              | non-specific            | 3               | 133           | 3.18e-09 | c02039          | cytidylyltransferase_like   | c00015                                                                      | Cytidylyltransferase-like domain                                             |
|              | non-specific            | 5               | 133           | 2.80e-08 | c02167          | NMMAT NadR                  | c00015                                                                      | Nicotinamide/nicotinate mononucleotide adenyltransferase                    |
|              | non-specific            | 1               | 66            | 2.88e-08 | COG1057         | NadD                        | c00015                                                                      | Nicotinamide adenyltransferase                                              |
|              | non-specific            | 1               | 66            | 3.34e-07 | PRK00071        | nadD                        | c00015                                                                      | nicotinamide adenyltransferase                                              |
|              | non-specific            | 1               | 87            | 4.45e-07 | COG0615         | TagD                        | c00015                                                                      | Glycerol-3-phosphate cytidylyltransferase, cytidylyltransferase family       |
|              | non-specific            | 1               | 35            | 4.80e-07 | COG1056         | NADR                        | c00015                                                                      | Nicotinamide mononucleotide adenyltransferase                              |
|              | non-specific            | 1               | 36            | 5.86e-07 | c02170          | cytidylyltransferase        | c00015                                                                      | cytidylyltransferase                                                        |
|              | non-specific            | 5               | 56            | 1.62e-06 | TIGR00482       | TIGR00482                   | c00015                                                                      | nicotinate (nicotinamide) nucleotide adenyltransferase                      |
|              | non-specific            | 3               | 39            | 1.08e-05 | c02156          | nt_trans                    | c00015                                                                      | nucleotide transferase superfamily                                         |
|              | non-specific            | 1               | 36            | 5.76e-05 | c02171          | G3P_Cytidylyltransferase    | c00015                                                                      | glycerol-3-phosphate cytidylyltransferase                                  |
|              | non-specific            | 5               | 58            | 6.21e-05 | TIGR01518       | g3p_cytidyltns              | c00015                                                                      | glycerol-3-phosphate cytidylyltransferase                                  |
|              | non-specific            | 1               | 134           | 9.28e-05 | PRK08099        | PRK08099                    | c28365                                                                      | bifunctional DNA-binding transcriptional repressor/ NMN adenyltransferase   |
| superfamily   | non-specific            | 1               | 134           | 9.28e-05 | c28365          | PRK08099 superfamily        | -                                                                           | bifunctional DNA-binding transcriptional repressor/ NMN adenyltransferase   |
| Query          | Hit type       | ID region start | ID region end | E-Value      | Accession          | Short name               | Superfamily                  | Definition                                                                 |
|----------------|----------------|-----------------|---------------|--------------|--------------------|--------------------------|-----------------------------|----------------------------------------------------------------------------|
| **M. primatum**| non-specific   | 13              | 39            | 0.000104     | pfam02569         | Pantoate ligase          | c00015                      | Pantoate-beta-alanine ligase                                            |
|                | non-specific   | 1               | 33            | 0.000108     | PRK00777         |                          | PRK00777                    | phosphopantetheine adenylyltransferase                                  |
|                | non-specific   | 1               | 133           | 0.000184     | TIGR01526        | nadR_NMn_Atrans         | PRK00365                    | nicotinamide-nucleotide adenylyltransferase                             |
|                | non-specific   | 2               | 35            | 0.000231     | PRK00113         |                          | PRK00113                    | nicotinamide-nucleotide adenylyltransferase                             |
|                | non-specific   | 3               | 42            | 0.00048      | cd02173           | ECT                      | c00015                      | CTP:phosphoethanolamine cytidylyltransferase (ECT)                        |
|                | non-specific   | 3               | 35            | 0.000531     | cd02166           | NNMAT_Archeae            | c00015                      | Nicotinamide/nicotinate mononucleotide adenylyltransferase               |
|                | non-specific   | 1               | 89            | 0.00074      | COG1019          |                          | c00015                      | Phosphopantetheine adenylyltransferase                                  |
|                | non-specific   | 3               | 46            | 0.001026     | TIGR01527         | arch_NMn_Atrans         | c00015                      | nicotinamide-nucleotide adenylyltransferase                             |
|                | specific       | 13              | 39            | 0.001088     | COG00560         | PantoC                   | c00015                      | Pantoate-beta-alanine ligase                                            |
|                | superfamily    | 4               | 35            | 0.001237     | PRK00379         |                          | PRK00379                    | bifunctional nicotinamide mononucleotide adenylyltransferase            |
|                |               | 13              | 39            | 0.001776     | COG00414         |                          | c00015                      | Panthothenate synthetase                                                 |
|                | non-specific   | 7               | 60            | 0.005073     | cd02164           |                          | PRK00125                    | phosphopantetheine adenylyltransferase                                  |
|                | specific       | 5               | 146           | 9.05e-49     | coaD              |                          | c00015                      | phosphopantetheine adenylyltransferase                                  |
|                | superfamily    | 5               | 146           | 9.05e-49     | cd00015          | nt_trans superfamily    | c00015                      | nicotinamide-nucleotide adenylyltransferase                             |
|                | superfamily    | 4               | 146           | 8.15e-57     | COG0069          | coaD                     | c00015                      | Phosphopantetheine adenylyltransferase                                  |
|                | non-specific   | 7               | 139           | 1.27e-39     | cd02163           |                          | PRK01510                    | nicotinamide-nucleotide adenylyltransferase                             |
|                | non-specific   | 5               | 139           | 5.99e-38     | PRK00168         | coaD                     | c00015                      | nicotinamide-nucleotide adenylyltransferase                             |
|                | non-specific   | 7               | 139           | 7.37e-38     | TIGR01510        | coaD_prev_kdB           | c00015                      | pantetheine-phosphate adenylyltransferase                               |
|                | specific       | 9               | 139           | 1.04e-19     | pfam01467        | CTP_trans_like          | c00015                      | Cytidylyltransferase-like                                               |
|                | non-specific   | 2               | 59            | 4.15e-12     | PRK00071         | coaD                     | c00015                      | nicotinamide-nucleotide adenylyltransferase                             |
|                | non-specific   | 7               | 67            | 2.33e-11     | TIGR00125        | cyt_tran_rel            | c00015                      | cytidylyltransferase-like domain                                       |
|                | superfamily    | 3               | 59            | 1.26e-09     | COG01057         |nadD                     | c00015                      | Nicotinamide/nicotinate mononucleotide adenylyltransferase               |
|                | non-specific   | 7               | 59             | 2.23e-09     | cd02165         | NNMAT                    | c00015                      | Nicotinamide/nicotinate mononucleotide adenylyltransferase               |
|                | superfamily    | 7               | 139           | 6.78e-09     | cd02039           | cytidylyltransferase     | c00015                      | Cytidylyltransferase-like domain                                       |
|                | non-specific   | 5               | 70             | 6.06e-07     | PRK07152         | nadD                     | c00015                      | putative nicotinamide-nucleotide adenylyltransferase                    |
|                | superfamily    | 5               | 70             | 6.06e-07     | cd02367         |                          | c00015                      | putative nicotinamide-nucleotide adenylyltransferase                    |
|                | non-specific   | 9               | 93             | 2.24e-06     | TIGR00482        | nadD superfamily        | c00015                      | putative nicotinamide-nucleotide adenylyltransferase                    |
|                | non-specific   | 7               | 70             | 4.89e-06     | PRK00379         | PRK05379                | PRK05379                    | bifunctional nicotinamide mononucleotide adenylyltransferase            |
|                | superfamily    | 1               | 70             | 4.89e-06     | cd02366         | PRK05379 superfamily    | c00015                      | bifunctional nicotinamide mononucleotide adenylyltransferase            |
|                | superfamily    | 8               | 63             | 8.69e-06     | cd02156         | nt_trans                | c00015                      | nicotinamide-nucleotide adenylyltransferase                             |
|                | non-specific   | 3               | 39             | 0.000122     | COG1056          | NadR                    | c00015                      | Nicotinamide mononucleotide adenylyltransferase                          |
|                | non-specific   | 7               | 139             | 0.000176     | cd02064          | FAD_synthetase_N         | c00015                      | FAD synthetase, N-terminal domain of the bifunctional enzyme            |
|                | non-specific   | 5               | 71             | 0.000571     | PRK00887         | PRK00887                | c00015                      | nicotinamide-nucleotide adenylyltransferase                             |
|                | non-specific   | 8               | 39             | 0.000958     | PRK00113         | PRK01153                | c00015                      | nicotinamide-nucleotide adenylyltransferase                             |
|                | non-specific   | 4               | 46             | 0.001423     | PTZ00308         | PTZ00308                | c00015                      | ethanolamine-phosphate cytidylyltransferase                              |
|                | superfamily    | 4               | 46             | 0.001423     | cd02266         | PLN02406 superfamily    | c00015                      | ethanolamine-phosphate cytidylyltransferase                              |
|                | superfamily    | 12              | 47             | 0.001912     | cd02174         |                          | c00015                      | CTP:phosphocholine cytidylyltransferase                                 |
|                | non-specific   | 7               | 146             | 0.001940     | cd02167         | NNMAT_NadR              | c00015                      | Nicotinamide/nicotinate mononucleotide adenylyltransferase               |
|                | non-specific   | 5               | 139             | 0.003724     | PRK00777         | PRK00777                | c00015                      | phosphopantetheine adenylyltransferase                                 |
|                | non-specific   | 8               | 39             | 0.004703     | COG00560         | NNMAT_Archeae            | c00015                      | Nicotinamide/nicotinate mononucleotide adenylyltransferase               |
|                | non-specific   | 7               | 29             | 0.004914     | cd02168         | NNMAT_Nudix              | c00015                      | Nicotinamide/nicotinate mononucleotide adenylyltransferase               |
| **M. pulmonis**| non-specific   | 1                | 35             | 0.0000176    | pfam02569        | Pantoate ligase          | c00015                      | Pantoate-beta-alanine ligase                                            |
| Query                                    | Hit type               | ID region start | ID region end | E-Value | Accession       | Short name               | Superfamily           | Definition                                                                 |
|------------------------------------------|------------------------|-----------------|----------------|---------|-----------------|--------------------------|-----------------------|--------------------------------------------------------------|
| **M. pulmonis**                          | non-specific           | 6               | 67             | 0.005299| PRK01170        | accD_prev_kdtB            | c00015                           | phosphopantetheine adenyltransferase                        |
|                                          | superfamily            | 6               | 67             | 0.005299| c000866         | NTPase I-T superfamily   | c00015                           | Protein of unknown function DUF84                          |
|                                          | non-specific           | 1               | 139            | 0.005711| COG1019         | CKB4                     | c00015                           | Phosphopantetheine adenyltransferase                        |
|                                          | non-specific           | 6               | 60             | 0.007006| c02171          | G3P Cytidylyltransferase  | c00015                           | glycero-3-phosphate cytidylyltransferase                    |
|                                          | superfamily            | 3               | 141            | 1.92e-54| TIGR01510       | c00015 nt_trans superfamily | -                               | nucleotidyl transferase superfamily                        |
|                                          | non-specific           | 1               | 140            | 1.67e-53| PRK13964        | coaD                      | c00015                           | phosphopantetheine adenyltransferase                        |
|                                          | non-specific           | 1               | 141            | 1.78e-53| PRK00168        | coaD                      | c00015                           | phosphopantetheine adenyltransferase                        |
|                                          | non-specific           | 3               | 141            | 1.79e-50| c02163           | PPAT                      | c00015                           | Phosphopantetheine adenyltransferase                        |
|                                          | non-specific           | 1               | 141            | 1.96e-50| COG0669         | CoaD                      | c00015                           | Phosphopantetheine adenyltransferase                        |
|                                          | non-specific           | 5               | 135            | 4.78e-15| pfam01467       | CTP trans/like            | c00015                           | Cytidylyltransferase-like                                   |
|                                          | non-specific           | 3               | 134            | 2.73e-12| c02039          | cytidylyltransferase_like | c00015                           | Cytidylyltransferase-like domain                             |
|                                          | non-specific           | 3               | 63             | 4.33e-12| TIGR00125       | cyt_tran_rel              | c00015                           | cytidylyltransferase-like domain                             |
|                                          | non-specific           | 1               | 66             | 1.60e-09| COG1057         | NaD                       | c00015                           | Nicotinic acid mononucleotide adenyltransferase             |
|                                          | non-specific           | 1               | 66             | 4.28e-08| PRK07152        | nadD                      | c028367                          | putative nicotinate-nucleotide adenyltransferase            |
|                                          | superfamily            | 6               | 66             | 4.38e-08| c028367         | nadD superfamily          | -                               | putative nicotinate-nucleotide adenyltransferase            |
|                                          | non-specific           | 3               | 66             | 2.30e-07| c02165          | NNMAT                     | c00015                           | Nicotinamide/nicotinate mononucleotide adenyltransferase    |
|                                          | non-specific           | 1               | 35             | 2.44e-07| COG1056         | NaD                       | c00015                           | Nicotinamide mononucleotide adenyltransferase               |
|                                          | non-specific           | 1               | 66             | 1.14e-06| PRK00071        | naD                       | c00015                           | nicotinic acid mononucleotide adenyltransferase             |
|                                          | non-specific           | 1               | 64             | 1.61e-05| TIGR01526       | nadR_NMN_Atrans           | c028365                          | nicotinamide-nucleotide adenyltransferase                   |
|                                          | superfamily            | 1               | 64             | 1.61e-05| c028365         | PRK08099 superfamily      | -                               | bifunctional DNA-binding transcriptional repressor/ NMN adenyltransferase |
|                                          | non-specific           | 8               | 134            | 1.66e-05| COG0615         | TagD                      | c00015                           | Glycerol-3-phosphate cytidylyltransferase, cytidylyltransferase family |
|                                          | non-specific           | 4               | 66             | 2.10e-05| TIGR01527       | arch_NMN_Atrans           | c00015                           | nicotinamide-nucleotide adenyltransferase                   |
|                                          | non-specific           | 3               | 39             | 4.29e-05| PRK05379        | PRK05379                  | c028366                          | bifunctional nicotinamide mononucleotide adenyltransferase |
|                                          | superfamily            | 3               | 39             | 4.29e-05| c028366         | PRK05379 superfamily      | -                               | bifunctional nicotinamide mononucleotide adenyltransferase |
|                                          | non-specific           | 4               | 35             | 0.00012 | c02166          | NNMAT_Archaea             | c00015                           | Nicotinamide/nicotinate mononucleotide adenyltransferase    |
|                                          | non-specific           | 8               | 97             | 0.000166| c02170          | cytidylyltransferase      | c00015                           | cytidylyltransferase                                       |
|                                          | non-specific           | 1               | 135            | 0.000191| c02171          | G3P Cytidylyltransferase  | c00015                           | glycero-3-phosphate cytidylyltransferase                    |
|                                          | non-specific           | 4               | 35             | 0.000215| PRK01153        | PRK01153                  | c00015                           | nicotinamide-nucleotide adenyltransferase                   |
|                                          | non-specific           | 3               | 66             | 0.000497| c02167          | NNMAT Nadu                 | c00015                           | Nicotinamide/nicotinate mononucleotide adenyltransferase    |
|                                          | non-specific           | 3               | 24             | 0.000885| c02168          | NNMAT Nadu                 | c00015                           | Nicotinamide/nicotinate mononucleotide adenyltransferase    |
|                                          | non-specific           | 4               | 130            | 0.001521| c02156          | nt trans                   | c00015                           | nucleotidyl transferase superfamily                        |
|                                          | non-specific           | 5               | 85             | 0.002241| TIGR008482      | TIGR008482                | c00015                           | nicotinate (nicotinamide) nucleotide adenyltransferase      |
|                                          | non-specific           | 1               | 33             | 0.002402| PRK00777        | PRK00777                  | c00015                           | phosphopantetheine adenyltransferase                        |
|                                          | non-specific           | 8               | 35             | 0.002999| c02174          | CCT                       | c00015                           | CTP:phosphocholine cytidylyltransferase                     |
|                                          | non-specific           | 1               | 140            | 7.69e-56| PRK13964        | coaD                      | c00015                           | phosphopantetheine adenyltransferase                        |
|                                          | superfamily            | 1               | 140            | 7.69e-56| c00015         | nt_trans superfamily      | -                               | nucleotidyl transferase superfamily                        |
| **M. simbae**                            | non-specific           | 1               | 134            | 2.68e-43| COG0669         | CoaD                      | c00015                           | Phosphopantetheine adenyltransferase                        |
|                                          | non-specific           | 3               | 133            | 6.47e-40| c02163          | PPAT                      | c00015                           | Phosphopantetheine adenyltransferase                        |
|                                          | non-specific           | 1               | 133            | 1.02e-38| PRK00168        | coaD                      | c00015                           | Phosphopantetheine adenyltransferase                        |
|                                          | non-specific           | 3               | 133            | 2.41e-35| TIGR01510       | coaD_prev_kdtB             | c00015                           | pantetheine-phosphate adenyltransferase                     |

**M. putrefaciens**

**M. simbae**
| Query | Hit type | ID region start | ID region end | E-Value | Accession | Short name | Superfamily | Definition |
|-------|----------|----------------|--------------|---------|-----------|------------|-------------|------------|
| specific | 5 | 135 | 3.01e-18 | pfam01467 | CTP transf like | c00015 | Cytidylyltransferase-like |
| non-specific | 5 | 133 | 1.67e-09 | cd02167 | NMNAT NadR | c00015 | Nicotinamide/nicotinate mononucleotide adenylyltransferase |
| non-specific | 3 | 46 | 1.73e-09 | TIGR00125 | cyt tran rel | c00015 | cytidylyltransferase-like domain |
| non-specific | 3 | 133 | 1.59e-07 | cd02039 | cytidylyltransferase like | c00015 | Cytidylyltransferase-like domain |
| non-specific | 1 | 35 | 1.63e-07 | COG1056 | NadR | c00015 | Nicotinamide mononucleotide adenylyltransferase |
| non-specific | 1 | 66 | 2.64e-07 | COG1057 | NadD | c00015 | Nicotinic acid mononucleotide adenylyltransferase |
| non-specific | 1 | 66 | 2.74e-07 | PRK07152 | nadD | c00015 | putative nicotinate-nucleotide adenylyltransferase |
| superfamily | 1 | 66 | 2.74e-07 | l28367 | nadD superfamily | | putative nicotinate-nucleotide adenylyltransferase |
| non-specific | 4 | 41 | 5.16e-07 | cd02165 | NMNAT | c00015 | Nicotinamide/nicotinate mononucleotide adenylyltransferase |
| non-specific | 1 | 52 | 4.38e-06 | PRK00071 | nadD | c00015 | nicotinic acid mononucleotide adenylyltransferase |
| non-specific | 5 | 66 | 7.52e-06 | TIGR00482 | TIGR00482 | c00015 | nicotinate (nicotinamide) nucleotide adenylyltransferase |
| non-specific | 1 | 133 | 1.05e-05 | TIGR01526 | nadB_NMN_Atrans | c00015 | nicotinamide-nucleotide adenylyltransferase |
| superfamily | 1 | 133 | 1.05e-05 | l28365 | PRK08099 superfamily | | bifunctional DNA-binding transcriptional repressor/ NMN adenylyltransferase |
| non-specific | 1 | 33 | 1.95e-05 | PRK00777 | PRK00777 | c00015 | phosphopantetheine adenylyltransferase |
| non-specific | 4 | 68 | 2.47e-05 | PRK05379 | PRK05379 | c00015 | bifunctional nicotinamide mononucleotide adenylyltransferase |
| superfamily | 4 | 68 | 2.47e-05 | l28366 | PRK05379 superfamily | | bifunctional nicotinamide mononucleotide adenylyltransferase |
| non-specific | 3 | 35 | 3.94e-05 | cd02166 | NMNAT_Archaeb | c00015 | Nicotinamide/nicotinate mononucleotide adenylyltransferase |
| non-specific | 1 | 35 | 5.06e-05 | PRK01153 | PRK01153 | c00015 | nicotinate-nucleotide adenylyltransferase |
| non-specific | 3 | 56 | 7.86e-05 | TIGR01527 | arch_NMN_Atrans | c00015 | nicotinamide-nucleotide adenylyltransferase |
| non-specific | 8 | 134 | 0.000172 | PRK08099 | PRK08099 | c00015 | bifunctional DNA-binding transcriptional repressor/ NMN adenylyltransferase |
| non-specific | 4 | 42 | 0.000416 | cd02168 | NMNAT Nudix | c00015 | Nicotinamide/nicotinate mononucleotide adenylyltransferase |
| non-specific | 1 | 56 | 0.000768 | COG1019 | CAB4 | c00015 | Phosphopantetheine adenylyltransferase |
| non-specific | 1 | 36 | 0.001184 | cd02171 | G3P Cytidylyltransferase | c00015 | glycerol-3-phosphate cytidylyltransferase |
| non-specific | 8 | 27 | 0.002250 | pfam06574 | FAD syn | c00015 | FAD synthetase |
| non-specific | 7 | 59 | 0.004095 | cd02164 | PPT1_CoAS | c00015 | phosphopantetheine adenylyltransferase |
| non-specific | 3 | 57 | 0.00418 | cd02156 | nt trans | c00015 | nucleotidyl transferase superfamily |
| non-specific | 1 | 43 | 0.004248 | COG0615 | TagD | c00015 | Glycerol-3-phosphate cytidylyltransferase, cytidylyltransferase family |
| non-specific | 8 | 50 | 0.004811 | PTZ00308 | PTZ00308 | c00015 | ethanolamine-phosphate cytidylyltransferase |
| superfamily | 8 | 50 | 0.004811 | l28362 | PLN02406 superfamily | | ethanolamine-phosphate cytidylyltransferase |
| M. sturni | non-specific | 3 | 142 | 5.48e-59 | PRK13964 | coaD | c00015 | phosphopantetheine adenylyltransferase |
| superfamily | 3 | 142 | 5.48e-59 | cd00015 | | | | |
| non-specific | 4 | 144 | 8.41e-51 | COG00669 | Coal | c00015 | phosphopantetheine adenylyltransferase |
| non-specific | 5 | 144 | 4.45e-46 | cd02163 | PPT1 | c00015 | phosphopantetheine adenylyltransferase |
| non-specific | 4 | 144 | 2.23e-43 | PRK00168 | coaD | c00015 | phosphopantetheine adenylyltransferase |
| M. sturni | non-specific | 5 | 144 | 3.64e-42 | TIGR01510 | coaD prev kdtB | c00015 | pantetheine-phosphate adenylyltransferase |
| specific | 7 | 135 | 7.58e-27 | pfam01467 | CTP transf like | c00015 | Cytidylyltransferase-like |
| non-specific | 5 | 65 | 6.76e-14 | TIGR00125 | | c00015 | cytidylyltransferase-like domain |
| non-specific | 1 | 68 | 2.33e-12 | PRK00071 | nadD | c00015 | nicotinic acid mononucleotide adenylyltransferase |
| non-specific | 1 | 68 | 2.90e-11 | COG1057 | NadD | c00015 | Nicotinic acid mononucleotide adenylyltransferase |
| non-specific | 4 | 68 | 1.19e-10 | PRK07152 | nadD | c00015 | putative nicotinate-nucleotide adenylyltransferase |
| Query         | Hit type | ID region start | ID region end | E-Value   | Accession | Short name         | Superfamily                                                                                      | Definition                                                                                   |
|--------------|----------|----------------|---------------|-----------|-----------|-------------------|-----------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------|
| superfamily  | 4        | 68             |               | 1.19e-10  | cI28367   | nadD superfamily  | -                                                                               | putative nicotinate-nucleotide adenylyltransferase                                           |
| non-specific | 5        | 135            | 3.63e-10      | c02039    | cytidylyltransferase like | c00015 | Cytidylyltransferase-like domain |                                                                         |
| non-specific | 5        | 68             | 4.80e-10      | c02165    | NNMAT     | c00015            | Nicotinamide/nicotinate mononucleotide adenylyltransferase                               |
| non-specific | 1        | 136            | 6.18e-08      | PRK08099  | PRK08099  | cI28365           | -                                                                               | bifunctional DNA-binding transcriptional repressor/ NMN adenylyltransferase                  |
| superfamily  | 1        | 136            | 6.18e-08      | cI28365   | PRK08099  | cI28365           | -                                                                               | bifunctional DNA-binding transcriptional repressor/ NMN adenylyltransferase                  |
| non-specific | 7        | 64             | 2.74e-07      | TIGR00482 | TIGR00482 | c00015            | nicotinate (nicotinamide) nucleotide adenylyltransferase                              |
| non-specific | 4        | 135            | 6.18e-07      | TIGR01526 | nadR NMN Atrans | cI28365 | nicotinamide-nucleotide adenylyltransferase                                   |
| non-specific | 1        | 37             | 6.44e-07      | COG1056   | NadR      | c00015            | Nicotinamide mononucleotide adenylyltransferase                                      |
| non-specific | 5        | 68             | 2.02e-06      | c02167    | NNMAT NadR | c00015            | Nicotinamide/nicotinate mononucleotide adenylyltransferase                      |
| non-specific | 6        | 92             | 2.35e-06      | c02156    | nt trans  | c00015            | nucleotidyl transferase superfamily                                                   |
| non-specific | 10       | 72             | 3.65e-05      | PRK00777  | PRK00777  | c00015            | phosphopantetheine adenylyltransferase                                                |
| non-specific | 6        | 37             | 8.73e-05      | PRK01153  | PRK01153  | c00015            | nicotinamide-nucleotide adenylyltransferase                                       |
| non-specific | 6        | 37             | 0.000192      | c02166    | NNMAT Archaia | c00015 | Nicotinamide/nicotinate mononucleotide adenylyltransferase                 |
| non-specific | 7        | 37             | 0.000354      | c02173    | ECT       | c00015            | CTP:phosphoethanolamine cytidylyltransferase (ECT)                                    |
| non-specific | 10       | 78             | 0.00064       | COG1019   | CAB4      | c00015            | Phosphopantetheine adenylyltransferase                                                |
| non-specific | 4        | 37             | 0.000661      | cI28366   | PRK05379  | cI28366           | -                                                                               | ethanolamine-phosphate cytidylyltransferase                                                  |
| non-specific | 4        | 43             | 0.000784      | TIGR02199 | rfaE dom II | c00015            | rfaE: bifunctional protein, domain II                                                    |
| non-specific | 10       | 38             | 0.001375      | c02170    | cytidylyltransferase | c00015 | cytidylyltransferase                                                    |
| non-specific | 10       | 42             | 0.003324      | COG0615   | TagD      | c00015            | Glycerol-3-phosphate cytidylyltransferase, cytidylyltransferase family                |
| non-specific | 1        | 36             | 0.006569      | PRK05379  | PRK05379  | cI28366           | bifunctional nicotinamide mononucleotide adenylyltransferase                         |
| superfamily  | 1        | 36             | 0.006569      | cI28366   | PRK05379  | cI28366           | -                                                                               | bifunctional nicotinamide mononucleotide adenylyltransferase                                |
| specific     | 7        | 145            | 1.02e-70      | PRK13964  | coaD      | c00015            | phosphopantetheine adenylyltransferase                                                |
| superfamily  | 7        | 145            | 1.02e-70      | c00015    | nt trans  | superfamily       | -                                                                               | nucleotidyl transferase superfamily                                                       |
| non-specific | 5        | 139            | 8.48e-46      | COG0669   | CoaD      | c00015            | Phosphopantetheine adenylyltransferase                                              |
| non-specific | 8        | 138            | 7.40e-43      | c02163    | PPAT      | c00015            | Phosphopantetheine adenylyltransferase                                              |
| non-specific | 8        | 138            | 7.70e-39      | PRK00168  | coaD      | c00015            | phosphopantetheine adenylyltransferase                                              |
| non-specific | 8        | 138            | 2.99e-38      | TIGR01510 | coaD prev kdB | c00015 | pantetheine-phosphate adenylyltransferase                                 |
| specific     | 10       | 138            | 1.75e-21      | pfam01467 | CTP transf like | c00015 | Cytidylyltransferase-like                                     |
| non-specific | 8        | 40             | 3.49e-12      | TIGR00125 | cyt tran rel | c00015 | cytidylyltransferase-like-domain                                       |
| non-specific | 8        | 138            | 2.88e-11      | c02039    | cytidylyltransferase like | c00015 | Cytidylyltransferase-like-domain                                      |
| specific     | 7        | 71             | 5.01e-08      | COG1057   | NadD      | c00015            | Nicotinic acid mononucleotide adenylyltransferase                                   |
| non-specific | 8        | 44             | 6.67e-08      | c02156    | nt trans  | c00015            | nucleotidyl transferase superfamily                                                  |
| non-specific | 10       | 138            | 7.22e-08      | c02167    | NNMAT NadR | c00015            | Nicotinamide/nicotinate mononucleotide adenylyltransferase                         |
| M. synoviae  | 9        | 71             | 7.22e-08      | c02165    | NNMAT     | c00015            | Nicotinamide/nicotinate mononucleotide adenylyltransferase                           |
| non-specific | 3        | 46             | 1.03e-06      | PRK00071  | nadD      | c00015            | nicotinic acid mononucleotide adenylyltransferan                                      |
| non-specific | 13       | 41             | 1.37e-06      | c02170    | cytidylyltransferase | c00015 | cytidylyltransferase                                               |
| non-specific | 10       | 67             | 1.89e-06      | TIGR00482 | TIGR00482 | c00015            | nicotinate (nicotinamide) nucleotide adenylyltransferase                             |
| M. synoviae  | 13       | 90             | 2.20e-06      | COG0615   | TagD      | c00015            | Glycerol-3-phosphate cytidylyltransferase, cytidylyltransferase family                |
| Query | Hit type | ID region start | ID region end | E-Value | Accession | Short name | Superfamily | Definition |
|-------|----------|----------------|--------------|---------|-----------|------------|-------------|------------|
| non-specific | 7 | 48 | 6.80e-06 | PRK07152 | nadD | c28367 | putative nicotinate-nucleotide adenylyltransferase |
| superfamily | 7 | 48 | 6.80e-06 | c28367 | nadD superfamily | c00015 | putative nicotinate-nucleotide adenylyltransferase |
| non-specific | 7 | 40 | 2.13e-05 | COG1056 | NadR | c00015 | Nicotinamide mononucleotide adenylyltransferase |
| non-specific | 13 | 38 | 0.000116 | PRK00777 | PRK00777 | c00015 | phosphopantetheine adenylyltransferase |
| non-specific | 10 | 41 | 0.000464 | TIGR01526 | nadR_NMN_Atrans | c28365 | nicotinamide-nucleotide adenylyltransferase |
| superfamily | 10 | 41 | 0.000464 | c28365 | PRK08099 superfamily | - | bifunctional DNA-binding transcriptional repressor/ NMN adenylyltransferase |
| non-specific | 13 | 46 | 0.000556 | c002174 | CCT | c00015 | CTP:phosphocholine cytidylyltransferase |
| non-specific | 7 | 40 | 0.001029 | PRK01153 | PRK01153 | c00015 | nicotinamide-nucleotide adenylyltransferase |
| non-specific | 8 | 40 | 0.001086 | c002166 | NMNAT_Archaear | c00015 | Nicotinamide/nicotinate mononucleotide adenylyltransferase |
| non-specific | 12 | 46 | 0.001356 | PTZ00308 | PTZ00308 | c28362 | ethanolamine-phosphate cytidylyltransferase |
| superfamily | 12 | 46 | 0.001356 | c28362 | PLN02406 superfamily | - | ethanolamine-phosphate cytidylyltransferase |
| non-specific | 7 | 41 | 0.001661 | c002171 | G3P Cytidylyltransferase | c00015 | glycerol-3-phosphate cytidylyltransferase |
| non-specific | 8 | 46 | 0.002191 | c002173 | ECT | c00015 | CTP:phosphoethanolamine cytidylyltransferase (ECT) |
| non-specific | 13 | 62 | 0.002334 | TIGR01518 | g3p cytidyltranscripts | c00015 | glycerol-3-phosphate cytidylyltransferase |
| non-specific | 3 | 88 | 0.007463 | COG1019 | CAB4 | c00015 | Phosphopantetheine adenylyltransferase |
| non-specific | 13 | 139 | 0.009413 | PRK08099 | PRK08099 | c28365 | bifunctional DNA-binding transcriptional repressor/ NMN adenylyltransferase |
| non-specific | 4 | 138 | 6.38e-51 | c002163 | PPAT | c00015 | Phosphopantetheine adenylyltransferase |
| superfamily | 4 | 138 | 6.38e-51 | c00015 | nt_trans superfamily | - | nucleotidyl transferase superfamily |
| non-specific | 3 | 138 | 5.73e-50 | PRK00168 | coaD | c00015 | phosphopantetheine adenylyltransferase |
| non-specific | 1 | 138 | 6.30e-50 | COG0669 | CoaD | c00015 | phosphopantetheine adenylyltransferase |
| non-specific | 4 | 138 | 4.10e-46 | TIGR01510 | coaD_prev_kdtB | c00015 | panteptide-phosphate adenylyltransferase |
| non-specific | 3 | 145 | 6.67e-38 | PRK13964 | coaD | c00015 | phosphopantetheine adenylyltransferase |
| specific | 6 | 137 | 1.45e-21 | pfam01467 | CTP trans. like | c00015 | Cytidylyltransferase-like |
| non-specific | 4 | 62 | 5.82e-13 | TIGR00125 | cyt.trans.rel | c00015 | cytidylyltransferase-like domain |
| non-specific | 1 | 87 | 9.30e-13 | PRK00071 | nadD | c00015 | nicotinic acid mononucleotide adenylyltransferase |
| non-specific | 4 | 135 | 5.30e-11 | c002093 | cytidylyltransferase_like | c00015 | Cytidylyltransferase-like domain |
| non-specific | 4 | 142 | 7.57e-11 | c002165 | NMNAT | c00015 | Nicotinamide/nicotinate mononucleotide adenylyltransferase |
| non-specific | 1 | 136 | 3.00e-10 | COG1057 | NadD | c00015 | Nicotinic acid mononucleotide adenylyltransferase |
| non-specific | 5 | 36 | 9.11e-09 | c002166 | NMNAT_Archaear | c00015 | Nicotinamide/nicotinate mononucleotide adenylyltransferase |
| non-specific | 5 | 36 | 2.08e-08 | PRK01153 | PRK01153 | c00015 | nicotinamide-nucleotide adenylyltransferase |
| non-specific | 3 | 36 | 6.77e-08 | COG1056 | Nad | c00015 | Nicotinamide mononucleotide adenylyltransferase |
| non-specific | 1 | 142 | 1.49e-07 | PRK08887 | PRK08887 | c00015 | nicotinic acid mononucleotide adenylyltransferase |
| non-specific | 6 | 103 | 8.88e-07 | TIGR00482 | TIGR00482 | c00015 | nicotinamide (nicotinamides) nucleotide adenylyltransferase |
| non-specific | 5 | 48 | 2.28e-06 | c002156 | nt_trans | c00015 | nucleotidyl transferase superfamily |
| non-specific | 5 | 67 | 2.29e-05 | TIGR01527 | arch_NMN_Atrans | c00015 | nicotinamide-nucleotide adenylyltransferase |
| non-specific | 3 | 87 | 2.33e-05 | PRK07152 | nadD | c28367 | putative nicotinate-nucleotide adenylyltransferase |
| superfamily | 3 | 87 | 2.33e-05 | c28367 | nadD superfamily | - | putative nicotinate-nucleotide adenylyltransferase |
| non-specific | 4 | 33 | 5.56e-05 | PRK05379 | PRK05379 | c28366 | bifunctional nicotinate mononucleotide adenylyltransferase |
| superfamily | 4 | 33 | 5.56e-05 | c28366 | PRK05379 superfamily | - | bifunctional nicotinate mononucleotide adenylyltransferase |
| non-specific | 2 | 36 | 8.10e-05 | PTZ00308 | PTZ00308 | c28362 | ethanolamine-phosphate cytidylyltransferase |
| superfamily | 2 | 36 | 8.10e-05 | c28362 | PLN02406 superfamily | - | ethanolamine-phosphate cytidylyltransferase |
| Query | Hit type | ID region start | ID region end | E-Value | Accession | Short name | Superfamily | Definition |
|-------|----------|----------------|--------------|---------|-----------|------------|-------------|------------|
| non-specific | 9 | 42 | 8.99e-05 | COG0615 | TagD | c00015 | Glycerol-3-phosphate cytidylyltransferase, cytidylyltransferase family |
| non-specific | 9 | 56 | 9.03e-05 | cd02170 | cytidylyltransferase | c00015 | cytidylyltransferase |
| non-specific | 3 | 36 | 0.000179 | cd02173 | ECT | c00015 | CTP-phosphoethanolamine cytidylyltransferase (ECT) |
| non-specific | 4 | 36 | 0.000766 | cd02168 | NMNAT Nudix | c00015 | Nicotinamide/nicotinate mononucleotide adenylyltransferase |
| non-specific | 3 | 37 | 0.001214 | cd02171 | G3P Cytidylyltransferase | c00015 | glycerol-3-phosphate cytidylyltransferase |
| non-specific | 1 | 36 | 0.003597 | PRK00777 | PRK00777 | c00015 | phosphopantetheine adenylyltransferase |
| superfamily | 3 | 139 | 2.57e-56 | TIGR01510 | coaD prev kdlB | c00015 | pantetheine-phosphate adenylyltransferase |
| superfamily | 1 | 135 | 9.05e-55 | PRK00168 | coaD | c00015 | phosphopantetheine adenylyltransferase |
| non-specific | 1 | 140 | 1.17e-53 | PRK13964 | coaD | c00015 | phosphopantetheine adenylyltransferase |
| non-specific | 1 | 140 | 1.38e-52 | COG0669 | CoaD | c00015 | phosphopantetheine adenylyltransferase |
| non-specific | 3 | 139 | 1.53e-52 | cd02163 | PPAT | c00015 | phosphopantetheine adenylyltransferase |
| specific | 5 | 135 | 3.84e-20 | pfam01467 | CTP transf like | c00015 | Cytidylyltransferase-like |
| non-specific | 3 | 63 | 1.68e-14 | TIGR00125 | cytid trans rel | c00015 | cytidylyltransferase-like domain |
| non-specific | 3 | 134 | 1.00e-13 | cd02039 | cytidylyltransferase like | c00015 | Cytidylyltransferase-like domain |
| non-specific | 3 | 66 | 1.63e-09 | cd02165 | NMNAT | c00015 | Nicotinamide/nicotinate mononucleotide adenylyltransferase |
| non-specific | 1 | 35 | 5.73e-09 | COG1056 | NadR | c00015 | Nicotinamide mononucleotide adenylyltransferase |
| non-specific | 1 | 60 | 2.21e-08 | COG1057 | NadD | c00015 | Nicotinic acid mononucleotide adenylyltransferase |
| superfamily | 1 | 66 | 1.18e-07 | TIGR07152 | nadD | c23867 | putative nicotinate-nucleotide adenylyltransferase |
| non-specific | 4 | 66 | 1.83e-07 | TIGR01527 | arch NMN Atrans | c00015 | nicotinamide-nucleotide adenylyltransferase |
| superfamily | 1 | 57 | 2.01e-07 | cd02171 | G3P Cytidylyltransferase | c00015 | glycerol-3-phosphate cytidylyltransferase |
| non-specific | 4 | 35 | 3.01e-07 | PRK01153 | PRK01153 | c00015 | nicotinamide-nucleotide adenylyltransferase |
| non-specific | 4 | 35 | 5.09e-07 | cd02166 | NMNAT_Archaea | c00015 | Nicotinamide/nicotinate mononucleotide adenylyltransferase |
| non-specific | 8 | 89 | 5.98e-07 | cd02170 | cytidylyltransferase | c00015 | cytidylyltransferase |
| non-specific | 1 | 69 | 7.93e-07 | TIGR01526 | nadR NMN Atrans | c23865 | nicotinamide-nucleotide adenylyltransferase |
| superfamily | 1 | 69 | 7.93e-07 | TIGR01526 | nadR NMN Atrans | c23865 | nicotinamide-nucleotide adenylyltransferase |
| superfamily | 3 | 55 | 9.84e-07 | TIGR01526 | nadR NMN Atrans | c23865 | nicotinamide-nucleotide adenylyltransferase |
| superfamily | 3 | 55 | 9.84e-07 | TIGR01526 | nadR NMN Atrans | c23865 | nicotinamide-nucleotide adenylyltransferase |
| non-specific | 1 | 66 | 1.10e-06 | PRK00071 | nadD | c00015 | nicotinic acid mononucleotide adenylyltransferase |
| non-specific | 4 | 130 | 4.04e-06 | cd02156 | nt trans | c00015 | nucleotidyl transferase superfamily |
| non-specific | 3 | 66 | 1.23e-05 | cd02167 | NMNAT_NadR | c00015 | Nicotinamide/nicotinate mononucleotide adenylyltransferase |
| superfamily | 8 | 89 | 1.30e-05 | COG0615 | TagD | c00015 | Glycerol-3-phosphate cytidylyltransferase, cytidylyltransferase family |
| superfamily | 8 | 37 | 5.40e-05 | cd02168 | NMNAT Nudix | c00015 | Nicotinamide/nicotinate mononucleotide adenylyltransferase |
| non-specific | 1 | 33 | 0.000427 | PRK00777 | PRK00777 | c00015 | phosphopantetheine adenylyltransferase |
| non-specific | 5 | 54 | 0.001052 | TIGR00482 | TIGR00482 | c00015 | nicotinate (nicotinamide) nucleotide adenylyltransferase |
| non-specific | 8 | 54 | 0.001145 | TIGR01518 | g3p cytidylms | c00015 | glycerol-3-phosphate cytidylyltransferase |
| superfamily | 8 | 134 | 0.001474 | PRK07143 | PRK07143 | c27514 | hypothetical protein |
| superfamily | 8 | 134 | 0.001474 | C27514 | Flavokinase superfamily | c00015 | flavokinase |
| non-specific | 2 | 35 | 0.001999 | PTZ00308 | PTZ00308 | c23862 | ethanolamine-phosphate cytidylyltransferase |
| Query       | Hit type     | ID region start | ID region end | E-Value    | Accession | Short name                        | Superfamily          | Definition                                      |
|-------------|--------------|-----------------|---------------|------------|-----------|-----------------------------------|----------------------|------------------------------------------------|
| superfamily | 2            | 35              |               | 0.001999   | cl28626   | PLN02406 superfamily              | -                    | ethanolamine-phosphate cytidylyltransferase      |
| non-specific| 8            | 134             |               | 0.002964   | COG0196   | Rubf                              | c27514               | FAD synthase                                    |
| non-specific| 5            | 33              |               | 0.006077   | cd02173   | ECT                              | cl000015             | CTP:phosphoethanolamine cytidylyltransferase (ECT) |
| non-specific| 12           | 73              |               | 0.00806    | cd02169   | Citrate lyase ligase              | cl000015             | Citrate lyase ligase                            |

**Supplementary Table 11 PPAT InterPro results**

| Mycoplasma species | Amino acid region | Database | Database ID | Database signature description | ID region start | ID region end | InterPro ID | ID type | Gene Ontology (GO) term |
|--------------------|-------------------|----------|-------------|---------------------------------|----------------|--------------|-------------|---------|------------------------|
| *M. agalactiae*    | 140               | Gene3D   | G3DSA:3.40.50.620 | Phosphopantetheine adenylyltransferase [coaD]. | 1              | 140          | IPR014729   | H       | GO:0004595; GO:0015937 |
|                    |                   | Hamap    | MF_00151    | Phosphopantetheine adenylyltransferase [coaD]. | 2              | 140          | IPR001980   | F       | GO:0004595; GO:0015937 |
|                    |                   | PANTHER  | PTHR21342-SF1 | Cytidylyltransferase-like         | 1              | 139          | IPR001980   | F       | GO:0004595; GO:0015937 |
|                    |                   | PANTHER  | PTHR21342    | Lipopolysaccharide core biosynthesis protein signature | 1             | 139          | IPR001980   | F       | GO:0004595; GO:0015937 |
|                    |                   | Pfam     | PF01467     | Lipopolysaccharide core biosynthesis protein signature | 5              | 134          | IPR004821   | D       | GO:0003824; GO:0009058 |
|                    |                   | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 2              | 20           | IPR001980   | F       | GO:0004595; GO:0015937 |
|                    |                   | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 49             | 73           | IPR001980   | F       | GO:0004595; GO:0015937 |
|                    |                   | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 20             | 41           | IPR001980   | F       | GO:0004595; GO:0015937 |
|                    |                   | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 113            | 135          | IPR001980   | F       | GO:0004595; GO:0015937 |
|                    |                   | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 86             | 102          | IPR001980   | F       | GO:0004595; GO:0015937 |
|                    |                   | SUPERFAMILY | SSF52374 | coaD_prev_kdB: pantetheine-phosphate adenylyltransferase | 2              | 139          | IPR001980   | F       | GO:0004595; GO:0015937 |
|                    |                   | TIGRFAM  | TIGR01510   | Cytidylyltransferase-like         | 4              | 134          | IPR001980   | F       | GO:0004595; GO:0015937 |
|                    |                   | TIGRFAM  | TIGR00125   | Cytidylyltransferase-like         | 4              | 58           | IPR004821   | D       | GO:0003824; GO:0009058 |
| *M. alligatoris*   | 145               | Gene3D   | G3DSA:3.40.50.620 | Phosphopantetheine adenylyltransferase [coaD]. | 1              | 144          | IPR014729   | H       | GO:0004595; GO:0015937 |
|                    |                   | Hamap    | MF_00151    | Phosphopantetheine adenylyltransferase [coaD]. | 5              | 145          | IPR001980   | F       | GO:0004595; GO:0015937 |
|                    |                   | PANTHER  | PTHR21342-SF1 | Cytidylyltransferase-like         | 5              | 140          | IPR001980   | F       | GO:0004595; GO:0015937 |
|                    |                   | PANTHER  | PTHR21342    | Citrate lyase ligase              | 5              | 140          | IPR001980   | F       | GO:0004595; GO:0015937 |
|                    |                   | Pfam     | PF01467     | Cytidylyltransferase-like         | 8              | 139          | IPR004821   | D       | GO:0003824; GO:0009058 |
| Mycoplasma species | Amino acid region | Database | Database ID | Database signature description | ID region start | ID region end | InterPro ID | ID type | Gene Ontology (GO) term |
|--------------------|------------------|----------|-------------|--------------------------------|----------------|---------------|-------------|---------|------------------------|
|                    |                  | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 118            | 140           | IPR01980 F  |         | GO:0004595; GO:0015937 |
|                    |                  | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 5              | 23            | IPR01980 F  |         | GO:0004595; GO:0015937 |
|                    |                  | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 91             | 107           | IPR01980 F  |         | GO:0004595; GO:0015937 |
|                    |                  | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 23             | 44            | IPR01980 F  |         | GO:0004595; GO:0015937 |
|                    |                  | SUPERFAMILY | SSF52374 |                     | 5              | 141           |             |         |                        |
| M. alligatoris     | 145              | TIGRFAM  | TIGR01510   | coaD_prev_kdtB: pantetheine-phosphate adenylyltransferase | 7              | 139           | IPR01980 F  |         | GO:0004595; GO:0015937 |
|                    |                  | TIGRFAM  | TIGR00125   | cyt_tran_rel: cytidylytransferase-like domain | 7              | 63            | IPR004821 D |         | GO:0003824; GO:0009058 |
|                    |                  | Gene3D   | 3.40.50.620 |                     | 1              | 149           | IPR014729 H |         |                        |
|                    |                  | Hamap    | MF_00151    | Phosphopantetheine adenylyltransferase [coaD]. | 4              | 151           | IPR01980 F  |         | GO:0004595; GO:0015937 |
|                    |                  | PANTHER  | PTHR21342   |                     | 4              | 140           | IPR01980 F  |         | GO:0004595; GO:0015937 |
|                    |                  | PANTHER  | PTHR21342:SF1 |                     | 4              | 140           | IPR01980 F  |         | GO:0004595; GO:0015937 |
|                    |                  | Pfam     | PF01467     | Cytidylytransferase-like | 7              | 137           | IPR004821 D |         | GO:0003824; GO:0009058 |
|                    |                  | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 22             | 43            | IPR01980 F  |         | GO:0004595; GO:0015937 |
|                    |                  | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 116            | 138           | IPR01980 F  |         | GO:0004595; GO:0015937 |
|                    |                  | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 89             | 105           | IPR01980 F  |         | GO:0004595; GO:0015937 |
|                    |                  | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 4              | 22            | IPR01980 F  |         | GO:0004595; GO:0015937 |
|                    |                  | SUPERFAMILY | SSF52374 |                     | 4              | 143           |             |         |                        |
|                    |                  | TIGRFAM  | TIGR00125   | cyt_tran_rel: cytidylytransferase-like domain | 5              | 39            | IPR004821 D |         | GO:0003824; GO:0009058 |
|                    |                  | TIGRFAM  | TIGR01510   | coaD_prev_kdtB: pantetheine-phosphate adenylyltransferase | 5              | 140           | IPR01980 F  |         | GO:0004595; GO:0015937 |
|                    |                  | Gene3D   | 3.40.50.620 |                     | 1              | 143           | IPR014729 H |         |                        |
|                    |                  | Hamap    | MF_00151    | Phosphopantetheine adenylyltransferase [coaD]. | 4              | 143           | IPR01980 F  |         | GO:0004595; GO:0015937 |
|                    |                  | PANTHER  | PTHR21342:SF1 |                     | 4              | 135           | IPR01980 F  |         | GO:0004595; GO:0015937 |
|                    |                  | PANTHER  | PTHR21342   |                     | 4              | 135           | IPR01980 F  |         | GO:0004595; GO:0015937 |
|                    |                  | Pfam     | PF01467     | Cytidylytransferase-like | 7              | 135           | IPR004821 D |         | GO:0003824; GO:0009058 |
|                    |                  | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 115            | 137           | IPR01980 F  |         | GO:0004595; GO:0015937 |

M. alvi

| Mycoplasma species | Amino acid region | Database | Database ID | Database signature description | ID region start | ID region end | InterPro ID | ID type | Gene Ontology (GO) term |
|--------------------|------------------|----------|-------------|--------------------------------|----------------|---------------|-------------|---------|------------------------|
|                    | 151              | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 22             | 43            | IPR01980 F  |         | GO:0004595; GO:0015937 |
|                    |                  | SUPERFAMILY | SSF52374 |                     | 4              | 143           |             |         |                        |
|                    |                  | TIGRFAM  | TIGR00125   | cyt_tran_rel: cytidylytransferase-like domain | 5              | 39            | IPR004821 D |         | GO:0003824; GO:0009058 |

M. anatis

| Mycoplasma species | Amino acid region | Database | Database ID | Database signature description | ID region start | ID region end | InterPro ID | ID type | Gene Ontology (GO) term |
|--------------------|------------------|----------|-------------|--------------------------------|----------------|---------------|-------------|---------|------------------------|
| Mycoplasma species | Amino acid region | Database | Database ID | Database signature description | ID region start | ID region end | InterPro ID | ID type | Gene Ontology (GO) term |
|--------------------|------------------|----------|-------------|--------------------------------|----------------|--------------|-------------|---------|----------------------|
| **M. anatis**       | 143              | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 22             | 43           | IPR01980    | F       | GO:0004595; GO:0015937 |
|                     |                  | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 88             | 104          | IPR01980    | F       | GO:0004595; GO:0015937 |
|                     |                  | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 51             | 75           | IPR01980    | F       | GO:0004595; GO:0015937 |
|                     |                  | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 4              | 22           | IPR01980    | F       | GO:0004595; GO:0015937 |
|                     |                  | SUPERFAMILY | SSF52374   |                                  | 4              | 138          |             |         |                      |
|                     |                  | TIGRFAM  | TIGR01510   | coaD_prev_kdtB: pantetheine-phosphate adenylyltransferase | 6              | 136          | IPR01980    | F       | GO:0004595; GO:0015937 |
|                     |                  | TIGRFAM  | TIGR00125   | cyt_tran_rel: cytidylyltransferase-like domain | 6              | 46           | IPR004821   | D       | GO:0003824; GO:0009058 |
|                     |                  | Gene3D   | G3DSA:3.40.50.620 |                      | 1              | 142          | IPR014729   | H       |                      |
|                     |                  | Hamap    | MF_00151    | Phosphopantetheine adenylyltransferase [coaD]. | 2              | 143          | IPR01980    | F       | GO:0004595; GO:0015937 |
|                     |                  | PANTHER  | PTHR21342-SF1 |                                      | 1              | 138          | IPR01980    | F       | GO:0004595; GO:0015937 |
|                     |                  | PANTHER  | PTHR21342   |                                  | 1              | 138          |             |         |                      |
|                     |                  | Pfam     | PF01467     | Cytidylyltransferase-like | 5              | 134          | IPR004821   | D       | GO:0003824; GO:0009058 |
|                     |                  | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 86             | 102          | IPR01980    | F       | GO:0004595; GO:0015937 |
|                     |                  | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 2              | 20           | IPR01980    | F       | GO:0004595; GO:0015937 |
|                     |                  | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 113            | 135          | IPR01980    | F       | GO:0004595; GO:0015937 |
|                     |                  | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 20             | 41           | IPR01980    | F       | GO:0004595; GO:0015937 |
|                     |                  | SUPERFAMILY | SSF52374   |                                  | 2              | 140          |             |         |                      |
|                     |                  | TIGRFAM  | TIGR01510   | coaD_prev_kdtB: pantetheine-phosphate adenylyltransferase | 4              | 134          | IPR01980    | F       | GO:0004595; GO:0015937 |
|                     |                  | TIGRFAM  | TIGR00125   | cyt_tran_rel: cytidylyltransferase-like domain | 4              | 55           | IPR004821   | D       | GO:0003824; GO:0009058 |
| **M. arginini**     | 143              | Gene3D   | G3DSA:3.40.50.620 |                      | 1              | 139          | IPR014729   | H       |                      |
|                     |                  | PANTHER  | PTHR21342-SF1 |                                      | 1              | 136          | IPR01980    | F       | GO:0004595; GO:0015937 |
|                     |                  | PANTHER  | PTHR21342   |                                  | 1              | 136          |             |         |                      |
|                     |                  | Pfam     | PF01467     | Cytidylyltransferase-like | 5              | 134          | IPR004821   | D       | GO:0003824; GO:0009058 |
|                     |                  | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 113            | 135          | IPR01980    | F       | GO:0004595; GO:0015937 |
| **M. bovigenitalium** | 140           | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 2              | 20           | IPR01980    | F       | GO:0004595; GO:0015937 |
| Mycoplasma species | Amino acid region | Database | Database ID | Database signature description | ID region start | ID region end | InterPro ID | ID type | Gene Ontology (GO) term |
|--------------------|-------------------|----------|-------------|-------------------------------|----------------|----------------|-------------|--------|------------------------|
| M. bovigenitalium | 140               | PR01020  | Lipopolysaccharide core biosynthesis protein signature | 86              | 102             | IPR001980   | F        | GO:0004595; GO:0015937 |
|                    |                   | PR01020  | Lipopolysaccharide core biosynthesis protein signature | 49              | 73              | IPR001980   | F        | GO:0004595; GO:0015937 |
|                    |                   | PR01020  | Lipopolysaccharide core biosynthesis protein signature | 20              | 41              | IPR001980   | F        | GO:0004595; GO:0015937 |
|                    |                   | SSF52374 |                          | 2                | 136             |             |          |                        |
|                    |                   | TIGRFAM  | TIGR01510                | 4                | 134             | IPR001980   | F        | GO:0004595; GO:0015937 |
|                    | 140               | TIGRFAM  | TIGR00125                | 4                | 59              | IPR004821   | D        | GO:0003824; GO:0009058 |
| M. bovis           | 140               | Gene3D   | G3DSA:3.40.50.620        | 1                | 140             | IPR014729   | H        |                          |
|                    |                   | Hamap    | MF_00151                 | 2                | 140             | IPR001980   | F        | GO:0004595; GO:0015937 |
|                    |                   | PANTHER  | PTHR21342                | 1                | 139             | IPR001980   | F        | GO:0004595; GO:0015937 |
|                    |                   | PANTHER  | PTHR21342:SF1            | 1                | 139             | IPR001980   | F        | GO:0004595; GO:0015937 |
|                    |                   | Pfam     | PF01467                  | 5                | 134             | IPR04821    | D        | GO:0003824; GO:0009058 |
|                    |                   | PR01020  | Lipopolysaccharide core biosynthesis protein signature | 49              | 73              | IPR001980   | F        | GO:0004595; GO:0015937 |
|                    |                   | PR01020  | Lipopolysaccharide core biosynthesis protein signature | 2                | 20              | IPR001980   | F        | GO:0004595; GO:0015937 |
|                    |                   | PR01020  | Lipopolysaccharide core biosynthesis protein signature | 20              | 41              | IPR001980   | F        | GO:0004595; GO:0015937 |
|                    |                   | PR01020  | Lipopolysaccharide core biosynthesis protein signature | 113             | 135             | IPR001980   | F        | GO:0004595; GO:0015937 |
|                    |                   | PR01020  | Lipopolysaccharide core biosynthesis protein signature | 86              | 102             | IPR001980   | F        | GO:0004595; GO:0015937 |
|                    |                   | SSF52374 |                          | 2                | 139             |             |          |                        |
|                    |                   | TIGRFAM  | TIGR00125                | 4                | 55              | IPR004821   | D        | GO:0003824; GO:0009058 |
|                    |                   | TIGRFAM  | TIGR01510                | 4                | 134             | IPR001980   | F        | GO:0004595; GO:0015937 |
| M. buteonis        | 148               | Coils    | Coil                     | 70               | 90              |             |          |                        |
|                    |                   | Gene3D   | G3DSA:3.40.50.620        | 3                | 147             | IPR014729   | H        |                          |
|                    |                   | Hamap    | MF_00151                 | 6                | 148             | IPR001980   | F        | GO:0004595; GO:0015937 |
|                    |                   | PANTHER  | PTHR21342                | 6                | 140             | IPR001980   | F        | GO:0004595; GO:0015937 |
|                    |                   | PANTHER  | PTHR21342:SF1            | 6                | 140             | IPR001980   | F        | GO:0004595; GO:0015937 |
|                    |                   | Pfam     | PF01467                  | 9                | 140             | IPR004821   | D        | GO:0003824; GO:0009058 |
| Mycoplasma species | Amino acid region | Database | Database ID | Database signature description | ID region start | ID region end | InterPro ID | ID type | Gene Ontology (GO) term |
|--------------------|-------------------|----------|-------------|-------------------------------|----------------|---------------|-------------|---------|-------------------------|
| M. buteonis        | 148               | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 24             | 45            | IPR001980   | F       | GO:0004595; GO:0015937  |
|                    | TIGRFAM           | TIGR01510| coaD_prev_kdtB: pantetheine-phosphate adenylyltransferase | 7              | 144           | IPR001980   | F       | GO:0004595; GO:0015937  |
|                    | TIGRFAM           | TIGR00125| cyt_tran_rel: cytidyltransferase-like domain | 7              | 62            | IPR004821   | D       | GO:0003824; GO:0009058  |
|                    | Gene3D            | G3DSA:3:40.50.620 |                | 1               | 142           | IPR014729   | H       |                     |
|                    | PANTHER           | PTHR21342:SF1 |                | 1               | 138           | IPR001980   | F       | GO:0004595; GO:0015937  |
|                    | Pfam              | PF01467   | Cytidylyltransferase-like | 5              | 134           | IPR004821   | D       | GO:0003824; GO:0009058  |
|                    | PRINTS            | PR01020   | Lipopolysaccharide core biosynthesis protein signature | 2              | 20            | IPR001980   | F       | GO:0004595; GO:0015937  |
|                    | PRINTS            | PR01020   | Lipopolysaccharide core biosynthesis protein signature | 86             | 102           | IPR001980   | F       | GO:0004595; GO:0015937  |
|                    | PRINTS            | PR01020   | Lipopolysaccharide core biosynthesis protein signature | 49             | 73            | IPR001980   | F       | GO:0004595; GO:0015937  |
|                    | PRINTS            | PR01020   | Lipopolysaccharide core biosynthesis protein signature | 113            | 135           | IPR001980   | F       | GO:0004595; GO:0015937  |
|                    | PRINTS            | PR01020   | Lipopolysaccharide core biosynthesis protein signature | 20             | 41            | IPR001980   | F       | GO:0004595; GO:0015937  |
|                    | SUPERFAMILY       | SSF52374  |                | 2               | 140           |              |         |                     |
|                    | TIGRFAM           | TIGR00125| cyt_tran_rel: cytidyltransferase-like domain | 4              | 57            | IPR004821   | D       | GO:0003824; GO:0009058  |
|                    | TIGRFAM           | TIGR01510| coaD_prev_kdtB: pantetheine-phosphate adenylyltransferase | 4              | 134           | IPR001980   | F       | GO:0004595; GO:0015937  |
| M. californicum    | 143               | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 89             | 105           | IPR001980   | F       | GO:0004595; GO:0015937  |
|                    | Coils             | Coils     |                | 46             | 66            |              |         |                     |
|                    | Gene3D            | G3DSA:3:40.50.620 |                | 1               | 142           | IPR014729   | H       |                     |
|                    | PANTHER           | PTHR21342 |                | 5               | 139           | IPR001980   | F       | GO:0004595; GO:0015937  |
|                    | PANTHER           | PTHR21342:SF1 |                | 5               | 139           | IPR001980   | F       | GO:0004595; GO:0015937  |
|                    | Pfam              | PF01467   | Cytidylyltransferase-like | 8              | 137           | IPR004821   | D       | GO:0003824; GO:0009058  |
|                    | PRINTS            | PR01020   | Lipopolysaccharide core biosynthesis protein signature |                 |               | IPR001980   | F       | GO:0004595; GO:0015937  |
| M. canis           | 143               | Coils     | Coils        | 46             | 66            |              |         |                     |
|                    | Gene3D            | G3DSA:3:40.50.620 |                | 1               | 142           | IPR014729   | H       |                     |
|                    | PANTHER           | PTHR21342 |                | 5               | 139           | IPR001980   | F       | GO:0004595; GO:0015937  |
|                    | PANTHER           | PTHR21342:SF1 |                | 5               | 139           | IPR001980   | F       | GO:0004595; GO:0015937  |
|                    | Pfam              | PF01467   | Cytidylyltransferase-like | 8              | 137           | IPR004821   | D       | GO:0003824; GO:0009058  |
|                    | PRINTS            | PR01020   | Lipopolysaccharide core biosynthesis protein signature |                 |               | IPR001980   | F       | GO:0004595; GO:0015937  |
| Mycoplasma species | Amino acid region | Database | Database ID | Database signature description | ID region start | ID region end | InterPro ID | ID type | Gene Ontology (GO) term |
|--------------------|-------------------|----------|-------------|-------------------------------|----------------|--------------|-------------|---------|------------------------|
| M. canis | 143 | PRINTS | PR01020 | Lipopolysaccharide core biosynthesis protein signature | 116 | 138 | IPR001980 | F | GO:0004595; GO:0015937 |
| | | PRINTS | PR01020 | Lipopolysaccharide core biosynthesis protein signature | 5 | 23 | IPR001980 | F | GO:0004595; GO:0015937 |
| | | PRINTS | PR01020 | Lipopolysaccharide core biosynthesis protein signature | 23 | 44 | IPR001980 | F | GO:0004595; GO:0015937 |
| | | SUPERFAMILY | SSF52374 | | 5 | 138 | | | |
| | | TIGRFAM | TIGR01510 | coaD_prev_kdtB: pantetheine-phosphate adenylyltransferase | 7 | 139 | IPR001980 | F | GO:0004595; GO:0015937 |
| M. capricolum | 140 | Gene3D | G3DSA:3.40.50.620 | | 1 | 137 | IPR014729 | H | |
| | | Hamap | MF_00151 | Phosphopantetheine adenylyltransferase [coaD]. | 2 | 140 | IPR001980 | F | GO:0004595; GO:0015937 |
| | | PANTHER | PTHR21342:SF1 | | 1 | 138 | IPR001980 | F | GO:0004595; GO:0015937 |
| | | PANTHER | PTHR21342 | | 5 | 134 | IPR004821 | D | GO:0003824; GO:0009058 |
| | | Pfam | PF01467 | Cytidylyltransferase-like | 2 | 140 | IPR004821 | D | GO:0003824; GO:0009058 |
| | | PRINTS | PR01020 | Lipopolysaccharide core biosynthesis protein signature | 113 | 135 | IPR001980 | F | GO:0004595; GO:0015937 |
| | | PRINTS | PR01020 | Lipopolysaccharide core biosynthesis protein signature | 2 | 20 | IPR001980 | F | GO:0004595; GO:0015937 |
| | | PRINTS | PR01020 | Lipopolysaccharide core biosynthesis protein signature | 49 | 73 | IPR001980 | F | GO:0004595; GO:0015937 |
| | | PRINTS | PR01020 | Lipopolysaccharide core biosynthesis protein signature | 86 | 102 | IPR001980 | F | GO:0004595; GO:0015937 |
| | | PRINTS | PR01020 | Lipopolysaccharide core biosynthesis protein signature | 20 | 41 | IPR001980 | F | GO:0004595; GO:0015937 |
| | | SUPERFAMILY | SSF52374 | | 2 | 138 | | | |
| | | TIGRFAM | TIGR01510 | coaD_prev_kdtB: pantetheine-phosphate adenylyltransferase | 3 | 139 | IPR001980 | F | GO:0004595; GO:0015937 |
| | | TIGRFAM | TIGR00125 | cyt_tran_rel: cytidyltransferase-like domain | 3 | 61 | IPR004821 | D | GO:0003824; GO:0009058 |
| M. collis | 147 | Gene3D | G3DSA:3.40.50.620 | | 2 | 143 | IPR014729 | H | |
| | | Hamap | MF_00151 | Phosphopantetheine adenylyltransferase [coaD]. | 8 | 147 | IPR001980 | F | GO:0004595; GO:0015937 |
| | | PANTHER | PTHR21342 | | 7 | 139 | IPR001980 | F | GO:0004595; GO:0015937 |
| | | PANTHER | PTHR21342:SF1 | | 7 | 139 | IPR001980 | F | GO:0004595; GO:0015937 |
| | | Pfam | PF01467 | Cytidylyltransferase-like | 11 | 136 | IPR004821 | D | GO:0003824; GO:0009058 |
| | | PRINTS | PR01020 | Lipopolysaccharide core biosynthesis protein signature | 55 | 79 | IPR001980 | F | GO:0004595; GO:0015937 |
| Mycoplasma species | Amino acid region | Database | Database ID | Database signature description | ID region start | ID region end | InterPro ID | ID type | Gene Ontology (GO) term |
|--------------------|-------------------|----------|-------------|--------------------------------|----------------|--------------|-------------|---------|------------------------|
|                    |                   | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 8              | 26           | IPR01980    | F       | GO:0004595; GO:0015937 |
|                    |                   | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 26             | 47           | IPR01980    | F       | GO:0004595; GO:0015937 |
|                    |                   | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 92             | 108          | IPR01980    | F       | GO:0004595; GO:0015937 |
|                    |                   | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 119            | 141          | IPR01980    | F       | GO:0004595; GO:0015937 |
|                    |                   | SUPERFAMILY | SSF52374     |                                      | 8              | 141          |             |         |                        |
| M. collis          | 147               | TIGRFAM  | TIGR01510   | coaD_prev_kdtB: pantetheine-phosphate adenylyltransferase | 10             | 139          | IPR01980    | F       | GO:0004595; GO:0015937 |
|                    |                   | TIGRFAM  | TIGR00125   | cyt_tran_rel: cytidylytransferase-like domain | 10             | 67           | IPR004821   | D       | GO:0003824; GO:0009058  |
|                    |                   | Gene3D   | G3DSA:3.40.50.620 |                                      | 1              | 141          | IPR014729   | H       |                        |
|                    |                   | Hamap    | MF_00151    | Phosphopantetheine adenylyltransferase [coaD]. | 3              | 142          | IPR01980    | F       | GO:0004595; GO:0015937 |
|                    |                   | PANTHER  | PTHR21342   |                                      | 1              | 138          | IPR01980    | F       | GO:0004595; GO:0015937 |
|                    |                   | Pfam     | PF01467     | Cytidylytransferase-like | 6              | 136          | IPR004821   | D       | GO:0003824; GO:0009058  |
|                    |                   | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 115            | 137          | IPR01980    | F       | GO:0004595; GO:0015937 |
|                    |                   | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 21             | 42           | IPR01980    | F       | GO:0004595; GO:0015937 |
|                    |                   | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 3              | 21           | IPR01980    | F       | GO:0004595; GO:0015937 |
|                    |                   | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 88             | 104          | IPR01980    | F       | GO:0004595; GO:0015937 |
|                    |                   | SUPERFAMILY | SSF52374     |                                      | 3              | 141          |             |         |                        |
|                    |                   | TIGRFAM  | TIGR00125   | cyt_tran_rel: cytidylytransferase-like domain | 4              | 57           | IPR004821   | D       | GO:0003824; GO:0009058  |
|                    |                   | TIGRFAM  | TIGR01510   | coaD_prev_kdtB: pantetheine-phosphate adenylyltransferase | 4              | 136          | IPR01980    | F       | GO:0004595; GO:0015937 |
|                    |                   | Gene3D   | G3DSA:3.40.50.620 |                                      | 1              | 139          | IPR014729   | H       |                        |
|                    |                   | Hamap    | MF_00151    | Phosphopantetheine adenylyltransferase [coaD]. | 4              | 141          | IPR01980    | F       | GO:0004595; GO:0015937 |
|                    |                   | PANTHER  | PTHR21342   |                                      | 4              | 136          | IPR01980    | F       | GO:0004595; GO:0015937 |
|                    |                   | Pfam     | PF01467     | Cytidylytransferase-like | 7              | 136          | IPR004821   | D       | GO:0003824; GO:0009058  |
|                    |                   | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 115            | 137          | IPR01980    | F       | GO:0004595; GO:0015937 |
| M. columbinum      | 142               | TIGRFAM  | TIGR00125   | cyt_tran_rel: cytidylytransferase-like domain | 4              | 57           | IPR004821   | D       | GO:0003824; GO:0009058  |
|                    |                   | TIGRFAM  | TIGR01510   | coaD_prev_kdtB: pantetheine-phosphate adenylyltransferase | 4              | 136          | IPR01980    | F       | GO:0004595; GO:0015937 |
| M. columborale     | 142               | Gene3D   | G3DSA:3.40.50.620 |                                      | 1              | 139          | IPR014729   | H       |                        |
|                    |                   | Hamap    | MF_00151    | Phosphopantetheine adenylyltransferase [coaD]. | 4              | 141          | IPR01980    | F       | GO:0004595; GO:0015937 |
|                    |                   | PANTHER  | PTHR21342   |                                      | 4              | 136          | IPR01980    | F       | GO:0004595; GO:0015937 |
|                    |                   | Pfam     | PF01467     | Cytidylytransferase-like | 7              | 136          | IPR004821   | D       | GO:0003824; GO:0009058  |
|                    |                   | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 115            | 137          | IPR01980    | F       | GO:0004595; GO:0015937 |
| Mycoplasma species | Amino acid region | Database | Database ID | Database signature description | ID region start | ID region end | InterPro ID | ID type | Gene Ontology (GO) term |
|--------------------|-------------------|----------|-------------|--------------------------------|----------------|--------------|-------------|---------|------------------------|
| **M. columborae**  | 142               | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 34             | 55           | IPR001980  | F       | GO:0004595; GO:0015937  |
|                    |                   | SUPERFAMILY | SSF52374   |                                | 5              | 136          | IPR001980  | F       | GO:0003824; GO:0009058  |
|                    |                   | TIGRFAM  | TIGR00125   | cyt_tran_rel: cytidyltransferase-like domain | 5              | 46           | IPR004821  | D       | GO:0003824; GO:0009058  |
|                    |                   | TIGRFAM  | TIGR01510   | coaD_prev_kdtB: pantetheine-phosphate adenylyltransferase | 5              | 136          | IPR001980  | F       | GO:0004595; GO:0015937  |
| M. conjunctivae    | 148               | Gene3D   | G3DSA:3.40.50.620 |                                | 2              | 145          | IPR014729  | H       |                            |
|                    |                   | Hamap    | MF_00151    | Phosphopantetheine adenylyltransferase [coaD]. | 11             | 147          | IPR001980  | F       | GO:0004595; GO:0015937  |
|                    |                   | PANTHER  | PTHR21342:SF1 |                                | 11             | 142          | IPR001980  | F       | GO:0004595; GO:0015937  |
|                    |                   | PANTHER  | PTHR21342   |                                | 11             | 142          | IPR001980  | F       | GO:0004595; GO:0015937  |
|                    |                   | Pfam     | PF01467     | Cytidylyltransferase-like       | 14             | 142          | IPR004821  | D       | GO:0003824; GO:0009058  |
|                    |                   | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 95             | 111          | IPR001980  | F       | GO:0004595; GO:0015937  |
|                    |                   | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 122            | 144          | IPR001980  | F       | GO:0004595; GO:0015937  |
|                    |                   | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 29             | 50           | IPR001980  | F       | GO:0004595; GO:0015937  |
|                    |                   | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 11             | 29           | IPR001980  | F       | GO:0004595; GO:0015937  |
|                    |                   | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 58             | 82           | IPR001980  | F       | GO:0004595; GO:0015937  |
|                    |                   | SUPERFAMILY | SSF52374   |                                | 11             | 144          | IPR001980  | F       | GO:0004595; GO:0015937  |
|                    |                   | TIGRFAM  | TIGR00125   | cyt_tran_rel: cytidyltransferase-like domain | 13             | 64           | IPR004821  | D       | GO:0003824; GO:0009058  |
|                    |                   | TIGRFAM  | TIGR01510   | coaD_prev_kdtB: pantetheine-phosphate adenylyltransferase | 13             | 142          | IPR001980  | F       | GO:0004595; GO:0015937  |
| M. cricetuli       | 142               | Gene3D   | G3DSA:3.40.50.620 |                                | 1              | 141          | IPR014729  | H       |                            |
|                    |                   | Hamap    | MF_00151    | Phosphopantetheine adenylyltransferase [coaD]. | 4              | 142          | IPR001980  | F       | GO:0004595; GO:0015937  |
|                    |                   | PANTHER  | PTHR21342:SF1 |                                | 4              | 138          | IPR001980  | F       | GO:0004595; GO:0015937  |
|                    |                   | PANTHER  | PTHR21342   |                                | 4              | 138          | IPR001980  | F       | GO:0004595; GO:0015937  |
|                    |                   | Pfam     | PF01467     | Cytidylyltransferase-like       | 7              | 136          | IPR004821  | D       | GO:0003824; GO:0009058  |
| Mycoplasma species | Amino acid region | Database | Database ID | Database signature description | ID region start | ID region end | InterPro ID | ID type | Gene Ontology (GO) term |
|-------------------|------------------|----------|------------|--------------------------------|----------------|--------------|-------------|---------|------------------------|
| M. cricetuli      | 142              | PRINTS   | PR01020    | Lipopolysaccharide core biosynthesis protein signature | 88             | 104          | IPR001980   | F       | GO:0004595; GO:0015937 |
|                   |                  | PRINTS   | PR01020    | Lipopolysaccharide core biosynthesis protein signature | 115            | 137          | IPR001980   | F       | GO:0004595; GO:0015937 |
|                   |                  | PRINTS   | PR01020    | Lipopolysaccharide core biosynthesis protein signature | 51             | 75           | IPR001980   | F       | GO:0004595; GO:0015937 |
|                   |                  | PRINTS   | PR01020    | Lipopolysaccharide core biosynthesis protein signature | 22             | 43           | IPR001980   | F       | GO:0004595; GO:0015937 |
|                   |                  | SUPERFAMILY | SSF52374  |                                  | 4              | 141          |             |         |                        |
|                   |                  | TIGRFAM  | TIGR00125  | cyt_tran_rel: cytidyltransferase-like domain | 5              | 59           | IPR004821   | D       | GO:0003824; GO:0009058 |
|                   |                  | TIGRFAM  | TIGR01510  | coaD_prev_kdtB: pantetheine-phosphate adenylyltransferase | 5              | 136          | IPR001980   | F       | GO:0004595; GO:0015937 |
|                   |                  | Gene3D   | G3DSA:3.40.50.620 |                         | 3              | 146          | IPR014729   | H       |                        |
|                   |                  | Hamap    | MF_00151   | Phosphopantetheine adenylyltransferase [coaD]. | 6              | 146          | IPR001980   | F       | GO:0004595; GO:0015937 |
|                   |                  | PANTHER  | PTHR21342  |                                  | 6              | 142          |             |         |                        |
|                   |                  | PANTHER  | PTHR21342:SF1 |                                    | 6              | 142          | IPR001980   | F       | GO:0004595; GO:0015937 |
|                   |                  | Pfam     | PF01467    | Cytidyltransferase-like | 9              | 139          | IPR004821   | D       | GO:0003824; GO:0009058 |
|                   |                  | PRINTS   | PR01020    | Lipopolysaccharide core biosynthesis protein signature | 92             | 108          | IPR001980   | F       | GO:0004595; GO:0015937 |
|                   |                  | PRINTS   | PR01020    | Lipopolysaccharide core biosynthesis protein signature | 119            | 141          | IPR001980   | F       | GO:0004595; GO:0015937 |
|                   |                  | PRINTS   | PR01020    | Lipopolysaccharide core biosynthesis protein signature | 24             | 45           | IPR001980   | F       | GO:0004595; GO:0015937 |
|                   |                  | PRINTS   | PR01020    | Lipopolysaccharide core biosynthesis protein signature | 6              | 24           | IPR001980   | F       | GO:0004595; GO:0015937 |
|                   |                  | SUPERFAMILY | SSF52374  |                                  | 6              | 145          |             |         |                        |
|                   |                  | TIGRFAM  | TIGR01510  | coaD_prev_kdtB: pantetheine-phosphate adenylyltransferase | 8              | 140          | IPR001980   | F       | GO:0004595; GO:0015937 |
|                   |                  | TIGRFAM  | TIGR00125  | cyt_tran_rel: cytidyltransferase-like domain | 8              | 62           | IPR004821   | D       | GO:0003824; GO:0009058 |
| M. crocodyli      | 146              | PRINTS   | PR01020    | Lipopolysaccharide core biosynthesis protein signature | 6              | 24           | IPR001980   | F       | GO:0004595; GO:0015937 |
| M. felisfium      | 146              | Coils    | Coil       |                                  | 46             | 66           |             |         |                        |
|                   |                  | Gene3D   | G3DSA:3.40.50.620 |                         | 1              | 142          | IPR014729   | H       |                        |
|                   |                  | Hamap    | MF_00151   | Phosphopantetheine adenylyltransferase [coaD]. | 4              | 146          | IPR001980   | F       | GO:0004595; GO:0015937 |
|                   |                  | PANTHER  | PTHR21342:SF1 |                                    | 4              | 141          | IPR001980   | F       | GO:0004595; GO:0015937 |
| Mycoplasma species | Amino acid region | Database | Database ID | Database signature description | ID region start | ID region end | InterPro ID | ID type | Gene Ontology (GO) term |
|-------------------|-------------------|----------|-------------|--------------------------------|----------------|--------------|-------------|---------|------------------------|
|                   |                   | Pfam     | PF01467     | Cytidylyltransferase-like      | 7              | 136          | IPR004821   | D       | GO:0003824; GO:0009058  |
|                   |                   | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 51             | 75           | IPR001980   | F       | GO:0004595; GO:0015937  |
|                   |                   | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 22             | 43           | IPR001980   | F       | GO:0004595; GO:0015937  |
|                   |                   | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 4              | 22           | IPR001980   | F       | GO:0004595; GO:0015937  |
|                   |                   | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 115            | 137          | IPR001980   | F       | GO:0004595; GO:0015937  |
|                   |                   | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 88             | 104          | IPR001980   | F       | GO:0004595; GO:0015937  |
|                   |                   | SUPERFAMILY | SSF52374 |        | 4              | 140          |             |         |                        |
|                   |                   | TIGRFAM  | TIGR00125   | cyt_tran_rel: cytidyltransferase-like domain | 5              | 62           | IPR004821   | D       | GO:0003824; GO:0009058  |
|                   |                   | TIGRFAM  | TIGR01510   | coaD_prev_kdtB: pantetheine-phosphate adenylyltransferase | 5              | 141          | IPR001980   | F       | GO:0004595; GO:0015937  |
|                   |                   | Gene3D   | G3DSA:3.40.50.620 |        | 1              | 135          | IPR014729   | H       |                        |
|                   |                   | PANTHER  | PTHR21342   |        | 1              | 133          | IPR001980   | F       | GO:0004595; GO:0015937  |
|                   |                   | PANTHER  | PTHR21342:SF1 |        | 1              | 133          | IPR001980   | F       | GO:0004595; GO:0015937  |
|                   |                   | Pfam     | PF01467     | Cytidylyltransferase-like      | 6              | 133          | IPR004821   | D       | GO:0003824; GO:0009058  |
|                   |                   | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 21             | 42           | IPR001980   | F       | GO:0004595; GO:0015937  |
|                   |                   | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 3              | 21           | IPR001980   | F       | GO:0004595; GO:0015937  |
|                   |                   | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 86             | 102          | IPR001980   | F       | GO:0004595; GO:0015937  |
|                   |                   | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 113            | 135          | IPR001980   | F       | GO:0004595; GO:0015937  |
|                   |                   | SUPERFAMILY | SSF52374 |        | 5              | 134          |             |         |                        |
|                   |                   | TIGRFAM  | TIGR00125   | cyt_tran_rel: cytidyltransferase-like domain | 5              | 49           | IPR004821   | D       | GO:0003824; GO:0009058  |
|                   |                   | TIGRFAM  | TIGR01510   | coaD_prev_kdtB: pantetheine-phosphate adenylyltransferase | 5              | 133          | IPR001980   | F       | GO:0004595; GO:0015937  |
|                   |                   | Gene3D   | G3DSA:3.40.50.620 |        | 2              | 142          | IPR014729   | H       |                        |
|                   |                   | Hamap    | MF_00151    | Phosphopantetheine adenylyltransferase [coaD]. | 3              | 142          | IPR001980   | F       | GO:0004595; GO:0015937  |
|                   |                   | PANTHER  | PTHR21342:SF1 |        | 1              | 141          | IPR001980   | F       | GO:0004595; GO:0015937  |
|                   |                   | PANTHER  | PTHR21342   |        | 1              | 141          |             |         |                        |
| M. fermentans     | 142               | Coils    | Coil       |        | 45             | 65           |             |         |                        |
|                   |                   | Gene3D   | G3DSA:3.40.50.620 |        | 2              | 142          | IPR014729   | H       |                        |
|                   |                   | Hamap    | MF_00151    | Phosphopantetheine adenylyltransferase [coaD]. | 3              | 142          | IPR001980   | F       | GO:0004595; GO:0015937  |
|                   |                   | PANTHER  | PTHR21342:SF1 |        | 1              | 141          | IPR001980   | F       | GO:0004595; GO:0015937  |
|                   |                   | PANTHER  | PTHR21342   |        | 1              | 141          |             |         |                        |
| Mycoplasma species | Amino acid region | Database | Database ID | Database signature description | ID region start | ID region end | InterPro ID | ID type | Gene Ontology (GO) term |
|--------------------|------------------|----------|-------------|--------------------------------|----------------|--------------|-------------|---------|------------------------|
|                    |                  | Pfam     | PF01467     | Cytidylyltransferase-like      | 6              | 135          | IPR004821   | D       | GO:0003824; GO:0009058  |
|                    | M. fermentans    | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 50             | 74           | IPR001980   | F       | GO:0004595; GO:0015937 |
|                    |                  | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 87             | 103          | IPR001980   | F       | GO:0004595; GO:0015937 |
|                    |                  | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 21             | 42           | IPR001980   | F       | GO:0004595; GO:0015937 |
|                    |                  | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 3              | 21           | IPR001980   | F       | GO:0004595; GO:0015937 |
|                    |                  | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 114            | 136          | IPR001980   | F       | GO:0004595; GO:0015937 |
|                    |                  | SUPERFAMILY | SSF52374  | Cyt_tran_rel: cytidyltransferase-like domain | 3              | 140          |             |         |                        |
|                    |                  | TIGRFAM  | TIGR00125   | coaD_prev_kdtB: pantetheine-phosphate adenylyltransferase | 5              | 137          | IPR001980   | F       | GO:0004595; GO:0015937 |
|                    |                  | Gene3D   | G3DSA:3.40.50.620 | Phosphopantetheine adenylyltransferase [coaD]. | 1              | 145          | IPR014729   | H       |                        |
|                    |                  | Hamap    | MF_00151    | Phosphopantetheine adenylyltransferase [coaD]. | 5              | 145          | IPR001980   | F       | GO:0004595; GO:0015937 |
|                    |                  | PANTHER  | PTHR21342:SF1 |              | 5              | 144          | IPR001980   | F       | GO:0004595; GO:0015937 |
|                    |                  | PANTHER  | PTHR21342   | Phosphopantetheine adenylyltransferase [coaD]. | 5              | 144          |             |         |                        |
|                    | M. gallinarum    | Pfam     | PF01467     | Cytidylyltransferase-like      | 8              | 137          | IPR004821   | D       | GO:0003824; GO:0009058  |
|                    |                  | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 52             | 76           | IPR001980   | F       | GO:0004595; GO:0015937 |
|                    |                  | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 5              | 23           | IPR001980   | F       | GO:0004595; GO:0015937 |
|                    |                  | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 116            | 138          | IPR001980   | F       | GO:0004595; GO:0015937 |
|                    |                  | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 23             | 44           | IPR001980   | F       | GO:0004595; GO:0015937 |
|                    |                  | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 89             | 105          | IPR001980   | F       | GO:0004595; GO:0015937 |
|                    |                  | SUPERFAMILY | SSF52374  | Cyt_tran_rel: cytidyltransferase-like domain | 5              | 144          |             |         |                        |
|                    |                  | TIGRFAM  | TIGR00125   | coaD_prev_kdtB: pantetheine-phosphate adenylyltransferase | 7              | 58           | IPR004821   | D       | GO:0003824; GO:0009058  |
|                    |                  | Gene3D   | G3DSA:3.40.50.620 | Phosphopantetheine adenylyltransferase [coaD]. | 1              | 139          | IPR014729   | H       | GO:0004595; GO:0015937 |
|                    |                  | Hamap    | MF_00151    | Phosphopantetheine adenylyltransferase [coaD]. | 3              | 141          | IPR001980   | F       | GO:0004595; GO:0015937 |
| Mycoplasma species | Amino acid region | Database | Database ID | Database signature description | ID region start | ID region end | InterPro ID | ID type | Gene Ontology (GO) term |
|--------------------|------------------|----------|-------------|--------------------------------|----------------|--------------|-------------|---------|------------------------|
| M. gallinarum | 141 | PANTHER | PTHR21342 |  |  | 1 | 137 | IPR001980 | F | GO:0004595; GO:0015937 |
| |  | PANTHER | PTHR21342:SF1 |  | Cytidylyltransferase-like | 6 | 133 | IPR004821 | D | GO:0003824; GO:0009058 |
| |  | Pfam | PF01467 | Lipopolysaccharide core biosynthesis protein signature | 87 | 103 | IPR001980 | F | GO:0004595; GO:0015937 |
| |  | PRINTS | PR01020 |  |  | 50 | 74 | IPR001980 | F | GO:0004595; GO:0015937 |
| |  | PRINTS | PR01020 | Lipopolysaccharide core biosynthesis protein signature | 21 | 42 | IPR001980 | F | GO:0004595; GO:0015937 |
| |  | PRINTS | PR01020 | Lipopolysaccharide core biosynthesis protein signature | 3 | 21 | IPR001980 | F | GO:0004595; GO:0015937 |
| |  | PRINTS | PR01020 | Lipopolysaccharide core biosynthesis protein signature | 114 | 136 | IPR001980 | F | GO:0004595; GO:0015937 |
| |  | SUPERFAMILY | SSF52374 |  |  | 3 | 137 |  |  |  |
| |  | TIGRFAM | TIGR01510 | coaD_prev_kdtB: pantetheine-phosphate adenylyltransferase | 4 | 140 | IPR001980 | F | GO:0004595; GO:0015937 |
| |  | TIGRFAM | TIGR000125 | cyt_tran_rel: cytidyltransferase-like domain | 4 | 60 | IPR004821 | D | GO:0003824; GO:0009058 |
| |  | Gene3D | G3DSA:3.40.50.620 |  |  | 1 | 145 | IPR014729 | H |  |
| |  | Hamap | MF_00151 | Phosphopantetheine adenylyltransferase [coaD] | 3 | 147 | IPR001980 | F | GO:0004595; GO:0015937 |
| |  | PANTHER | PTHR21342:SF1 |  |  | 1 | 136 | IPR001980 | F | GO:0004595; GO:0015937 |
| |  | Pfam | PF01467 | Cytidylyltransferase-like | 6 | 132 | IPR004821 | D | GO:0003824; GO:0009058 |
| |  | PRINTS | PR01020 | Lipopolysaccharide core biosynthesis protein signature | 3 | 21 | IPR001980 | F | GO:0004595; GO:0015937 |
| |  | PRINTS | PR01020 | Lipopolysaccharide core biosynthesis protein signature | 114 | 136 | IPR001980 | F | GO:0004595; GO:0015937 |
| |  | PRINTS | PR01020 | Lipopolysaccharide core biosynthesis protein signature | 50 | 74 | IPR001980 | F | GO:0004595; GO:0015937 |
| |  | PRINTS | PR01020 | Lipopolysaccharide core biosynthesis protein signature | 87 | 103 | IPR001980 | F | GO:0004595; GO:0015937 |
| |  | PRINTS | PR01020 | Lipopolysaccharide core biosynthesis protein signature | 21 | 42 | IPR001980 | F | GO:0004595; GO:0015937 |
| |  | SUPERFAMILY | SSF52374 |  |  | 3 | 138 |  |  |  |
| |  | TIGRFAM | TIGR01510 | coaD_prev_kdtB: pantetheine-phosphate adenylyltransferase | 5 | 140 | IPR001980 | F | GO:0004595; GO:0015937 |
| |  | TIGRFAM | TIGR00125 | cyt_tran_rel: cytidyltransferase-like domain | 4 | 46 | IPR004821 | D | GO:0003824; GO:0009058 |
| M. iowae | 144 | Gene3D | G3DSA:3.40.50.620 |  |  | 1 | 144 | IPR014729 | H |  |
| Mycoplasma species | Amino acid region | Database | Database ID | Database signature description | ID region start | ID region end | InterPro ID | ID type | Gene Ontology (GO) term |
|--------------------|-------------------|----------|-------------|--------------------------------|----------------|-------------|------------|--------|------------------------|
|                    |                   | PANTHER  | PTHR21342   |                                | 6              | 136         | IPR001980  | F      | GO:0004595; GO:0015937  |
| M. iowae           | 144               | PANTHER  | PTHR21342:SF1 | Cytidylytransferase-like      | 6              | 136         | IPR004821  | D      | GO:0004595; GO:0015937  |
|                    |                   | Pfam     | PF01467     | Lipopolysaccharide core biosynthesis protein signature | 9              | 137         | IPR001980  | F      | GO:0004595; GO:0015937  |
|                    |                   | PRINTS   | PR01020     |                                | 6              | 24          | IPR001980  | F      | GO:0004595; GO:0015937  |
|                    |                   | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 117             | 139         | IPR001980  | F      | GO:0004595; GO:0015937  |
|                    |                   | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 24             | 45          | IPR001980  | F      | GO:0004595; GO:0015937  |
|                    |                   | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 90             | 106         | IPR001980  | F      | GO:0004595; GO:0015937  |
|                    |                   | SUPERFAMILY | SSF52374   |                                | 8              | 142         | IPR004821  | D      | GO:0003824; GO:0009058   |
|                    |                   | TIGRFAM  | TIGR00125   | cyt_tran_rel: cytidyltransferase-like domain | 8              | 63          | IPR001980  | F      | GO:0004595; GO:0015937  |
|                    |                   | TIGRFAM  | TIGR01510   | coaD_prev_kdtB: pantetheine-phosphate adenylyltransferase | 8              | 136         | IPR001980  | F      | GO:0004595; GO:0015937  |
|                    |                   | Gene3D   | G3DSA:3.40.50.620 |                                | 1              | 137         | IPR014729  | H      |                          |
|                    |                   | Hamap    | MF_00151    | Phosphopantetheine adenylyltransferase [coaD]. | 2              | 140         | IPR001980  | F      | GO:0004595; GO:0015937  |
|                    |                   | PANTHER  | PTHR21342:SF1 |                                | 1              | 138         | IPR001980  | F      | GO:0004595; GO:0015937  |
|                    |                   | PANTHER  | PTHR21342   |                                | 1              | 138         |             |        | GO:0004595; GO:0015937  |
|                    |                   | Pfam     | PF01467     | Cytidylytransferase-like      | 5              | 134         | IPR004821  | D      | GO:0003824; GO:0009058   |
|                    |                   | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 86             | 102         | IPR001980  | F      | GO:0004595; GO:0015937  |
|                    |                   | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 113             | 135         | IPR001980  | F      | GO:0004595; GO:0015937  |
|                    |                   | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 49             | 73          | IPR001980  | F      | GO:0004595; GO:0015937  |
|                    |                   | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 20             | 41          | IPR001980  | F      | GO:0004595; GO:0015937  |
|                    |                   | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 2              | 20          | IPR001980  | F      | GO:0004595; GO:0015937  |
|                    |                   | SUPERFAMILY | SSF52374   |                                | 2              | 138         |             |        | GO:0004595; GO:0015937  |
|                    |                   | TIGRFAM  | TIGR00125   | cyt_tran_rel: cytidyltransferase-like domain | 4              | 62          | IPR004821  | D      | GO:0003824; GO:0009058   |
|                    |                   | TIGRFAM  | TIGR01510   | coaD_prev_kdtB: pantetheine-phosphate adenylyltransferase | 3              | 139         | IPR001980  | F      | GO:0004595; GO:0015937  |
|                    |                   | Gene3D   | G3DSA:3.40.50.620 |                                | 1              | 136         | IPR014729  | H      | GO:0004595; GO:0015937  |
| M. leachii         | 140               | PANTHER  | PTHR21342   |                                | 1              | 138         |             |        | GO:0004595; GO:0015937  |
|                    |                   | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 5              | 134         | IPR004821  | D      | GO:0003824; GO:0009058   |
|                    |                   | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 86             | 102         | IPR001980  | F      | GO:0004595; GO:0015937  |
|                    |                   | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 113             | 135         | IPR001980  | F      | GO:0004595; GO:0015937  |
|                    |                   | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 49             | 73          | IPR001980  | F      | GO:0004595; GO:0015937  |
|                    |                   | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 20             | 41          | IPR001980  | F      | GO:0004595; GO:0015937  |
|                    |                   | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 2              | 20          | IPR001980  | F      | GO:0004595; GO:0015937  |
|                    |                   | SUPERFAMILY | SSF52374   |                                | 2              | 138         |             |        | GO:0004595; GO:0015937  |
|                    |                   | TIGRFAM  | TIGR00125   | cyt_tran_rel: cytidyltransferase-like domain | 4              | 62          | IPR004821  | D      | GO:0003824; GO:0009058   |
|                    |                   | TIGRFAM  | TIGR01510   | coaD_prev_kdtB: pantetheine-phosphate adenylyltransferase | 3              | 139         | IPR001980  | F      | GO:0004595; GO:0015937  |
|                    |                   | Gene3D   | G3DSA:3.40.50.620 |                                | 1              | 136         | IPR014729  | H      | GO:0004595; GO:0015937  |
| M. leonicaptivi    | 137               | PANTHER  | PTHR21342:SF1 |                                | 1              | 138         |             |        | GO:0004595; GO:0015937  |
| Mycoplasma species | Amino acid region | Database | Database ID | Database signature description | ID region start | ID region end | InterPro ID | ID type | Gene Ontology (GO) term |
|-------------------|------------------|----------|-------------|--------------------------------|----------------|--------------|-------------|---------|------------------------|
| *M. leonicaptivi* | 137 Coils       | PANTHER  | PTHR21342   |                                | 4              | 135          |             |         |                        |
|                   |                 | Pfam     | PF01467     | Cytidylyltransferase-like       | 8              | 135          | IPR004821   | D       | GO:0003824; GO:0009058 |
|                   |                 | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 22             | 43           | IPR001980   | F       | GO:0004595; GO:0015937 |
|                   |                 | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 87             | 103          | IPR001980   | F       | GO:0004595; GO:0015937 |
|                   | 137 Coils       | ProDom   | PD016147    | Ligase Lyase Citrate Pro-3S-Lyase Synthetase Transferase Cytidylyltransferase-Related:Citrate:Acetate:SH-Citrate Citrate Plasmid | 5              | 67           |             |         |                        |
|                   |                 | SUPERFAMILY | SSF52374 |                                | 5              | 135          |             |         |                        |
|                   |                 | TIGRFAM  | TIGR00125   | cyt_tran_rel: cytidyltransferase-like domain | 5              | 46           | IPR004821   | D       | GO:0003824; GO:0009058 |
|                   |                 | TIGRFAM  | TIGR01510   | coaD_prev_kdtB: pantetheine-phosphate adenylyltransferase | 6              | 135          | IPR001980   | F       | GO:0004595; GO:0015937 |
| *M. lipofaciens*  | 140 Coils       | Coils    | G3DSA:3.40.50.620 |                            | 1              | 140          | IPR014729   | H       |                        |
|                   |                 | Hamap    | MF_00151    | Phosphopantetheine adenylyltransferase [coaD]. | 2              | 140          | IPR001980   | F       | GO:0004595; GO:0015937 |
|                   |                 | PANTHER  | PTHR21342:SF1 |                                | 1              | 139          | IPR001980   | F       | GO:0004595; GO:0015937 |
|                   |                 | PANTHER  | PTHR21342   |                                | 1              | 139          |             |         |                        |
|                   |                 | Pfam     | PF01467     | Cytidylyltransferase-like       | 5              | 134          | IPR004821   | D       | GO:0003824; GO:0009058 |
|                   |                 | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 2              | 20           | IPR001980   | F       | GO:0004595; GO:0015937 |
|                   |                 | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 113             | 135          | IPR001980   | F       | GO:0004595; GO:0015937 |
|                   |                 | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 49              | 73           | IPR001980   | F       | GO:0004595; GO:0015937 |
|                   |                 | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 86              | 102          | IPR001980   | F       | GO:0004595; GO:0015937 |
|                   |                 | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 20              | 41           | IPR001980   | F       | GO:0004595; GO:0015937 |
|                   |                 | SUPERFAMILY | SSF52374 |                                | 2              | 139          |             |         |                        |
|                   |                 | TIGRFAM  | TIGR00125   | cyt_tran_rel: cytidyltransferase-like domain | 4              | 60           | IPR004821   | D       | GO:0003824; GO:0009058 |
|                   |                 | TIGRFAM  | TIGR01510   | coaD_prev_kdtB: pantetheine-phosphate adenylyltransferase | 4              | 134          | IPR001980   | F       | GO:0004595; GO:0015937 |
| *M. mobile*       | 145 Coils       | Coils    |             |                                | 44             | 64           |             |         |                        |
| **Mycoplasma** species | **Amino acid region** | **Database** | **Database ID** | **Database signature description** | **ID region start** | **ID region end** | **InterPro ID** | **ID type** | **Gene Ontology (GO) term** |
|------------------------|----------------------|--------------|----------------|-----------------------------------|------------------|----------------|-----------------|------------|--------------------------|
| **M. mobile**          | 145                  | Gene3D       | G3DSA:3.40.50.620 |                                   | 2                | 141            | IPR014729       | H          | GO:0003824; GO:0009058   |
|                        |                      | Pfam         | PF01467        | Cytidylyltransferase-like          | 12               | 72             | IPR004821       | D          | GO:0004595; GO:0015937   |
|                        |                      | PRINTS       | PR01020        | Lipopolysaccharide core biosynthesis protein signature | 9               | 27             | IPR001980       | F          | GO:0004595; GO:0015937   |
|                        |                      | PRINTS       | PR01020        | Lipopolysaccharide core biosynthesis protein signature | 27              | 48             | IPR001980       | F          | GO:0004595; GO:0015937   |
|                        |                      | PRINTS       | PR01020        | Lipopolysaccharide core biosynthesis protein signature | 56              | 80             | IPR001980       | F          | GO:0004595; GO:0015937   |
|                        |                      | SUPERFAMILY  | SSF52374       | cyt_tran_rel: cytidyltransferase-like domain | 9               | 126            | IPR004821       | D          | GO:0003824; GO:0009058   |
|                        |                      | TIGRFAM      | TIGR00125      |                                   | 11               | 61             | IPR004821       | D          | GO:0003824; GO:0009058   |
| **M. molare**          | 143                  | Gene3D       | G3DSA:3.40.50.620 |                                   | 1                | 138            | IPR014729       | H          | GO:0003824; GO:0009058   |
|                        |                      | Hamap        | MF_00151       | Phosphopantetheine adenyllytransferase [coaD]. | 2               | 143            | IPR001980       | F          | GO:0004595; GO:0015937   |
|                        |                      | PANTHER      | PTHR21342:SF1  |                                   | 1                | 134            | IPR001980       | F          | GO:0004595; GO:0015937   |
|                        |                      | PANTHER      | PTHR21342      |                                   | 1                | 138            | IPR001980       | F          | GO:0004595; GO:0015937   |
|                        |                      | Pfam         | PF01467        | Cytidylyltransferase-like          | 5                | 133            | IPR004821       | D          | GO:0003824; GO:0009058   |
|                        |                      | PRINTS       | PR01020        | Lipopolysaccharide core biosynthesis protein signature | 113              | 135            | IPR001980       | F          | GO:0004595; GO:0015937   |
|                        |                      | PRINTS       | PR01020        | Lipopolysaccharide core biosynthesis protein signature | 49              | 73             | IPR001980       | F          | GO:0004595; GO:0015937   |
|                        |                      | PRINTS       | PR01020        | Lipopolysaccharide core biosynthesis protein signature | 2               | 20             | IPR001980       | F          | GO:0004595; GO:0015937   |
|                        |                      | PRINTS       | PR01020        | Lipopolysaccharide core biosynthesis protein signature | 86              | 102            | IPR001980       | F          | GO:0004595; GO:0015937   |
|                        |                      | PRINTS       | PR01020        | Lipopolysaccharide core biosynthesis protein signature | 20              | 41             | IPR001980       | F          | GO:0004595; GO:0015937   |
|                        |                      | ProDom       | PD016147       | Ligase Lyase Citrate Pro-3S-Lyase Synthetase Transferase Transferase Cytidylyltransferase-Related: Citrate:Acetate:SH-Citrate Ctic Plasmid | 11              | 75             | IPR001980       | F          | GO:0004595; GO:0015937   |
|                        |                      | SUPERFAMILY  | SSF52374       | cyt_tran_rel: cytidyltransferase-like domain | 4               | 138            | IPR004821       | D          | GO:0003824; GO:0009058   |
|                        |                      | TIGRFAM      | TIGR00125      | cyt_tran_rel: cytidyltransferase-like domain | 4               | 56             | IPR004821       | D          | GO:0003824; GO:0009058   |
|                        |                      | TIGRFAM      | TIGR01510      | coaD_prev_kdtB: pantetheine-phosphate adenyllytransferase | 4               | 134            | IPR001980       | F          | GO:0004595; GO:0015937   |
| **M. mycoides subsp. capri** | 140              | Gene3D       | G3DSA:3.40.50.620 |                                   | 1                | 137            | IPR014729       | H          | GO:0003824; GO:0009058   |
|                        |                      | Hamap        | MF_00151       | Phosphopantetheine adenyllytransferase [coaD]. | 2               | 140            | IPR001980       | F          | GO:0004595; GO:0015937   |
|                        |                      | PANTHER      | PTHR21342:SF1  |                                   | 1                | 138            | IPR001980       | F          | GO:0004595; GO:0015937   |
|                        |                      | PANTHER      | PTHR21342      |                                   | 1                | 138            | IPR001980       | F          | GO:0004595; GO:0015937   |
| Mycoplasma species | Amino acid region | Database | Database ID | Database signature description | ID region start | ID region end | InterPro ID | ID type | Gene Ontology (GO) term |
|--------------------|-------------------|----------|-------------|--------------------------------|----------------|--------------|-------------|--------|------------------------|
| M. mycoides subsp. capri | 140 | Pfam | PF01467 | Cytidylyltransferase-like | 5 | 134 | IPR004821 | D | GO:0003824; GO:0009058 |
| | | PRINTS | PR01020 | Lipopolysaccharide core biosynthesis protein signature | 113 | 135 | IPR001980 | F | GO:0004595; GO:0015937 |
| | | PRINTS | PR01020 | Lipopolysaccharide core biosynthesis protein signature | 49 | 73 | IPR001980 | F | GO:0004595; GO:0015937 |
| | | PRINTS | PR01020 | Lipopolysaccharide core biosynthesis protein signature | 2 | 20 | IPR001980 | F | GO:0004595; GO:0015937 |
| | | PRINTS | PR01020 | Lipopolysaccharide core biosynthesis protein signature | 86 | 102 | IPR001980 | F | GO:0004595; GO:0015937 |
| | | PRINTS | PR01020 | Lipopolysaccharide core biosynthesis protein signature | 20 | 41 | IPR001980 | F | GO:0004595; GO:0015937 |
| | | SUPERFAMILY | SSF52374 |  | 2 | 138 | | | |
| | | TIGRFAM | TIGR01510 | coaD_prev_kdtB: pantetheine-phosphate adenylyltransferase | 3 | 139 | IPR001980 | F | GO:0004595; GO:0015937 |
| | | TIGRFAM | TIGR00125 | cyt_tran_rel: cytidyltransferase-like domain | 3 | 61 | IPR004821 | D | GO:0003824; GO:0009058 |
| | | Gene3D | G3DSA:3.40.50.620 |  | 1 | 137 | IPR014729 | H | |
| | | Hamap | MF_00151 | Phosphopantetheine adenylyltransferase [coaD]. | 2 | 140 | IPR001980 | F | GO:0004595; GO:0015937 |
| | | PANTHER | PTHR21342:SF1 |  | 1 | 138 | IPR001980 | F | GO:0004595; GO:0015937 |
| | | PANTHER | PTHR21342 |  | 1 | 138 | | | |
| | | Pfam | PF01467 | Cytidylyltransferase-like | 5 | 134 | IPR004821 | D | GO:0003824; GO:0009058 |
| | | PRINTS | PR01020 | Lipopolysaccharide core biosynthesis protein signature | 49 | 73 | IPR001980 | F | GO:0004595; GO:0015937 |
| | | PRINTS | PR01020 | Lipopolysaccharide core biosynthesis protein signature | 113 | 135 | IPR001980 | F | GO:0004595; GO:0015937 |
| | | PRINTS | PR01020 | Lipopolysaccharide core biosynthesis protein signature | 2 | 20 | IPR001980 | F | GO:0004595; GO:0015937 |
| | | PRINTS | PR01020 | Lipopolysaccharide core biosynthesis protein signature | 20 | 41 | IPR001980 | F | GO:0004595; GO:0015937 |
| | | PRINTS | PR01020 | Lipopolysaccharide core biosynthesis protein signature | 86 | 102 | IPR001980 | F | GO:0004595; GO:0015937 |
| | | SUPERFAMILY | SSF52374 |  | 2 | 138 | | | |
| | | TIGRFAM | TIGR00125 | cyt_tran_rel: cytidyltransferase-like domain | 4 | 62 | IPR004821 | D | GO:0003824; GO:0009058 |
| | | TIGRFAM | TIGR01510 | coaD_prev_kdtB: pantetheine-phosphate adenylyltransferase | 3 | 139 | IPR001980 | F | GO:0004595; GO:0015937 |
| M. opalescens | 145 | Gene3D | G3DSA:3.40.50.620 | | 1 | 143 | IPR014729 | H | GO:0004595; GO:0015937 |
| | | Hamap | MF_00151 | Phosphopantetheine adenylyltransferase [coaD]. | 2 | 145 | IPR001980 | F | GO:0004595; GO:0015937 |
| Mycoplasma species | Amino acid region | Database | Database ID | Database signature description | ID region start | ID region end | InterPro ID | ID type | Gene Ontology (GO) term |
|-------------------|-------------------|----------|-------------|-------------------------------|----------------|--------------|-------------|---------|-----------------------|
| **M. opalescens** | 145               | PANTHER  | PTHR21342:SF1 |                               | 1              | 139          | IPR001980   | F       | GO:0004595; GO:0015937 |
|                   |                   | PANTHER  | PTHR21342     |                               | 1              | 139          |             |         |                       |
|                   |                   | Pfam     | PF01467       | Cytidylyltransferase-like      | 5              | 134          | IPR004821   | D       | GO:0003824; GO:0009058 |
|                   |                   | PRINTS   | PR01020       | Lipopolysaccharide core biosynthesis protein signature | 2              | 20           | IPR001980   | F       | GO:0004595; GO:0015937 |
|                   |                   | PRINTS   | PR01020       | Lipopolysaccharide core biosynthesis protein signature | 87             | 103          | IPR001980   | F       | GO:0004595; GO:0015937 |
|                   |                   | PRINTS   | PR01020       | Lipopolysaccharide core biosynthesis protein signature | 20             | 41           | IPR001980   | F       | GO:0004595; GO:0015937 |
|                   |                   | SUPERFAMILY | Ssf52374 |                              | 2              | 140          |             |         |                       |
|                   |                   | TIGRFAM  | Tigr00125     | cyt_tran_rel: cytidyltransferase-like domain | 4              | 43           | IPR004821   | D       | GO:0003824; GO:0009058 |
|                   |                   | TIGRFAM  | Tigr01510     | coAD_prev_kdtB: pantetheine-phosphate adenylyltransferase | 4              | 135          | IPR001980   | F       | GO:0004595; GO:0015937 |
|                   |                   | Coils    |              |                               | 49             | 69           |             |         |                       |
|                   |                   | Gene3D   | G3DSA:3.40.50.620 |                               | 2              | 149          | IPR014729   | H       | GO:0004595; GO:0015937 |
|                   |                   | Hamap    | MF_00151      | Phosphopantetheine adenylyltransferase [coAD]. | 8              | 149          | IPR001980   | F       | GO:0004595; GO:0015937 |
|                   |                   | PANTHER  | PTHR21342     |                               | 8              | 136          | IPR001980   | F       | GO:0004595; GO:0015937 |
|                   |                   | Pfam     | PF01467       | Cytidylyltransferase-like      | 11             | 140          | IPR004821   | D       | GO:0003824; GO:0009058 |
|                   |                   | PRINTS   | PR01020       | Lipopolysaccharide core biosynthesis protein signature | 8              | 26           | IPR001980   | F       | GO:0004595; GO:0015937 |
|                   |                   | PRINTS   | PR01020       | Lipopolysaccharide core biosynthesis protein signature | 119            | 141          | IPR001980   | F       | GO:0004595; GO:0015937 |
|                   |                   | PRINTS   | PR01020       | Lipopolysaccharide core biosynthesis protein signature | 92             | 108          | IPR001980   | F       | GO:0004595; GO:0015937 |
|                   |                   | PRINTS   | PR01020       | Lipopolysaccharide core biosynthesis protein signature | 26             | 47           | IPR001980   | F       | GO:0004595; GO:0015937 |
|                   |                   | SUPERFAMILY | Ssf52374 |                              | 8              | 147          |             |         |                       |
|                   |                   | TIGRFAM  | Tigr01510     | coAD_prev_kdtB: pantetheine-phosphate adenylyltransferase | 10             | 147          | IPR001980   | F       | GO:0004595; GO:0015937 |
|                   |                   | TIGRFAM  | Tigr00125     | cyt_tran_rel: cytidyltransferase-like domain | 11             | 65           | IPR004821   | D       | GO:0003824; GO:0009058 |
| **M. penetrans**  | 150               | PANTHER  | PTHR21342:SF1 |                               | 8              | 136          | IPR001980   | F       | GO:0004595; GO:0015937 |
|                   |                   | Pfam     | PF01467       | Cytidylyltransferase-like      | 11             | 140          | IPR004821   | D       | GO:0003824; GO:0009058 |
|                   |                   | PRINTS   | PR01020       | Lipopolysaccharide core biosynthesis protein signature | 8              | 26           | IPR001980   | F       | GO:0004595; GO:0015937 |
|                   |                   | PRINTS   | PR01020       | Lipopolysaccharide core biosynthesis protein signature | 119            | 141          | IPR001980   | F       | GO:0004595; GO:0015937 |
|                   |                   | PRINTS   | PR01020       | Lipopolysaccharide core biosynthesis protein signature | 92             | 108          | IPR001980   | F       | GO:0004595; GO:0015937 |
|                   |                   | PRINTS   | PR01020       | Lipopolysaccharide core biosynthesis protein signature | 26             | 47           | IPR001980   | F       | GO:0004595; GO:0015937 |
|                   |                   | SUPERFAMILY | Ssf52374 |                              | 8              | 147          |             |         |                       |
|                   |                   | TIGRFAM  | Tigr01510     | coAD_prev_kdtB: pantetheine-phosphate adenylyltransferase | 10             | 147          | IPR001980   | F       | GO:0004595; GO:0015937 |
|                   |                   | TIGRFAM  | Tigr00125     | cyt_tran_rel: cytidyltransferase-like domain | 11             | 65           | IPR004821   | D       | GO:0003824; GO:0009058 |
| **M. pirum**      | 151               | Gene3D   | G3DSA:3.40.50.620 |                               | 1              | 149          | IPR014729   | H       | GO:0004595; GO:0015937 |
|                   |                   | Hamap    | MF_00151      | Phosphopantetheine adenylyltransferase [coAD]. | 4              | 151          | IPR001980   | F       | GO:0004595; GO:0015937 |
| Mycoplasma species | Amino acid region | Database | Database ID | Database signature description | ID region start | ID region end | InterPro ID | ID type | Gene Ontology (GO) term |
|-------------------|------------------|----------|-------------|-------------------------------|----------------|-------------|-------------|---------|------------------------|
| **M. pirum**      | 151              | PANTHER  | PTHR21342:SF1 |                                | 4              | 141         | IPR001980   | F       | GO:0004595; GO:0015937 |
|                   |                  | PANTHER  | PTHR21342    |                                | 4              | 141         |             |         |                        |
| Pfam              |                  | PF01467  | Cytidylytransferase-like |                              |                |             | IPR004821   | D       | GO:0003824; GO:0009058 |
| PRINTS            | PR01020          | Lipopolysaccharide core biosynthesis protein signature | 4 | 22 | IPR001980  | F | GO:0004595; GO:0015937 |
| PRINTS            | PR01020          | Lipopolysaccharide core biosynthesis protein signature | 22 | 43 | IPR001980  | F | GO:0004595; GO:0015937 |
| PRINTS            | PR01020          | Lipopolysaccharide core biosynthesis protein signature | 89 | 105 | IPR001980 | F | GO:0004595; GO:0015937 |
| PRINTS            | PR01020          | Lipopolysaccharide core biosynthesis protein signature | 116 | 138 | IPR001980 | F | GO:0004595; GO:0015937 |
| SUPERFAMILY       | SSF52374         |          |              |                               | 4              | 143         |             |         |                        |
| TIGRFAM           | TIGR01510        | coaD_prev_kdtB: pantetheine-phosphate adenylyltransferase | 5 | 140 | IPR001980 | F | GO:0004595; GO:0015937 |
| TIGRFAM           | TIGR00125        | cyt_tran_rel: cytidyltransferase-like domain | 5 | 62 | IPR004821 | D | GO:0003824; GO:0009058 |
| Gene3D            | G3DSA:3.40.50.620 |          |              |                               | 1              | 140         | IPR014729   | H       |                        |
| Hamap             | MF_00151         | Phosphopantetheine adenylyltransferase [coaD]. | 2 | 140 | IPR001980 | F | GO:0004595; GO:0015937 |
| PANTHER           | PTHR21342:SF1    |                                | 1 | 139 | IPR001980 | F | GO:0004595; GO:0015937 |
| PANTHER           | PTHR21342        |                                | 1 | 139 | IPR001980 | F | GO:0004595; GO:0015937 |
| Pfam              | PF01467          | Cytidylytransferase-like | 5 | 134 | IPR004821 | D | GO:0003824; GO:0009058 |
| PRINTS            | PR01020          | Lipopolysaccharide core biosynthesis protein signature | 113 | 135 | IPR001980 | F | GO:0004595; GO:0015937 |
| PRINTS            | PR01020          | Lipopolysaccharide core biosynthesis protein signature | 49 | 73 | IPR001980 | F | GO:0004595; GO:0015937 |
| PRINTS            | PR01020          | Lipopolysaccharide core biosynthesis protein signature | 86 | 102 | IPR001980 | F | GO:0004595; GO:0015937 |
| PRINTS            | PR01020          | Lipopolysaccharide core biosynthesis protein signature | 2 | 20 | IPR001980 | F | GO:0004595; GO:0015937 |
| PRINTS            | PR01020          | Lipopolysaccharide core biosynthesis protein signature | 20 | 41 | IPR001980 | F | GO:0004595; GO:0015937 |
| SUPERFAMILY       | SSF52374         |          |              |                               | 2              | 139         |             |         |                        |
| TIGRFAM           | TIGR00125        | cyt_tran_rel: cytidyltransferase-like domain | 4 | 59 | IPR004821 | D | GO:0003824; GO:0009058 |
| TIGRFAM           | TIGR01510        | coaD_prev_kdtB: pantetheine-phosphate adenylyltransferase | 4 | 134 | IPR001980 | F | GO:0004595; GO:0015937 |
| **M. primatum**   | 140              | Gene3D   | G3DSA:3.40.50.620 |                                | 2              | 143         | IPR014729   | H       |                        |
| Hamap             | MF_00151         | Phosphopantetheine adenylyltransferase [coaD]. | 6 | 148 | IPR001980 | F | GO:0004595; GO:0015937 |
| **M. pulmonis**   | 149              | Gene3D   | G3DSA:3.40.50.620 |                                | 2              | 143         | IPR014729   | H       |                        |
| Mycoplasma species | Amino acid region | Database | Database ID | Database signature description | ID region start | ID region end | InterPro ID | ID type | Gene Ontology (GO) term |
|--------------------|-------------------|----------|-------------|--------------------------------|----------------|---------------|-------------|---------|------------------------|
|                    |                   | PANTHER  | PTHR21342   |                                | 6              | 140           | IPR001980   | F       | GO:0004595; GO:015937   |
|                    |                   | PANTHER  | PTHR21342:SF1 |                                | 6              | 140           | IPR004821   | D       | GO:0003824; GO:009058   |
|                    |                   | Pfam     | PF01467     | Cytidylyltransferase-like      | 9              | 140           | IPR01980    | F       | GO:0004595; GO:015937   |
|                    |                   | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 119            | 141           | IPR01980    | F       | GO:0004595; GO:015937   |
|                    |                   | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 24             | 45            | IPR001980   | F       | GO:0004595; GO:015937   |
|                    |                   | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 92             | 108           | IPR001980   | F       | GO:0004595; GO:015937   |
|                    |                   | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 6              | 24            | IPR001980   | F       | GO:0004595; GO:015937   |
|                    |                   | ProDom   | PD016147    | Ligase Lyase Citrate Pro-3S-Lyase Synthetase Transferase Cytidylyltransferase-Related:Citrate:Acetate:SH-Citrate Citc Plasmid | 4              | 103           | IPR0014729  | H       |                          |
|                    |                   | SUPERFAMILY | SSF52374 |                                | 6              | 140           | IPR001980   | F       | GO:0004595; GO:015937   |
|                    |                   | TIGRFAM  | TIGR01510   | coaD_prev_kdhB: pantetheine-phosphate adenylyltransferase | 7              | 140           | IPR001980   | F       | GO:0004595; GO:015937   |
|                    |                   | TIGRFAM  | TIGR00125   | cyt_tran_rel: cytidyltransferase-like domain | 7              | 64            | IPR004821   | D       | GO:0003824; GO:009058   |
|                    |                   | Gene3D   | G3DSA:3.40.50.620 |                                | 1              | 137           | IPR01980    | F       | GO:0004595; GO:015937   |
|                    |                   | Hamap    | MF_00151    | Phosphopantetheine adenylyltransferase [coaD] | 2              | 141           | IPR001980   | F       | GO:0004595; GO:015937   |
|                    |                   | PANTHER  | PTHR21342   |                                | 1              | 139           | IPR001980   | F       | GO:0004595; GO:015937   |
|                    |                   | PANTHER  | PTHR21342:SF1 |                                | 1              | 139           | IPR001980   | F       | GO:0004595; GO:015937   |
|                    |                   | Pfam     | PF01467     | Cytidylyltransferase-like      | 5              | 134           | IPR004821   | D       | GO:0003824; GO:009058   |
|                    |                   | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 86             | 102           | IPR001980   | F       | GO:0004595; GO:015937   |
|                    |                   | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 113            | 135           | IPR001980   | F       | GO:0004595; GO:015937   |
|                    |                   | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 20             | 41            | IPR001980   | F       | GO:0004595; GO:015937   |
|                    |                   | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 2              | 20            | IPR001980   | F       | GO:0004595; GO:015937   |
|                    |                   | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 49             | 73            | IPR001980   | F       | GO:0004595; GO:015937   |
|                    |                   | ProDom   | PD016147    | Ligase Lyase Citrate Pro-3S-Lyase Synthetase Transferase Cytidylyltransferase-Related:Citrate:Acetate:SH-Citrate Citc Plasmid | 2              | 75            |                         |         |                          |
|                    |                   | SUPERFAMILY | SSF52374 |                                | 2              | 138           |                         |         |                          |
| Mycoplasma species | Amino acid region | Database | Database ID | Database signature description | ID region start | ID region end | InterPro ID | ID type | Gene Ontology (GO) term |
|--------------------|-------------------|----------|-------------|--------------------------------|----------------|---------------|-------------|---------|------------------------|
|                    |                   | TIGRFAM  | TIGR01510   | coaD_prev_kdtB: pantetheine-phosphate adenylyltransferase | 3              | 141           | IPR001980   | F       | GO:0004595; GO:0015937 |
|                    |                   | TIGRFAM  | TIGR00125   | cyt_tran_rel: cytidyltransferase-like domain          | 3              | 62            | IPR004821   | D       | GO:0003824; GO:0009058 |
| M. simbae          | 142               | Gene3D   | G3DSA:3.40.50.620 |                               | 1              | 138           | IPR014729   | H       |                           |
|                    |                   | PANTHER  | PTHR21342   |                               | 1              | 136           | IPR001980   | F       | GO:0004595; GO:0015937 |
|                    |                   | PANTHER  | PTHR21342:SF1 |                               | 1              | 136           | IPR001980   | F       | GO:0004595; GO:0015937 |
|                    |                   | Pfam     | PF01467     | Cytidyltransferase-like       | 5              | 134           | IPR004821   | D       | GO:0003824; GO:0009058 |
|                    |                   | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 20             | 41            | IPR001980   | F       | GO:0004595; GO:0015937 |
|                    |                   | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 2              | 20            | IPR001980   | F       | GO:0004595; GO:0015937 |
|                    |                   | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 113            | 135           | IPR001980   | F       | GO:0004595; GO:0015937 |
|                    |                   | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 49             | 73            | IPR001980   | F       | GO:0004595; GO:0015937 |
|                    |                   | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 86             | 102           | IPR001980   | F       | GO:0004595; GO:0015937 |
|                    |                   | SUPERFAMILY | SSF52374 |                               | 2              | 135           |             |         |                         |
|                    |                   | TIGRFAM  | TIGR01510   | coaD_prev_kdtB: pantetheine-phosphate adenylyltransferase | 4              | 134           | IPR001980   | F       | GO:0004595; GO:0015937 |
|                    |                   | TIGRFAM  | TIGR00125   | cyt_tran_rel: cytidyltransferase-like domain          | 4              | 56            | IPR004821   | D       | GO:0003824; GO:0009058 |
|                    |                   | Gene3D   | G3DSA:3.40.50.620 |                               | 1              | 144           | IPR014729   | H       |                           |
|                    |                   | Hamap    | MF_00151    | Phosphopantetheine adenylyltransferase [coaD].        | 4              | 143           | IPR001980   | F       | GO:0004595; GO:0015937 |
|                    |                   | PANTHER  | PTHR21342:SF1 |                               | 4              | 143           | IPR001980   | F       | GO:0004595; GO:0015937 |
|                    |                   | PANTHER  | PTHR21342   |                               | 4              | 143           | IPR001980   | F       | GO:0004595; GO:0015937 |
|                    |                   | Pfam     | PF01467     | Cytidyltransferase-like       | 7              | 136           | IPR004821   | D       | GO:0003824; GO:0009058 |
|                    |                   | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 4              | 22            | IPR001980   | F       | GO:0004595; GO:0015937 |
|                    |                   | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 22             | 43            | IPR001980   | F       | GO:0004595; GO:0015937 |
|                    |                   | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 115            | 137           | IPR001980   | F       | GO:0004595; GO:0015937 |
|                    |                   | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 51             | 75            | IPR001980   | F       | GO:0004595; GO:0015937 |
|                    |                   | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 88             | 104           | IPR001980   | F       | GO:0004595; GO:0015937 |
|                    |                   | SUPERFAMILY | SSF52374 |                               | 4              | 142           |             |         |                         |
| Mycoplasma species | Amino acid region | Database | Database ID     | Database signature description                           | ID start | ID end | InterPro ID   | ID type | Gene Ontology (GO) term                  |
|-------------------|------------------|----------|----------------|----------------------------------------------------------|----------|--------|---------------|---------|------------------------------------------|
| TIGRFAM           | TIGR01510        | coaD_prev_kdtB: pantetheine-phosphate adenyltransferase | 5 | 144 | IPR001980 | F | GO:0004595; GO:0015937 |
| TIGRFAM           | TIGR00125        | cyt_tran_rel: cytidyltransferase-like domain | 5 | 62 | IPR004821 | D | GO:0003824; GO:0009058 |
| M. synoviae       | 148              | Gene3D   | G3DSA:3.40.50.620 |                                                                     | 1 | 147 | IPR014729 | H |                                           |
|                   |                  | Hamap    | MF_00151       | Phosphopantetheine adenyltransferase [coaD].                | 7 | 148 | IPR001980 | F | GO:0004595; GO:0015937 |
|                   |                  | PANTHER  | PTHR21342:SF1  |                                                                 | 7 | 143 |                     |         |                                          |
| M. synoviae       | 148              | PANTHER  | PTHR21342:SF1  |                                                                 | 7 | 143 | IPR001980 | F | GO:0004595; GO:0015937 |
| Pfam              | PF01467          | Cytidyltransferase-like | 10 | 139 | IPR004821 | D | GO:0003824; GO:0009058 |
| PRINTS            | PR01020          | Lipopolysaccharide core biosynthesis protein signature | 7 | 25 | IPR001980 | F | GO:0004595; GO:0015937 |
| PRINTS            | PR01020          | Lipopolysaccharide core biosynthesis protein signature | 118 | 140 | IPR001980 | F | GO:0004595; GO:0015937 |
| PRINTS            | PR01020          | Lipopolysaccharide core biosynthesis protein signature | 25 | 46 | IPR001980 | F | GO:0004595; GO:0015937 |
| PRINTS            | PR01020          | Lipopolysaccharide core biosynthesis protein signature | 91 | 107 | IPR001980 | F | GO:0004595; GO:0015937 |
| SUPERFAMILY       | SSF52374         |                                                   | 7 | 145 |                     |         |                     |
| TIGRFAM           | TIGR00125        | cyt_tran_rel: cytidyltransferase-like domain | 9 | 60 | IPR004821 | D | GO:0003824; GO:0009058 |
| TIGRFAM           | TIGR01510        | coaD_prev_kdtB: pantetheine-phosphate adenyltransferase | 9 | 139 | IPR001980 | F | GO:0004595; GO:0015937 |
| M. testudinis      | 151              | Gene3D   | G3DSA:3.40.50.620 |                                                                     | 1 | 149 | IPR014729 | H |                                           |
|                   |                  | Hamap    | MF_00151       | Phosphopantetheine adenyltransferase [coaD].                | 3 | 150 | IPR001980 | F | GO:0004595; GO:0015937 |
|                   |                  | PANTHER  | PTHR21342:SF1  |                                                                 | 1 | 142 | IPR001980 | F | GO:0004595; GO:0015937 |
| PANTHER           | PTHR21342:SF1    |                                                   | 1 | 142 |                     |         |                     |
| Pfam              | PF01467          | Cytidyltransferase-like | 6 | 136 | IPR004821 | D | GO:0003824; GO:0009058 |
| PRINTS            | PR01020          | Lipopolysaccharide core biosynthesis protein signature | 3 | 21 | IPR001980 | F | GO:0004595; GO:0015937 |
| PRINTS            | PR01020          | Lipopolysaccharide core biosynthesis protein signature | 21 | 42 | IPR001980 | F | GO:0004595; GO:0015937 |
| PRINTS            | PR01020          | Lipopolysaccharide core biosynthesis protein signature | 88 | 104 | IPR001980 | F | GO:0004595; GO:0015937 |
| PRINTS            | PR01020          | Lipopolysaccharide core biosynthesis protein signature | 115 | 137 | IPR001980 | F | GO:0004595; GO:0015937 |
| SUPERFAMILY       | SSF52374         |                                                   | 3 | 142 |                     |         |                     |
| TIGRFAM           | TIGR00125        | cyt_tran_rel: cytidyltransferase-like domain | 4 | 61 | IPR004821 | D | GO:0003824; GO:0009058 |
| Mycoplasma species | Amino acid region | Database | Database ID | Database signature description | ID region start | ID region end | InterPro ID | ID type | Gene Ontology (GO term) |
|--------------------|------------------|----------|-------------|-------------------------------|----------------|--------------|-------------|---------|--------------------------|
| M. yeatsii         | 140              | Gene3D   | G3DAS:3.40.50.620 | coaD_prev_didB: pantetheine-phosphate adenylyltransferase | 4              | 140          | IPR001980  | F       | GO:0004595; GO:0015937   |
|                    |                  | Hanap    | MF_00151    | Phosphopantetheine adenylyltransferase [coaD] | 2              | 140          | IPR001980  | F       | GO:0004595; GO:0015937   |
|                    |                  | PANTHER  | PTHR21342   |                                | 1              | 138          | IPR014729  | H       | GO:0004595; GO:0015937   |
| M. yeatsii         | 140              | Pfam     | PF01467     | Cytidyltransferase-like        | 5              | 134          | IPR004821  | D       | GO:0003824; GO:0009058   |
|                    |                  | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 86             | 102          | IPR001980  | F       | GO:0004595; GO:0015937   |
|                    |                  | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 20             | 41           | IPR001980  | F       | GO:0004595; GO:0015937   |
|                    |                  | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 2              | 20           | IPR001980  | F       | GO:0004595; GO:0015937   |
|                    |                  | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 49             | 73           | IPR001980  | F       | GO:0004595; GO:0015937   |
|                    |                  | PRINTS   | PR01020     | Lipopolysaccharide core biosynthesis protein signature | 113            | 135          | IPR001980  | F       | GO:0004595; GO:0015937   |
|                    |                  | SUPERFAMILY | SSFS2374 | cyt_tran_rel: cytidyltransferase-like domain | 2              | 138          | IPR014729  | H       | GO:0004595; GO:0015937   |
|                    |                  | TIGRFAM  | TIGR00125   |                                | 3              | 61           | IPR004821  | D       | GO:0003824; GO:0009058   |
|                    |                  | TIGRFAM  | TIGR01510   | coaD_prev_didB: pantetheine-phosphate adenylyltransferase | 3              | 139          | IPR001980  | F       | GO:0004595; GO:0015937   |

1ID type abbreviations – H, Homologous superfamily; F, Family; D, Domain
2InterPro ID – IPR014729: Rossmann-like alpha/beta/alpha sandwich fold; IPR001980: Phosphopantetheine adenylyltransferase; IPR004821: Cytidyltransferase-like domain
3GO term (Biological Process) – GO:0009058: Biosynthetic process; GO:0015937: Coenzyme A biosynthetic process
GO term (Molecular Function) – GO:0003824: Catalytic activity; GO:0004595: Pantetheine-phosphate adenylyltransferase activity

Supplementary Table 12 PPAT MEME + motif locations

| Mycoplasma species | p-value | Motif 1 | Motif 2 | Motif 3 | Motif 4 |
|--------------------|---------|---------|---------|---------|---------|
| M. agalactiae      | 8.04e-99| 1-42    | 47-61   | 63-83   | 85-134  |
| M. alligatoris     | 4.76e-92| 4-45    | 50-64   | 68-88   | 90-139  |
| M. alvi            | 4.46e-57| 3-44    | 49-63   | -       | 88-137  |
| M. anatis          | 8.32e-97| 3-44    | 49-63   | 65-85   | 87-136  |
| M. arginini        | 9.84e-101| 1-42   | 47-61   | 63-83   | 85-134  |
| M. bovigenitalium  | 1.33e-88| 1-42    | 47-61   | 63-83   | 85-134  |
| Mycoplasma species            | p-value     | Motif 1 | Motif 2 | Motif 3 | Motif 4 |
|------------------------------|-------------|---------|---------|---------|---------|
| M. bovis                     | 9.01e-101   | 1-42    | 47-61   | 63-83   | 85-134  |
| M. buteonis                  | 3.59e-77    | 5-46    | 51-65   | 69-89   | 91-140  |
| M. Californicum              | 6.44e-91    | 1-42    | 47-61   | 63-83   | 85-134  |
| M. canis                     | 5.39e-74    | 4-45    | 49-63   | 66-86   | 88-137  |
| M. capricolum                | 1.01e-89    | 1-42    | 47-61   | 63-83   | 85-134  |
| M. collis                    | 1.04e-81    | 7-48    | 53-67   | 69-89   | 91-140  |
| M. columbinum                | 1.37e-97    | 2-43    | 48-62   | 65-85   | 87-136  |
| M. columborale               | 4.20e-89    | 3-44    | 49-63   | 65-85   | 87-136  |
| M. conjunctivae              | 2.15e-95    | 10-51   | 56-70   | 72-92   | 94-143  |
| M. crociuli                  | 3.14e-91    | 5-46    | 51-65   | 69-89   | 91-140  |
| M. felis                     | 7.02e-97    | 3-44    | 49-63   | 65-85   | 87-136  |
| M. felis                     | 9.55e-85    | 2-43    | 47-61   | 63-83   | 85-134  |
| M. fermentans                | 8.34e-94    | 2-43    | 48-62   | 64-84   | 86-135  |
| M. gallinaceum               | 6.43e-91    | 4-45    | 50-64   | 66-86   | 88-137  |
| M. gallinarum                | 1.52e-99    | 2-43    | 48-62   | 64-84   | 86-135  |
| M. iners                     | 4.14e-87    | 2-43    | 48-62   | 64-84   | 86-135  |
| M. iowae                     | 1.23e-60    | 5-46    | 50-64   | -       | 89-138  |
| M. leachii                   | 6.70e-90    | 1-42    | 47-61   | 63-83   | 85-134  |
| M. leonidiae                 | 6.91e-72    | 3-44    | 48-62   | 64-84   | 86-135  |
| M. lipofaciens               | 2.75e-95    | 1-42    | 47-61   | 63-83   | 85-134  |
| M. mobile                    | 7.89e-27    | 8-49    | 54-68   | -       | -       |
| M. molare                    | 1.33e-89    | 1-42    | 47-61   | 63-83   | 85-134  |
| M. mycoides subsp. capri     | 1.37e-89    | 1-42    | 47-61   | 63-83   | 85-134  |
| M. mycoides subsp. mycoides  | 1.05e-87    | 1-42    | 47-61   | 63-83   | 85-134  |
| M. opalescens                | 5.58e-90    | 1-42    | 47-61   | 64-84   | 86-135  |
| M. penetrans                 | 4.73e-53    | 7-48    | 52-66   | -       | 91-140  |
| M. pirum                     | 1.88e-59    | 3-44    | 49-63   | -       | 88-137  |
| M. primatun                  | 7.48e-105   | 1-42    | 47-61   | 63-83   | 85-134  |
| M. pulmonis                  | 5.26e-87    | 5-46    | 51-65   | 69-89   | 91-140  |
| M. putrefaciens              | 4.92e-74    | 1-42    | 47-61   | 63-83   | 85-134  |
| M. simbae                    | 2.98e-93    | 1-42    | 47-61   | 63-83   | 85-134  |
| M. sturni                    | 1.22e-91    | 3-44    | 49-63   | 65-85   | 87-136  |
| M. synoviae                  | 5.65e-98    | 6-47    | 52-66   | 68-88   | 90-139  |
### Supplementary Table 13 DPCK CDD results

| Query | Hit type | ID region start | ID region end | E-Value | Accession | Short name | Superfamily | Definition |
|-------|----------|-----------------|---------------|---------|-----------|------------|-------------|------------|
| M. sp. Ms02 | non-specific | 1 | 122 | 1.50e-13 | COG0237 | CoaE | cI30785 | Dephospho-CoA kinase |
| | superfamily | 1 | 122 | 1.50e-13 | cI30785 | CoaE superfamily | - | Dephospho-CoA kinase |
| | non-specific | 1 | 122 | 6.33e-11 | cd02022 | DPCK | cI17190 | Dephospho-CoA kinase |
| | superfamily | 1 | 122 | 6.33e-11 | cI17190 | NK superfamily | - | Nucleoside/nucleotide kinase superfamily |
| | non-specific | 2 | 122 | 2.20e-08 | TIGR00152 | TIGR00152 | cI17190 | Dephospho-CoA kinase |
| | non-specific | 2 | 120 | 2.87e-05 | PRK00081 | coaE | cI17190 | Dephospho-CoA kinase |
| | non-specific | 2 | 48 | 0.000637 | cd01983 | Fer4_NifH | cI28886 | The Fer4_NifH superfamily |
| | superfamily | 2 | 48 | 0.000637 | cI28886 | Fer4_NifH superfamily | - | The Fer4_NifH superfamily |
| | non-specific | 1 | 33 | 0.001471 | COG1936 | Fap7 | cI17190 | Broad-specificity NMP kinase |
| M. agalactiae | non-specific | 1 | 143 | 2.34e-23 | COG0237 | CoaE | cI30785 | Dephospho-CoA kinase |
| | superfamily | 1 | 143 | 2.34e-23 | cI30785 | CoaE superfamily | - | Dephospho-CoA kinase |
| | specific | 1 | 143 | 8.86e-21 | cd02022 | DPCK | cI17190 | Dephospho-CoA kinase |
| | superfamily | 1 | 143 | 8.86e-21 | cI17190 | NK superfamily | - | Nucleoside/nucleotide kinase superfamily |
| | non-specific | 2 | 186 | 2.85e-14 | TIGR00152 | TIGR00152 | cI17190 | Dephospho-CoA kinase |
| | non-specific | 2 | 146 | 2.73e-13 | PRK00081 | coaE | cI17190 | Dephospho-CoA kinase |
| | non-specific | 2 | 142 | 1.59e-06 | pfam01121 | CoaE | cI17190 | Dephospho-CoA kinase |
| | non-specific | 1 | 121 | 9.07e-06 | COG1936 | Fap7 | cI17190 | Broad-specificity NMP kinase |
| | non-specific | 1 | 92 | 0.004474 | PLN02422 | PLN02422 | cI17190 | Dephospho-CoA kinase |
| | non-specific | 2 | 129 | 0.007723 | COG0572 | Udk | cI28606 | Uracil kinase superfamily |
| | superfamily | 2 | 129 | 0.007723 | cI28606 | Udk superfamily | - | Uracil kinase superfamily |
| | non-specific | 2 | 35 | 0.009588 | PRK03839 | PRK03839 | cI17190 | putative kinase |
| M. alligatoris | non-specific | 1 | 132 | 1.34e-11 | COG0237 | CoaE | cI30785 | Dephospho-CoA kinase |
| | superfamily | 1 | 132 | 1.34e-11 | cI30785 | CoaE superfamily | - | Dephospho-CoA kinase |
| | non-specific | 1 | 132 | 4.77e-11 | cd02022 | DPCK | cI17190 | Dephospho-CoA kinase |
| | superfamily | 1 | 132 | 4.77e-11 | cI17190 | NK superfamily | - | Nucleoside/nucleotide kinase superfamily |
| | non-specific | 2 | 132 | 2.79e-05 | PRK00081 | coaE | cI17190 | Dephospho-CoA kinase |
| | non-specific | 2 | 136 | 0.000429 | TIGR00152 | TIGR00152 | cI17190 | Dephospho-CoA kinase |
| M. allv | non-specific | 2 | 188 | 2.29e-24 | TIGR00152 | TIGR00152 | cI17190 | Dephospho-CoA kinase |
| | superfamily | 2 | 188 | 2.29e-24 | cI17190 | NK superfamily | - | Nucleoside/nucleotide kinase superfamily |
| Query          | Hit type         | ID region start | ID region end | E-Value  | Accession       | Short name | Superfamily                        | Definition                                                                 |
|---------------|------------------|-----------------|---------------|----------|----------------|------------|------------------------------------|---------------------------------------------------------------------------|
| specific      | 2                | 151             |               | 1.45e-21 | cd02022        | DPCK       | cl17190                            | Dephospho-CoA kinase                                                      |
| non-specific  | 1                | 191             | 5.20e-20      | 2.24e-17 | COG0237        | CoaE       | cl130785                           | Dephospho-CoA kinase                                                      |
| superfamily   | 1                | 191             | 5.20e-20      | 2.52e-12 | pfam01121      | CoaE       | cl17190                            | Dephospho-CoA kinase                                                      |
| non-specific  | 2                | 106             | 8.98e-11      | 8.36e-06 | PLN02422       | coaE       | cl17190                            | Dephospho-CoA kinase                                                      |
| non-specific  | 5                | 89              | 1.98e-08      | 1.83e-06 | PRK14730       | coaE       | cl17190                            | Dephospho-CoA kinase                                                      |
| non-specific  | 2                | 194             |               | 0.002608 | PRK04040       | coaE       | cl17190                            | adenylate kinase                                                         |
| M. alvi       | non-specific     | 2               | 44            | 0.003877 | cd03255        | ABC_MJ0796_LolCDE_FtsE | cl25403  | ATP-binding cassette domain of the transporters involved in export of lipoprotein and macrolide, and cell division protein |
|               | superfamily      | 2               | 44            | 0.003877 | cl25403        | ABC_ATPase superfamily | -       | ATP-binding cassette transporter nucleotide-binding domain               |
|               | non-specific     | 1               | 21            | 0.005459 | COG2019        | AdkA       | cl17190                            | Archaeal adenylate kinase                                                  |
| non-specific  | 1                | 21              | 0.005635      | 0.007481 | COG1936        | Fad7       | cl17190                            | Broad-specificity NMP kinase                                               |
|               | non-specific     | 2               | 44            | 0.00671  | cd03263        | ABC_subfamily_A | cl125403 | ATP-binding cassette domain of the lipid transporters, subfamily A          |
| superfamily   | 2                | 50              | 0.007481      | 2.61e-13 | TIGR02982      | heterocyst DevA | cl28181  | ABC exporter ATP-binding subunit, DevA family                              |
| M. anatis     | non-specific     | 1                | 137           | 0.005459 | CGO237         | CoaE       | cl130785                           | Dephospho-CoA kinase                                                      |
|               | superfamily      | 1                | 137           | 0.005635 | COG0237        | CoaE       | cl130785                           | Dephospho-CoA kinase                                                      |
|               | non-specific     | 1                | 137           | 2.26e-09  | CD02022        | DPCK       | cl17190                            | Dephospho-CoA kinase                                                      |
| superfamily   | 1                | 137             | 2.26e-09      | 2.61e-13 | CD02022        | DPCK       | cl17190                            | Dephospho-CoA kinase                                                      |
|               | non-specific     | 2                | 137           | 4.69e-05  | TIGR00152      | TIGR00152  | cl17190                            | Dephospho-CoA kinase                                                      |
|               | non-specific     | 2                | 137           | 4.71e-05  | PRK00081       | coaE       | cl17190                            | Dephospho-CoA kinase                                                      |
| superfamily   | 2                | 50              | 0.007481      | 2.61e-13 | CGO237         | CoaE       | cl17190                            | ATPases associated with a variety of cellular activities                 |
| M. arginini   | non-specific     | 1                | 141           | 5.25e-13  | CGO237         | CoaE       | cl130785                           | Dephospho-CoA kinase                                                      |
|               | superfamily      | 1                | 141           | 5.25e-13  | CGO237         | CoaE       | cl130785                           | Dephospho-CoA kinase                                                      |
|               | non-specific     | 1                | 141           | 2.86e-11  | CD02022        | DPCK       | cl17190                            | Dephospho-CoA kinase                                                      |
| superfamily   | 1                | 147             | 2.86e-11      | 2.61e-13 | CD02022        | DPCK       | cl17190                            | Dephospho-CoA kinase                                                      |
|               | non-specific     | 2                | 147           | 5.29e-07  | TIGR00152      | TIGR00152  | cl17190                            | Dephospho-CoA kinase                                                      |
| superfamily   | 1                | 76              | 0.009556      | 2.86e-11 | CD02022        | DPCK       | cl17190                            | Virulence-associated protein E (these proteins contain a P-loop motif)    |
| M. bovigenitalium | non-specific  | 1                | 178           | 3.64e-12  | CD02022        | DPCK       | cl17190                            | Dephospho-CoA kinase                                                      |
|               | superfamily      | 1                | 178           | 3.64e-12  | CD02022        | DPCK       | cl17190                            | Dephospho-CoA kinase                                                      |
|               | superfamily      | 1                | 178           | 3.64e-12  | CD02022        | DPCK       | cl17190                            | Nucleoside/nucleotide kinase superfamily                                |
| Query | Hit type | ID region start | ID region end | E-Value | Accession | Short name | Superfamily | Definition |
|-------|----------|-----------------|---------------|---------|-----------|------------|-------------|------------|
| M. bovis | non-specific | 2 | 137 | 2.67e-07 | TIGR00152 | TIGR00152 | cl17190 | Dephospho-CoA kinase |
| M. bovis | non-specific | 2 | 88 | 6.80e-06 | PRK00081 | coaE | cl17190 | Dephospho-CoA kinase |
| M. bovis | non-specific | 1 | 117 | 0.00034 | PRK14732 | coaE | cl17190 | Dephospho-CoA kinase |
| M. bovis | superfamily | 1 | 149 | 4.53e-21 | COG0237 | CoaE superfamily | - | Dephospho-CoA kinase |
| M. bovis | specific | 1 | 146 | 6.23e-20 | cd02022 | DPCK | cl17190 | Dephospho-CoA kinase |
| M. bovis | superfamily | 1 | 146 | 6.23e-20 | TIGR00152 | CoaE superfamily | - | Dephospho-CoA kinase |
| M. bovis | non-specific | 2 | 177 | 1.36e-11 | TIGR00152 | CoaE superfamily | - | Dephospho-CoA kinase |
| M. bovis | non-specific | 2 | 146 | 4.16e-11 | PRK00081 | coaE | cl17190 | Dephospho-CoA kinase |
| M. bovis | superfamily | 1 | 78 | 2.40e-06 | COG1936 | Fap7 | cl17190 | Broad-specificity NMP kinase |
| M. bovis | non-specific | 1 | 91 | 0.00063 | PRK14731 | coaE | cl17190 | Dephospho-CoA kinase |
| M. bovis | non-specific | 2 | 33 | 0.00111 | cd01983 | Fer4 NifH superfamily | - | The Fer4 NifH superfamily |
| M. bovis | specific | 1 | 263 | 9.47e-37 | COG0561 | CoF | cl26787 | Hydroxymethylpyrimidine pyrophosphatase and other HAD family phosphatases (Coenzyme transport and metabolism, General function prediction only) |
| M. bovis | superfamily | 1 | 263 | 9.47e-37 | PRK00081 | HAD_3 superfamily | - | HAD-like hydrolase-like hydrolase |
| M. bovis | non-specific | 7 | 242 | 7.44e-36 | pfam08282 | Hydrolase 3 | cl26787 | HAD-like hydrolase-like hydrolase |
| M. bovis | non-specific | 7 | 256 | 2.02e-33 | TIGR00099 | CoF-subfamily | cl26787 | HAD phosphatase, similar to Escherichia coli CoF and Thermotoga maritima TM0651 |
| M. bovis | specific | 7 | 258 | 7.41e-31 | cd07516 | HAD_Pase | cl21460 | HAD phosphatase, similar to Bacteroides thetaotaomicron VPI-5482 BT4131 hexose phosphate phosphatase |
| M. bovis | superfamily | 7 | 258 | 7.41e-31 | PRK01158 | HAD-like superfamily | - | HAD phosphatase, similar to Bacteroides thetaotaomicron VPI-5482 BT4131 hexose phosphate phosphatase |
| M. bovis | non-specific | 1 | 261 | 1.23e-14 | PRK01158 | PRK01158 | cl26787 | Phosphoglycerate phosphatase |
| M. bovis | non-specific | 4 | 244 | 6.09e-14 | cd07517 | HAD_HPP | cl21460 | Phosphoglycerate phosphatase |
| M. bovis | non-specific | 8 | 259 | 3.25e-12 | TIGR01482 | SPP-subfamily | cl26787 | Sucrose-phosphate phosphatase subfamily |
| M. bovis | non-specific | 266 | 400 | 5.02e-12 | COG0237 | CoaE | cl30785 | Dephospho-CoA kinase |
| M. bovis | superfamily | 266 | 393 | 2.03e-11 | TIGR00152 | CoaE superfamily | - | Dephospho-CoA kinase |
| M. bovis | superfamily | 266 | 393 | 2.03e-11 | PRK10976 | CoaE | cl17190 | Dephospho-CoA kinase |
| M. bovis | non-specific | 7 | 218 | 1.49e-10 | TIGR01484 | HAD-SF-III | cl26787 | HAD phosphatase, sugar phosphate phosphatase, similar to Synecocystis sp PCC 6803 SPP |
| M. bovis | non-specific | 9 | 218 | 2.48e-09 | cd02605 | HAD_SPP | cl21460 | HAD phosphatase, sugar phosphate phosphatase, similar to Synecocystis sp PCC 6803 SPP |
| M. bovis | non-specific | 4 | 244 | 4.82e-08 | TIGR01482 | Phosphoglycerate phosphatase | cl26787 | Phosphoglycerate phosphatase, TA0175-type |
| M. bovis | non-specific | 266 | 391 | 9.33e-07 | TIGR00152 | coaE | cl17190 | Dephospho-CoA kinase |
| M. bovis | non-specific | 3 | 240 | 9.70e-07 | PRK10976 | PRK10976 | cl26787 | Phosphoglycerate phosphatase, TA0175-type |
| M. bovis | non-specific | 1 | 261 | 1.95e-06 | PRK10513 | PRK10513 | cl26787 | Phosphoglycerate phosphatase, TA0175-type |
| M. bovis | non-specific | 266 | 394 | 2.91e-05 | PRK00081 | coaE | cl17190 | Dephospho-CoA kinase |
| Query | Hit type | ID region start | ID region end | E-Value | Accession | Short name | Superfamily | Definition |
|-------|----------|----------------|---------------|---------|-----------|------------|-------------|------------|
|       | non-specific | 148 | 257 | 3.67e-05 | cd07518 | HAD_YbiV-Like | cl21460 | Escherichia coli YbiV sugar phosphatase/phosphotransferase and related proteins |
|       | non-specific | 2 | 259 | 7.30e-05 | PLN02887 | PLN02887 | c126787 | Nuclease/nucleotide kinase superfamily |
|       | non-specific | 5 | 75 | 0.00369 | TIGR01486 | HAD-SF-IIB-MPGP | c126786 | Predicted mannosyl-3-phosphoglycerate phosphatase, HAD superfamily |
|       | superfamily | 5 | 75 | 0.00369 | c126786 | YeD superfamily |  | |
|       | non-specific | 178 | 218 | 0.004772 | pfam01116 | S6P | c126787 | Sucrose-6-fucose phosphohydrolase |
|       | non-specific | 175 | 259 | 0.008491 | cd07514 | HAD_Pase | cl21460 | |
| M. bovoculi (HAD-DPCk) | | | | | | | | |
|       | non-specific | 1 | 185 | 5.06e-12 | COG0237 | CoA | c130785 | Dephospho-CoA kinase |
|       | superfamily | 1 | 185 | 5.06e-12 | c130785 | CoA superfamily |  | |
|       | non-specific | 1 | 129 | 2.49e-09 | cd02022 | DPCK | c117190 | Dephospho-CoA kinase |
|       | superfamily | 1 | 129 | 2.49e-09 | c117190 | Nk superfamily |  | |
|       | non-specific | 2 | 128 | 2.01e-06 | TIGR00152 | c117190 | Dephospho-CoA kinase | |
|       | non-specific | 1 | 189 | 3.53e-15 | COG0237 | CoA | c130785 | Dephospho-CoA kinase |
| M. buteonis | | | | | | | | |
|       | superfamily | 1 | 189 | 3.53e-15 | c130785 | CoA superfamily |  | |
|       | non-specific | 1 | 148 | 1.98e-14 | cd02022 | DPCK | c117190 | Dephospho-CoA kinase |
|       | superfamily | 1 | 148 | 1.98e-14 | c117190 | Nk superfamily |  | |
|       | non-specific | 2 | 148 | 5.93e-08 | PRK00083 | c117190 | Dephospho-CoA kinase | |
|       | non-specific | 2 | 189 | 6.62e-08 | TIGR0152 | c117190 | Dephospho-CoA kinase | |
|       | non-specific | 2 | 137 | 0.00019 | pfam01121 | c117190 | Dephospho-CoA kinase | |
| M. californicum | | | | | | | | |
|       | non-specific | 1 | 129 | 8.82e-10 | COG0237 | CoA | c130785 | Dephospho-CoA kinase |
|       | superfamily | 1 | 129 | 8.82e-10 | c130785 | CoA superfamily |  | |
|       | non-specific | 2 | 173 | 5.03e-06 | TIGR00152 | TIGR00152 | c117190 | Dephospho-CoA kinase |
|       | superfamily | 2 | 173 | 5.03e-06 | c117190 | Nk superfamily |  | |
|       | non-specific | 1 | 129 | 1.37e-05 | cd02022 | DPCK | c117190 | Dephospho-CoA kinase |
|       | non-specific | 2 | 34 | 0.001443 | cd01983 | Fer4 NifH superfamily |  | |
|       | superfamily | 2 | 34 | 0.001443 | c128886 | Fer4 NifH superfamily |  | |
| M. canis | | | | | | | | |
|       | non-specific | 1 | 88 | 0.006613 | COG0488 | c128181 | ATPase components of ABC transporters with duplicated ATPase domains [General function prediction only] |
|       | superfamily | 1 | 88 | 0.006613 | c128181 | AAA superfamily |  | |
| M. capricolum subsp. capricolum | | | | | | | | |
|       | specific | 6 | 179 | 2.24e-38 | cd02022 | DPCK | c117190 | Dephospho-CoA kinase |
|       | superfamily | 6 | 179 | 2.24e-38 | c117190 | Nk superfamily |  | |
|       | non-specific | 4 | 174 | 1.85e-26 | PRK00083 | c117190 | Dephospho-CoA kinase | |
|       | non-specific | 4 | 179 | 1.75e-23 | COG0237 | c117190 | Dephospho-CoA kinase | |
|       | non-specific | 4 | 179 | 1.75e-23 | c130785 | CoA superfamily |  | |
|       | non-specific | 5 | 174 | 3.75e-23 | pfam01121 | c117190 | Dephospho-CoA kinase | |
|       | non-specific | 6 | 174 | 7.13e-18 | TIGR0152 | TIGR00152 | c117190 | Dephospho-CoA kinase | |
|       | non-specific | 6 | 188 | 5.99e-12 | PRK14730 | c117190 | Dephospho-CoA kinase | |
| Query | Hit type | ID | ID region start | ID region end | E-Value | Accession | Short name | Definition |
|-------|----------|----|----------------|--------------|---------|-----------|------------|------------|
| non-specific | 6 | 179 | 7.13e-11 | PRK14732 | coalE | c1l7190 | Dephospho-CoA kinase |
| non-specific | 7 | 174 | 4.72e-08 | PRK14733 | coalE | c1l7190 | Dephospho-CoA kinase |
| non-specific | 6 | 179 | 2.23e-05 | PLN02422 | PLN02422 | c1l7190 | Dephospho-CoA kinase |
| non-specific | 7 | 174 | 0.000153 | PRK14734 | coalE | c1l7190 | Dephospho-CoA kinase |
| non-specific | 3 | 174 | 0.000277 | PRK14731 | coalE | c1l7190 | Dephospho-CoA kinase |
| superfamily | 2 | 175 | 1.30e-36 | cd02022 | DPCK | c1l7190 | Dephospho-CoA kinase |
| specific | 2 | 175 | 1.30e-36 | ci17190 | NK superfamily | - | Nucleoside/nucleotide kinase superfamily |
| non-specific | 1 | 170 | 1.6e-24 | PRK00081 | coalE | c1l7190 | Dephospho-CoA kinase |
| non-specific | 1 | 175 | 1.93e-22 | COG0237 | CoalE | c130785 | Dephospho-CoA kinase |
| superfamily | 1 | 175 | 1.93e-22 | ci30785 | CoalE | c1l7190 | Dephospho-CoA kinase |
| specific | 1 | 170 | 3.53e-22 | pfam01121 | CoalE | c1l7190 | Dephospho-CoA kinase |
| specific | 2 | 175 | 1.19e-16 | TIGR00152 | TIGR00152 | c1l7190 | Dephospho-CoA kinase |
| non-specific | 2 | 184 | 2.12e-11 | PRK14730 | coalE | c1l7190 | Dephospho-CoA kinase |
| non-specific | 2 | 175 | 2.21e-11 | PRK14732 | coalE | c1l7190 | Dephospho-CoA kinase |
| non-specific | 3 | 170 | 5.81e-08 | PRK14733 | coalE | c1l7190 | Dephospho-CoA kinase |
| specific | 2 | 175 | 0.001038 | PLN02422 | PLN02422 | c1l7190 | Dephospho-CoA kinase |
| specific | 2 | 170 | 0.001838 | PRK14731 | coalE | c1l7190 | Dephospho-CoA kinase |
| specific | 1 | 129 | 9.11e-25 | COG0237 | CoalE | c130785 | Dephospho-CoA kinase |
| superfamily | 1 | 129 | 9.11e-25 | ci30785 | CoalE superfamily | - | Dephospho-CoA kinase |
| specific | 1 | 148 | 1.10e-20 | cd02022 | DPCK | c1l7190 | Dephospho-CoA kinase |
| superfamily | 1 | 148 | 1.10e-20 | ci17190 | NK superfamily | - | Nucleoside/nucleotide kinase superfamily |
| non-specific | 2 | 148 | 3.80e-17 | TIGR00152 | TIGR00152 | c1l7190 | Dephospho-CoA kinase |
| specific | 2 | 148 | 6.58e-15 | PRK00081 | coalE | c1l7190 | Dephospho-CoA kinase |
| non-specific | 2 | 150 | 4.58e-07 | PRK14730 | coalE | c1l7190 | Dephospho-CoA kinase |
| non-specific | 1 | 80 | 4.87e-07 | COG1936 | Fap7 | c1l7190 | Broad-specificity NMP kinase |
| specific | 2 | 129 | 9.87e-06 | pfam01121 | CoalE | c1l7190 | Dephospho-CoA kinase |
| non-specific | 2 | 33 | 2.26e-05 | cd01983 | Fer4_NifH | c128886 | The Fer4_NifH superfamily |
| superfamily | 2 | 33 | 2.26e-05 | cl28386 | Fer4_NifH superfamily | - | The Fer4_NifH superfamily |
| non-specific | 2 | 80 | 0.000107 | PRK03839 | PRK03839 | c1l7190 | putative kinase |
| specific | 2 | 92 | 0.000163 | PRK04182 | PRK04182 | c128332 | Cytidine kinase |
| superfamily | 2 | 92 | 0.000163 | cl28332 | CmkB superfamily | - | Cytidine kinase |
| non-specific | 1 | 86 | 0.000597 | PLN02422 | PLN02422 | c1l7190 | Dephospho-CoA kinase |
| specific | 2 | 124 | 0.000634 | smart00382 | AAA | c128181 | ATPases associated with a variety of cellular activities |
| superfamily | 2 | 124 | 0.000634 | cl28181 | AAA superfamily | - | ATPases associated with a variety of cellular activities |
| non-specific | 2 | 73 | 0.001659 | COG1102 | CmkB | c128332 | Cytidine kinase |
| non-specific | 2 | 42 | 0.001875 | PRK04040 | PRK04040 | c1l7190 | adenyline kinase |
| non-specific | 1 | 20 | 0.002192 | cd03255 | ABC_MJ0796_LolCDE_FtsE | c125403 | ATP-binding cassette domain of the transporters involved in export of lipoprotein and macrolide, and cell division protein |
| superfamily | 1 | 20 | 0.002192 | cl25403 | ABC_ATPase superfamily | - | ATP-binding cassette transporter nucleotide-binding domain |
| Query | Hit type | ID region start | ID region end | E-Value | Accession | Short name | Superfamily | Definition |
|-------|----------|----------------|--------------|---------|-----------|------------|-------------|------------|
| non-specific | 5 | 81 | 0.00335 | pfam13207 | AAA_17 | c121455 | AAA domain | |
| superfamily | 5 | 81 | 0.00335 | c121455 | P-loop_NTPase superfamily | - | P-loop containing Nucleoside Triphosphate Hydrolases | |
| non-specific | 1 | 26 | 0.003507 | cd03116 | MobB | c128886 | Molybdenum is an essential trace element in the form of molybdenum cofactor (Moco) which is associated with the metabolism of nitrogen, carbon and sulfur by redox active enzymes. In E. coli, the synthesis of Moco involves genes from several loci: mxa, mob, mod, moe and mog. The mob locus contains mobA and mobB genes. MobB catalyzes the attachment of the guanine dinucleotide to molybdopterin. | |
| non-specific | 2 | 26 | 0.003758 | pfam13521 | AAA_28 | c121455 | AAA domain | |
| non-specific | 1 | 20 | 0.006373 | COG1136 | LoI | c128181 | ABC-type lipoprotein export system, ATPase component [Cell wall/membrane/envelope biogenesis] | |
| non-specific | 2 | 73 | 0.00661 | cd02034 | CooC | c128886 | The accessory protein CooC, which contains a nucleotide-binding domain (P-loop) near the N-terminus, participates in the maturation of the nickel center of carbon monoxide dehydrogenase (CODH). | |
| non-specific | 2 | 151 | 0.007951 | cd01851 | GBP | c121455 | Guanylate-binding protein (GBP) family (N-terminal domain) | |
| non-specific | 1 | 92 | 0.009239 | TIGR02173 | cyt_kin_arch | c128332 | Cytidine monophosphate kinase | |
| non-specific | 2 | 28 | 0.009861 | cd02020 | CMPK | c17190 | Cytidine monophosphate kinase | |
| non-specific | 1 | 137 | 1.47e-22 | COG0237 | CoaE | c130785 | Dephospho-CoA kinase | |
| superfamily | 1 | 137 | 1.47e-22 | c130785 | CoaE superfamily | - | Dephospho-CoA kinase | |
| specific | 1 | 137 | 4.33e-22 | cd02022 | DPCK | c17190 | Dephospho-CoA kinase | |
| superfamily | 1 | 137 | 4.33e-22 | c17190 | NK superfamily | - | Nucleoside/nucleotide kinase superfamily | |
| non-specific | 2 | 137 | 1.79e-12 | PRK14733 | coaE | c17190 | Dephospho-CoA kinase | |
| non-specific | 2 | 140 | 5.95e-12 | TIGR00152 | TIGR00152 | c17190 | Dephospho-CoA kinase | |
| non-specific | 2 | 137 | 2.38e-07 | pfam01121 | CoaE | c17190 | Dephospho-CoA kinase | |
| non-specific | 1 | 88 | 0.000169 | PRK14732 | coaE | c17190 | Dephospho-CoA kinase | |
| non-specific | 2 | 126 | 0.000305 | pfam13238 | AAA_18 | c121455 | AAA domain | |
| superfamily | 2 | 126 | 0.000305 | c121455 | P-loop_NTPase superfamily | - | P-loop containing Nucleoside Triphosphate Hydrolases | |
| non-specific | 1 | 89 | 0.000568 | PRK14731 | coaE | c17190 | Dephospho-CoA kinase | |
| non-specific | 9 | 136 | 0.007099 | pfam13207 | AAA_17 | c121455 | AAA domain | |
| non-specific | 1 | 181 | 4.64e-11 | COG0237 | CoaE | c130785 | Dephospho-CoA kinase | |
| superfamily | 1 | 181 | 4.64e-11 | c130785 | CoaE superfamily | - | Dephospho-CoA kinase | |
| non-specific | 1 | 144 | 1.93e-07 | cd02022 | DPCK | c17190 | Dephospho-CoA kinase | |
| superfamily | 1 | 144 | 1.93e-07 | c17190 | NK superfamily | - | Nucleoside/nucleotide kinase superfamily | |
| non-specific | 1 | 156 | 2.71e-05 | PRK00081 | coaE | c17190 | Dephospho-CoA kinase | |
| non-specific | 2 | 136 | 0.000544 | TIGR00152 | TIGR00152 | c17190 | Dephospho-CoA kinase | |

**M. collinum**

**M. columburne**
### Query: M. conjunctivae

| Hit type | ID region start | ID region end | E-Value | Accession | Short name | Superfamily | Definition |
|----------|----------------|---------------|---------|-----------|------------|-------------|------------|
| non-specific | 4 | 137 | 0.000723 | PRK14731 | coaE | e171790 | Dephospho-CoA kinase |
| non-specific | 1 | 93 | 0.000804 | PRK14732 | coaE | e171790 | Dephospho-CoA kinase |
| M. columborale | non-specific | 1 | 30 | 0.006918 | PRK14734 | coaE | e171790 | Dephospho-CoA kinase |

| Specific | 3 | 264 | 1.60e-34 | COG0561 | CoF | e126787 | Hydroxymethylpyrimidine pyrophosphatase and other HAD family phosphatases [Coenzyme transport and metabolism, General function prediction only] |
| Superfamily | 3 | 264 | 1.60e-34 | cl26787 | Hydrolyase 3 superfamily | - | haloacid dehalogenase-like hydrolase |
| non-specific | 7 | 257 | 2.72e-33 | pfam08282 | Hydrolyase 3 | e126787 | haloacid dehalogenase-like hydrolase |
| non-specific | 6 | 259 | 1.10e-26 | cd07516 | HAD_Pase | e121460 | phosphatase, similar to Escherichia coli CoF and Thermotoga maritima TM0651 |

| Superfamily | 6 | 259 | 1.10e-26 | cl21460 | HAD_like superfamily | - | Haloacid Dehalogenase-like Hydrolases |
| non-specific | 6 | 257 | 2.46e-26 | TIGR00099 | CoF-subfamily | e126787 | CoF subfamily of IIB subfamily of haloacid dehalogenase superfamily |
| non-specific | 1 | 260 | 1.17e-13 | PRK01158 | - | e126787 | phosphoglycolate phosphatase |
| non-specific | 6 | 220 | 8.35e-13 | TIGR01484 | HAD-SF-IIB | e126787 | HAD-superfamily |
| non-specific | 10 | 263 | 2.26e-12 | TIGR01482 | SPP-subfamily | e126787 | sucrose-phosphate phosphatase subfamily |
| non-specific | 5 | 260 | 2.08e-11 | cd07517 | HAD_HPP | e121460 | phosphatase, similar to Bacteroides thetaiotaomicron VPI-5482 BT4131 hexasphosphate phosphatase |
| non-specific | 267 | 393 | 8.59e-10 | COG0237 | CoaE | e130785 | Dephospho-CoA kinase |
| superfamily | 267 | 393 | 8.59e-10 | cl30785 | CoaE superfamily | - | Dephospho-CoaA kinase |
| non-specific | 267 | 401 | 2.23e-09 | cd02022 | DPCK | e17190 | Dephospho-CoA kinase |
| superfamily | 267 | 401 | 2.23e-09 | cl17190 | NK superfamily | - | Nucleoside/nucleotide kinase superfamily |

| non-specific | 5 | 257 | 5.30e-09 | TIGR01487 | Pglycolate_Arch | e126787 | phosphoglycolate phosphatase, TA0175-type |
| non-specific | 5 | 261 | 9.68e-09 | PRK10513 | PRK10513 | e126787 | sugar phosphate phosphatase |

| M. conjunctivae (HAD-DPCK) |
|-----------------------------|
| non-specific | 186 | 260 | 5.79e-08 | cd07514 | HAD_Pase | e121460 | phosphatase, similar to Thermoplasma acidophilum TA0175 phosphoglycolate phosphatase (PCPase), and Pyrococcus horikoshii PH1421, a magnesium-dependent phosphatase |
| non-specific | 267 | 414 | 1.65e-07 | TIGR00152 | TIGR00152 | e171790 | Dephospho-CoA kinase |
| non-specific | 6 | 219 | 2.86e-07 | PRK10976 | PRK10976 | e126787 | putative hydrolase |
| non-specific | 122 | 258 | 5.35e-05 | cd07518 | HAD_YbiV-Like | e121460 | Escherichia coli YbiV sugar phosphatase/phosphotransferase and related proteins |
| non-specific | 157 | 260 | 0.000276 | cd02605 | HAD_SPP | e121460 | sucrose-phosphatase, similar to Synechocystis sp PCC 6803 SPP |
| non-specific | 3 | 102 | 0.000756 | COG1877 | OtsB | e128591 | Trehalose-6-phosphatase [Carbohydrate transport and metabolism] |
| superfamily | 3 | 102 | 0.000756 | cl28591 | OtsB superfamily | - | Trehalose-6-phosphatase [Carbohydrate transport and metabolism] |
| non-specific | 1 | 76 | 0.001366 | PRK00192 | PRK00192 | e126786 | mannosyl-3-phosphoglycerate phosphatase |
| superfamily | 1 | 76 | 0.001366 | cl26786 | YedP superfamily | - | Predicted mannosyl-3-phosphoglycerate phosphatase, HAD superfamily |

### Query: M. cricetuli

| non-specific | 1 | 183 | 2.25e-17 | COG0237 | CoaE | e130785 | Dephospho-CoA kinase |

| superfamily | 1 | 183 | 2.25e-17 | cl30785 | CoaE superfamily | - | Dephospho-CoA kinase |
| Query       | Hit type       | ID region start | ID region end | E-Value       | Accession   | Short name | Superfamily                  | Definition                                                                 |
|------------|----------------|-----------------|---------------|---------------|-------------|------------|-----------------------------|-----------------------------------------------------------------------------|
|            | non-specific   | 1 136           |               | 6.93e-13      | cd02022     | DPCK       | cl17190                     | Dephospho-CoA kinase                                                       |
|            | superfamily    | 1 136           |               | 6.93e-13      | cl17190     | NK superfamily | Nucleoside/nucleotide kinase superfamily |                                                           |
|            | non-specific   | 2 142           |               | 3.58e-08      | TIGR00152   | TIGR00152  | cl17190                     | Dephospho-CoA kinase                                                       |
|            | non-specific   | 2 136           |               | 3.11e-06      | PRK00081    | coaE       | cl17190                     | Dephospho-CoA kinase                                                       |
|            | non-specific   | 1 41            |               | 0.002388      | COG1936     | Fap7       | cl17190                     | Broad-specificity NMP kinase                                               |
| M. crocodyli | superfamily    | 2 137           |               | 0.004333      | COG0572     | Udk        | cl28606                     | Uridine kinase superfamily                                                 |
|            | non-specific   | 1 190           |               | 1.56e-15      | COG0237     | CoaE       | cl30785                     | Dephospho-CoA kinase                                                       |
|            | superfamily    | 1 190           |               | 1.56e-15      | cl30785     | CoaE superfamily | Dephospho-CoA kinase |                                                           |
|            | non-specific   | 1 137           |               | 1.08e-14      | cd02022     | DPCK       | cl17190                     | Dephospho-CoA kinase                                                       |
|            | superfamily    | 1 137           |               | 1.08e-14      | cl17190     | NK superfamily | Nucleoside/nucleotide kinase superfamily |                                                           |
|            | non-specific   | 2 173           |               | 6.02e-11      | TIGR00152   | TIGR00152  | cl17190                     | Dephospho-CoA kinase                                                       |
|            | non-specific   | 2 137           |               | 1.15e-08      | PRK00081    | coaE       | cl17190                     | Dephospho-CoA kinase                                                       |
|            | non-specific   | 2 137           |               | 3.04e-05      | pfam01121   | CoaE       | cl17190                     | Dephospho-CoA kinase                                                       |
|            | non-specific   | 7 221           |               | 1.49e-29      | pfam08282   | Hydrolase 3 | cl26787                     | Haloacid dehalogenase-like hydrolase                                      |
|            | superfamily    | 7 221           |               | 1.49e-29      | cl26787     | Hydrolase 3 superfamily | Haloacid dehalogenase-like hydrolase |                                                           |
|            | specific       | 1 266           |               | 4.21e-29      | COG0561     | Cof        | cl26787                     | Hydroxymethylpyrimidine pyrophosphatase and other HAD family phosphatases [Coenzyme transport and metabolism, General function prediction only] |
|            | non-specific   | 7 221           |               | 3.98e-24      | cd07516     | HAD_Pase   | cl21460                     | Phosphatase, similar to Escherichia coli Cof and Thermotoga maritima TIM0651 |
|            | superfamily    | 7 221           |               | 3.98e-24      | cl21460     | HAD_like superfamily | Haloacid Dehalogenase-like Hydrolases |                                                           |
|            | non-specific   | 7 221           |               | 8.47e-23      | TIGR00099   | Cof-subfamily | Cof subfamily of IIB subfamily of haloacid dehalogenase superfamily |                                                           |
|            | non-specific   | 7 221           |               | 5.10e-14      | TIGR01484   | HAD-SF-IIB | cl26787                     | HAD-superfamily                                                            |
| M. dispar (HAD-DPCK) | non-specific   | 269 396        |               | 7.14e-13      | COG0237     | CoaE superfamily | Dephospho-CoA kinase |                                                           |
|            | superfamily    | 269 396         |               | 7.14e-13      | cl30785     | CoaE superfamily | Dephospho-CoA kinase |                                                           |
|            | non-specific   | 4 108           |               | 1.70e-11      | cd07517     | HAD_HPP    | cl21460                     | Phosphatase, similar to Bacteroides thetaotaomicron VPI-5482 BT4131 hexose phosphate phosphatase |
|            | superfamily    | 269 396         |               | 3.50e-08      | cd02022     | DPCK       | cl17190                     | Dephospho-CoA kinase                                                       |
|            | non-specific   | 269 396         |               | 3.50e-08      | cl17190     | NK superfamily | Nucleoside/nucleotide kinase superfamily |                                                           |
|            | non-specific   | 1 221           |               | 4.95e-06      | PRK01158    | PRK01158   | cl26787                     | Phosphoglycerate phosphatase                                               |
|            | non-specific   | 269 428         |               | 8.47e-06      | TIGR00152   | TIGR00152  | cl17190                     | Dephospho-CoA kinase                                                       |
|            | non-specific   | 9 220           |               | 9.22e-06      | TIGR01482   | SPP-subfamily | sucrose-phosphate phosphatase subfamily |                                                           |
|            | non-specific   | 9 220           |               | 8.38e-05      | TIGR01487   | Pglycolate_arch | phosphoglycerate phosphatase, TA0175-type |                                                           |
|            | non-specific   | 2 92            |               | 0.000353      | PRK10976    | PRK10976   | cl26787                     | Putative hydrolase                                                        |
|            | non-specific   | 7 49            |               | 0.000784      | pfam02358   | Trehalose PPass | Trehalose-phosphatase |                                                           |
|            | non-specific   | 7 48            |               | 0.001349      | cd01627     | HAD_TPP    | cl21460                     | Trehalose-phosphatase similar to Escherichia coli trehalose-6-phosphate phosphatase OtD and Saccharomyces cerevisiae trehalose-phosphatase TPS2 |
| M. dispar (HAD-DPCK) | non-specific   | 7 78            |               | 0.004988      | COG1877     | OrtB       | cl28591                     | Trehalose-6-phosphatase [Carbohydrate transport and metabolism]            |
| Query                         | Hit type | ID    | ID    | E-Value | Accession | Short name        | Superfamily | Definition                                                                 |
|-------------------------------|----------|-------|-------|---------|-----------|-------------------|-------------|---------------------------------------------------------------------------|
|                               | superfamily | 7     | 78    | 0.004988 | cl28591   | OtSB superfamily  | -           | Trehalose-6-phosphatase [Carbohydrate transport and metabolism]            |
|                               | non-specific | 1     | 146   | 3.67e-16 | COG0237   | CoaE              | cl30785     | Dephospho-CoA kinase                                                      |
|                               | superfamily | 1     | 146   | 3.67e-16 | cl30785   | CoaE superfamily  | -           | Dephospho-CoA kinase                                                      |
|                               | non-specific | 1     | 136   | 4.80e-15 | cd02022   | DPCK             | cl17190     | Dephospho-CoA kinase                                                      |
|                               | superfamily | 1     | 136   | 4.80e-15 | cl17190   | NK superfamily    | -           | Nucleoside/nucleotide kinase superfamily                                 |
|                               | non-specific | 2     | 186   | 8.51e-11 | TIGR00152 | TIGR00152        | cl17190     | Dephospho-CoA kinase                                                      |
|                               | non-specific | 2     | 136   | 2.85e-07 | PRK00081  | coaE             | cl17190     | Dephospho-CoA kinase                                                      |
|                               | non-specific | 2     | 137   | 0.003639 | pfam01121 | CoaE             | cl17190     | Dephospho-CoA kinase                                                      |
|                               | non-specific | 3     | 122   | 3.08e-14 | cd02022   | DPCK             | cl17190     | Dephospho-CoA kinase                                                      |
|                               | superfamily | 3     | 122   | 3.08e-14 | cl17190   | NK superfamily    | -           | Nucleoside/nucleotide kinase superfamily                                 |
|                               | non-specific | 1     | 107   | 2.19e-11 | cl30785   | CoaE superfamily  | -           | Dephospho-CoA kinase                                                      |
|                               | M. felinae | non-specific | 4     | 133   | 3.29e-08 | TIGR00152       | cl17190     | Dephospho-CoA kinase                                                      |
|                               | non-specific | 1     | 122   | 6.46e-08 | PRK00081  | coaE             | cl17190     | Dephospho-CoA kinase                                                      |
|                               | non-specific | 4     | 107   | 0.001021 | pfam01121 | CoaE             | cl17190     | Dephospho-CoA kinase                                                      |
|                               | non-specific | 4     | 107   | 0.002914 | PRK14732  | coaE             | cl17190     | Dephospho-CoA kinase                                                      |
|                               | non-specific | 1     | 26    | 0.003529 | PRK15467  | PRK15467         | cl21455     | Ethanolamine utilization protein EutP                                      |
|                               | superfamily | 1     | 26    | 0.003529 | cl21455   | P-loop_NTPase superfamily | - | P-loop containing Nucleoside Triphosphate Hydrolases                     |
|                               | non-specific | 2     | 40    | 0.00391  | COG1936   | Fap7             | cl17190     | Broad-specificity NMP kinase                                              |
|                               | superfamily | 1     | 146   | 7.45e-23 | COG0237   | CoaE             | cl30785     | Dephospho-CoA kinase                                                      |
|                               | specific   | 1     | 146   | 7.45e-23 | cl30785   | CoaE superfamily  | -           | Dephospho-CoA kinase                                                      |
|                               | superfamily | 1     | 146   | 2.70e-20 | cd02022   | DPCK             | cl17190     | Dephospho-CoA kinase                                                      |
|                               | non-specific | 1     | 146   | 2.70e-20 | cl17190   | NK superfamily    | -           | Nucleoside/nucleotide kinase superfamily                                 |
|                               | non-specific | 2     | 146   | 1.34e-14 | PRK00081  | coaE             | cl17190     | Dephospho-CoA kinase                                                      |
|                               | non-specific | 2     | 146   | 8.01e-14 | TIGR00152 | TIGR00152        | cl17190     | Dephospho-CoA kinase                                                      |
|                               | M. fermentans | non-specific | 1     | 187   | 8.48e-07 | PRK14732        | cl17190     | Dephospho-CoA kinase                                                      |
|                               | non-specific | 2     | 137   | 3.08e-06 | PRK14733  | coaE             | cl17190     | Dephospho-CoA kinase                                                      |
|                               | non-specific | 2     | 146   | 3.22e-06 | pfam01121 | CoaE             | cl17190     | Dephospho-CoA kinase                                                      |
|                               | non-specific | 7     | 258   | 1.96e-37 | pfam08282 | Hydrolase 3      | cl26787     | Halocid dehalogenase-like hydrolase                                       |
|                               | superfamily | 7     | 258   | 1.96e-37 | cl26787   | Hydrolase 3 superfamily | - | Halocid dehalogenase-like hydrolase                                       |
|                               | specific   | 1     | 263   | 3.22e-34 | COG0561   | CoF              | cl26787     | Hydroxymethylpyrimidine pyrophosphatase and other HAD family phosphatases [Coenzyme transport and metabolism, General function prediction only] |
|                               | non-specific | 7     | 260   | 7.20e-31 | cd07516   | HAD_Pase         | cl21460     | Phosphatase, similar to Escherichia coli CoF and Thermotoga maritima TM0651 |
|                               | M. flocculare (HAD-DPCK) | non-specific | 7     | 260   | 7.20e-31 | cl21460         | HAD_like superfamily | Halocid Dehalogenase-like Hydrolases                                   |
|                               | non-specific | 7     | 257   | 9.73e-30 | TIGR00099 | Cof-subfamily     | cl26787     | Cof subfamily of IIB subfamily of haloacid dehalogenase superfamily       |
|                               | M. flocculare (HAD-DPCK) | non-specific | 4     | 246   | 5.58e-17 | cd07517         | cl21460     | Phosphatase, similar to Bacteroides thetaotomacron VPI-5482 BT4131 hexose phosphate phosphatase |
| Query          | Hit type           | ID region start | ID region end | E-Value | Accession | Short name | Superfamily | Definition                                                                 |
|---------------|--------------------|-----------------|---------------|---------|-----------|------------|-------------|---------------------------------------------------------------------------|
| non-specific  | 268 395            | 1.17e-14        | COG0237       |         | CoaE      |             |              | Dephospho-CoA kinase                                                     |
| superfamily   | 268 395            | 1.17e-14        | cI30785       |         | CoaE superfamily |             |              | Dephospho-CoA kinase                                                     |
| non-specific  | 7 232              | 2.46e-12        | TIGR01484     |         | HAD-SF-IIB |             |              | HAD-superfamily                                                          |
| non-specific  | 1 246              | 5.34e-10        | PRK01158      |         |             |             |              | phosphoglycolate phosphatase                                             |
| non-specific  | 268 395            | 1.46e-09        | cd02022       |         | DPCK      |             |              | Dephospho-CoA kinase                                                     |
| superfamily   | 268 395            | 1.46e-09        | cI17190       |         | NK superfamily |             |              | -                                                                        |
| non-specific  | 9 250              | 4.25e-07        | TIGR01482     |         | SPP-subfamily |             |              | sucrose-phosphate phosphatase subfamily                                  |
| non-specific  | 9 246              | 1.63e-06        | TIGR01487     |         | Pglycolate_arch |             |              | phosphoglycolate phosphatase, TA0175-type                                |
| non-specific  | 167 263            | 8.18e-05        | PRK14502      |         | PRK14502  |             |              | bifunctional mannosyl-3-phosphoglycerate synthase/mannosyl-3-phosphoglycerate phosphatase, TA0175-type |
| superfamily   | 167 263            | 8.18e-05        | cI26786       |         | YedP superfamily |             |              | Predicted mannosyl-3-phosphoglycerate phosphatase, HAD superfamily       |
| non-specific  | 1 263              | 0.00034         | PRK10513      |         | PRK10513  |             |              | Dephospho-CoA kinase                                                     |
| non-specific  | 191 246            | 0.000356        | cd07514       |         | HAD_Pase  |             |              | sugar phosphate phosphatase                                              |
| non-specific  | 268 405            | 0.000473        | TIGR00152     |         |            |             |              | -                                                                        |
| non-specific  | 268 395            | 0.004105        | PRK00081      |         | coalE      |             |              | Dephospho-CoA kinase                                                     |
| non-specific  | 246 285            | 0.004508        | cd03257       |         | ABC_NikE_OppD_transporters |             |              | Predicted mannosyl-3-phosphoglycerate phosphatase, TA0175-type |
| superfamily   | 246 285            | 0.004508        | cI25403       |         | ABC_ATPase superfamily |             |              | -                                                                        |
| non-specific  | 7 74               | 0.006724        | cd01627       |         | HAD_TPP   |             |              | ATP-binding cassette transporter nucleotide-binding domain               |

**M. gallinarum**

| non-specific  | 1 145              | 3.41e-15        | COG0237       |         | CoaE      |             |              | Dephospho-CoA kinase                                                     |
| superfamily   | 1 145              | 3.41e-15        | cI30785       |         | CoaE superfamily |             |              | Dephospho-CoA kinase                                                     |
| non-specific  | 1 136              | 4.53e-13        | cd02022       |         | DPCK      |             |              | Dephospho-CoA kinase                                                     |
| superfamily   | 1 136              | 4.53e-13        | cI17190       |         | NK superfamily |             |              | Dephospho-CoA kinase                                                     |
| non-specific  | 2 145              | 2.67e-09        | TIGR00152     |         |            |             |              | Nucleoside/nucleotide kinase superfamily                               |
| superfamily   | 2 151              | 2.01e-05        | PRK00081      |         | coalE      |             |              | Nucleoside/nucleotide kinase superfamily                               |
| non-specific  | 25 199             | 6.87e-19        | COG0237       |         | CoaE      |             |              | Dephospho-CoA kinase                                                     |
| superfamily   | 25 199             | 6.87e-19        | cI30785       |         | CoaE superfamily |             |              | Dephospho-CoA kinase                                                     |
| non-specific  | 24 194             | 4.11e-18        | PRK00081      |         | coaE      |             |              | Dephospho-CoA kinase                                                     |
| superfamily   | 24 194             | 4.11e-18        | cI17190       |         | NK superfamily |             |              | Dephospho-CoA kinase                                                     |
| non-specific  | 23 186             | 9.11e-17        | TIGR00152     |         | TIGR00152 |             |              | Dephospho-CoA kinase                                                     |
| non-specific  | 17 181             | 6.24e-12        | cd02022       |         | DPCK      |             |              | Dephospho-CoA kinase                                                     |
| non-specific  | 88                  | 5.55e-08        | plam01121     |         | CoaE      |             |              | Dephospho-CoA kinase                                                     |
| non-specific  | 18 195             | 2.61e-07        | PLN02422      |         |            |             |              | Dephospho-CoA kinase                                                     |
| superfamily   | 27 194             | 3.52e-07        | PRK14732      |         | coalE      |             |              | Dephospho-CoA kinase                                                     |

**M. gallisepticum**

| non-specific  | 23 186             | 9.11e-17        | TIGR00152     |         | TIGR00152 |             |              | Dephospho-CoA kinase                                                     |
| non-specific  | 17 181             | 6.24e-12        | cd02022       |         | DPCK      |             |              | Dephospho-CoA kinase                                                     |
| non-specific  | 23 186             | 9.11e-17        | TIGR00152     |         | TIGR00152 |             |              | Dephospho-CoA kinase                                                     |
| non-specific  | 17 181             | 6.24e-12        | cd02022       |         | DPCK      |             |              | Dephospho-CoA kinase                                                     |

**M. genitalium**

| specific      | 2 182              | 5.10e-78        | TIGR00152     |         | TIGR00152 |             |              | Dephospho-CoA kinase                                                     |
| superfamily   | 2 182              | 5.10e-78        | cI17190       |         | NK superfamily |             |              | Nucleoside/nucleotide kinase superfamily                               |
| Query | Hit type | ID region start | ID region end | E-Value | Accession | Short name | Superfamily | Definition |
|-------|----------|----------------|---------------|---------|-----------|------------|-------------|------------|
| specific | 1 | 198 | 1.74e-45 | COG0237 | CoaE | c130785 | Dephospho-CoA kinase |
| superfamily | 1 | 198 | 1.74e-45 | c130785 | CoaE superfamily | c130785 | Dephospho-CoA kinase |
| specific | 2 | 169 | 1.84e-37 | cd02022 | DPCK | c130785 | Dephospho-CoA kinase |
| non-specific | 3 | 128 | 1.43e-18 | PRK00081 | coaE | c17190 | Dephospho-CoA kinase |
| non-specific | 3 | 106 | 8.84e-10 | PRK14730 | coaE | c17190 | Dephospho-CoA kinase |
| non-specific | 1 | 110 | 8.42e-08 | pfam01121 | CoaE | c17190 | Dephospho-CoA kinase |
| non-specific | 2 | 98 | 2.74e-05 | PLN02422 | PLN02422 | c17190 | Dephospho-CoA kinase |
| non-specific | 2 | 114 | 9.20e-05 | PRK14732 | coaE | c17190 | Dephospho-CoA kinase |
| non-specific | 3 | 75 | 0.000209 | pfam13521 | AAA_28 | c121455 | AAA domain |
| superfamily | 3 | 75 | 0.000209 | cl121455 | P-loop_NTase superfamily | - | P-loop containing Nucleoside Triphosphate Hydrolases |
| non-specific | 1 | 172 | 0.000756 | PTZ00451 | PTZ00451 | c17190 | Dephospho-CoA kinase |
| non-specific | 6 | 77 | 0.002063 | pfam13207 | AAA_17 | c121455 | AAA domain |
| non-specific | 2 | 82 | 0.002657 | PRK14731 | coaE | c17190 | Dephospho-CoA kinase |
| non-specific | 3 | 50 | 0.003221 | TIGR00231 | small GTP | c12769 | small GTP-binding protein domain |
| superfamily | 3 | 50 | 0.003221 | cl27669 | GTP_NTase superfamily | - | Elongation factor Ta GTP binding domain |

M. hyopneumoniae (HAD-DPCK)

| specific | 1 | 265 | 8.37e-32 | COG0561 | Cof | c126787 | Hydroxymethylpyrimidine pyrophosphatase and other HAD family phosphatases [Coenzyme transport and metabolism, General function prediction only] |
| superfamily | 1 | 265 | 8.37e-32 | cl26787 | Hydrolyase 3 superfamily | - | haloacid dehalogenase-like hydrolase |
| non-specific | 7 | 258 | 1.25e-29 | pfam08282 | Hydrolyase 3 | c126787 | haloacid dehalogenase-like hydrolase |
| non-specific | 5 | 258 | 3.30e-27 | TIGR00099 | Cof-subfamily | c126787 | Cof subfamily of IIB subfamily of haloacid dehalogenase superfamily |
| non-specific | 7 | 260 | 9.11e-25 | cd07516 | HAD_Pase | c121460 | phosphatase, similar to Escherichia coli Cof and Thermotoga maritima TM0651 |
| superfamily | 7 | 260 | 9.11e-25 | cl21460 | HAD like superfamily | - | Haloacid Dehalogenase-like hydrolases |
| non-specific | 269 | 428 | 1.87e-13 | COG0237 | CoaE | c130785 | Dephospho-CoA kinase |
| superfamily | 269 | 428 | 1.87e-13 | cl30785 | CoaE superfamily | - | Dephospho-CoA kinase |
| non-specific | 4 | 246 | 2.03e-12 | cd07517 | HAD_HPP | c121460 | phosphatase, similar to Bacteroides thetaiotaomicron VPI-5482 BT4131 hексозе phosphate phosphatase |
| non-specific | 7 | 221 | 3.80e-11 | TIGR01484 | HAD-SF-IIb | c126787 | HAD-superfamily |
| non-specific | 9 | 250 | 3.14e-09 | TIGR01482 | SPP-subfamily | c126787 | sucrose-phosphate phosphatase subfamily |
| superfamily | 269 | 395 | 1.51e-08 | cd02022 | DPCK | c17190 | Dephospho-CoA kinase |
| superfamily | 269 | 395 | 1.51e-08 | cl17190 | NK superfamily | - | Nucleoside/nucleotide kinase superfamily |
| specific | 1 | 263 | 3.41e-08 | PRK01158 | PRK01158 | c126787 | phosphoglycolate phosphatase |
| non-specific | 269 | 428 | 2.04e-07 | TIGR00152 | TIGR00152 | c17190 | Dephospho-CoA kinase |
| non-specific | 191 | 246 | 1.35e-06 | cd07514 | HAD_Pase | c121460 | phosphatase, similar to Thermoplasma acidophilum TA0175 phosphoglycolate phosphatase (PCPase), and Pyrococcus horikoshii PH1421, a magnesium-dependent phosphatase |
| non-specific | 7 | 215 | 6.16e-06 | pfam02358 | Trehalose_PPhase | c121460 | Trehalose-phosphatase |
| non-specific | 9 | 246 | 3.75e-05 | TIGR01487 | Pglycolate_arch | c126787 | phosphoglycolate phosphatase, TA0175-type |
| Query | Hit type | ID region | ID region | E-Value | Accession | Short name | Superfamily | Definition |
|-------|----------|-----------|-----------|---------|-----------|------------|-------------|------------|
| M. hyorhinis | non-specific | 7 | 48 | 0.000556 | cd01627 | HAD_TPP | cl21460 | trehalose-phosphate phosphatase similar to Escherichia coli trehalose-6-phosphate phosphatase OtsB and Saccharomyces cerevisiae trehalose-phosphate TPS2 |
| | non-specific | 182 | 258 | 0.000585 | PLN02887 | PLN02887 | cl26787 | hydrolase family proteins |
| | non-specific | 183 | 263 | 0.001299 | PRK10513 | PRK10513 | cl26787 | sugar phosphate phosphatase |
| | non-specific | 7 | 58 | 0.002792 | TGR00685 | T6PP | cl21460 | trehalose-phosphatase |
| | non-specific | 183 | 258 | 0.009025 | cd07518 | HAD_YbiV-Like | cl21460 | Escherichia coli YbiV sugar phosphate/phosphotransferase and related proteins |
| | non-specific | 9 | 141 | 1.14e-15 | COG0237 | CoaE | cl30785 | Diphospho-CoA kinase |
| | superfamily | 9 | 141 | 1.14e-15 | cd30785 | CoaE superfamily | - | Diphospho-CoA kinase |
| | non-specific | 12 | 141 | 2.74e-13 | cd02022 | DPCK | cl17190 | Diphospho-CoA kinase |
| | superfamily | 12 | 141 | 2.74e-13 | cl17190 | NK superfamily | - | Nucleoside/nucleotide kinase superfamily |
| | non-specific | 9 | 140 | 1.34e-08 | TIGR00152 | TIGR00152 | cl17190 | Diphospho-CoA kinase |
| | non-specific | 12 | 141 | 5.89e-06 | PRK00881 | coaE | cl17190 | Diphospho-CoA kinase |
| | specific | 7 | 196 | 6.69e-24 | COG0237 | CoaE | cl30785 | Diphospho-CoA kinase |
| | superfamily | 7 | 196 | 6.69e-24 | cd30785 | CoaE superfamily | - | Diphospho-CoA kinase |
| M. imitans | non-specific | 9 | 193 | 6.46e-23 | TIGR00152 | TIGR00152 | cl17190 | Diphospho-CoA kinase |
| | superfamily | 9 | 193 | 6.46e-23 | cl17190 | NK superfamily | - | Nucleoside/nucleotide kinase superfamily |
| | specific | 9 | 182 | 3.99e-20 | cd02022 | DPCK | cl17190 | Diphospho-CoA kinase |
| | non-specific | 12 | 194 | 1.25e-19 | PRK00081 | coaE | cl17190 | Diphospho-CoA kinase |
| | non-specific | 9 | 196 | 1.11e-11 | PLN02422 | PLN02422 | cl17190 | Diphospho-CoA kinase |
| | non-specific | 8 | 90 | 9.35e-11 | pfam01121 | CoaE | cl17190 | Diphospho-CoA kinase |
| | non-specific | 9 | 97 | 2.22e-05 | PRK14732 | coaE | cl17190 | Diphospho-CoA kinase |
| | specific | 12 | 194 | 2.64e-05 | PRK14730 | coaE | cl17190 | Diphospho-CoA kinase |
| M. iners | non-specific | 187 | 263 | 2.66e-13 | COG0237 | CoaE | cl30785 | Diphospho-CoA kinase |
| | superfamily | 187 | 263 | 2.66e-13 | cd30785 | CoaE superfamily | - | Diphospho-CoA kinase |
| | non-specific | 1 | 160 | 5.90e-12 | cd02022 | DPCK | cl17190 | Diphospho-CoA kinase |
| | superfamily | 1 | 160 | 5.90e-12 | cl17190 | NK superfamily | - | Nucleoside/nucleotide kinase superfamily |
| | non-specific | 2 | 100 | 5.22e-07 | TIGR00152 | TIGR00152 | cl17190 | Diphospho-CoA kinase |
| | non-specific | 1 | 20 | 4.04e-05 | cd03213 | ABCG_EPDR | cl25403 | Eye pigment and drug resistance transporter subfamily G of the ATP-binding cassette superfamily |
| | superfamily | 1 | 20 | 4.04e-05 | cl25403 | ABC_ATPase superfamily | - | ATP-binding cassette transporter nucleotide-binding domain |
| | non-specific | 2 | 123 | 6.79e-05 | PRK00081 | coaE | cl17190 | Diphospho-CoA kinase |
| M. iners | non-specific | 1 | 19 | 0.000177 | cd03255 | ABC_MJ0796_LolCDE_FisE | cl25403 | ATP-binding cassette domain of the transporters involved in export of lipoprotein and macrolide, and cell division protein |
| | non-specific | 1 | 22 | 0.000252 | pfam00005 | ABC_tran | cl21455 | ABC transporter |
| | superfamily | 1 | 22 | 0.000252 | pfam01455 | P-loop_NTPase superfamily | - | P-loop containing Nucleoside Triphosphate Hydrolases |
| | non-specific | 2 | 22 | 0.000398 | pfam01926 | MMR_HSR1 | cl21455 | 50S ribosome-binding GTPase |
| Query         | Hit type       | ID region start | ID region end | E-Value  | Accession   | Short name       | Superfamily   | Definition                                                                 |
|--------------|----------------|-----------------|---------------|----------|-------------|------------------|---------------|-----------------------------------------------------------------------------|
| non-specific | 1              | 17              |               | 0.000429 | COG1136     | LolD             | c128181       | ABC-type lipoprotein export system, ATPase component [Cell wall/membrane/envelope biogenesis] |
| superfamily  | 1              | 17              |               | 0.000429 | c128181     | AAA superfamily  | -             | ATPases associated with a variety of cellular activities                  |
| non-specific | 1              | 16              |               | 0.000478 | cd03256     | ABC_PhnC_transporter | c125403       | ATP-binding cassette domain of the binding protein-dependent phosphonate transport system |
| non-specific | 1              | 20              |               | 0.000505 | PRK10771    | thiQ             | c128181       | thiamine transporter ATP-binding subunit                                   |
| non-specific | 1              | 21              |               | 0.000512 | cd03228     | ABCC_MRP_Like    | c125403       | ATP-binding cassette domain of multidrug resistance protein-like transporters |
| non-specific | 2              | 23              |               | 0.000831 | PRK11174    | PRK11174         | c126602       | cytochrome/glutathione ABC transporter membrane/ATP-binding component     |
| superfamily  | 2              | 23              |               | 0.000831 | c126602     | SunT superfamily | -             | ABC-type bacteriocin/antibiotic exporters, contain an N-terminal double-glycine peptidase domain [Defense mechanisms] |
| non-specific | 2              | 28              |               | 0.001139 | COG4987     | CydC             | c126602       | ABC-type transport system involved in cytochrome bd biosynthesis, fused ATPase and permease components [Energy production and conversion, Posttranslational modification, protein turnover, chaperones] |
| non-specific | 2              | 20              |               | 0.001175 | COG1116     | TauB             | c128181       | ABC-type nitrate/sulfonate/bicarbonate transport system, ATPase component [Inorganic ion transport and metabolism] |
| non-specific | 1              | 19              |               | 0.001453 | TIGR02857   | CydD             | c126602       | thiol reductant ABC exporter, CydD subunit                                 |
| non-specific | 2              | 19              |               | 0.001626 | COG4988     | CydD             | c126602       | ABC-type transport system involved in cytochrome bd biosynthesis, ATPase and permease components [Energy production and conversion, Posttranslational modification, protein turnover, chaperones] |
| non-specific | 2              | 133             |               | 0.001635 | pfam01122   | CoaE             | c127190       | Dephospho-CoA kinase                                                       |
| non-specific | 1              | 48              |               | 0.001853 | COG3638     | PhnC             | c128181       | ABC-type phosphate/phosphonate transport system, ATPase component [Inorganic ion transport and metabolism] |
| non-specific | 1              | 19              |               | 0.002362 | PRK10535    | PRK10535         | c128180       | macrolide transporter ATP-binding/permease protein                         |
| M. iners     | superfamily    | 1              | 19             | 0.002362 | c128180     | PRK10535 superfamily | -             | macrolide transporter ATP-binding/permease protein                         |
| non-specific | 1              | 21              |               | 0.002445 | COG1135     | AbcC             | c128181       | ABC-type methionine transport system, ATPase component [Amino acid transport and metabolism] |
| non-specific | 1              | 22              |               | 0.002501 | COG0488     | Uup              | c128181       | ATPase components of ABC transporters with duplicated ATPase domains [General function prediction only] |
| non-specific | 3              | 22              |               | 0.002813 | cd00880     | Era_like         | c121455       | E. coli Ras-like protein (Era-like) GTPase                                 |
| Query | Hit type | ID region start | ID region end | E-Value | Accession | Short name | Superfamily | Definition |
|-------|----------|----------------|--------------|---------|-----------|------------|-------------|------------|
| non-specific | 2 | 28 | 0.003096 | cd03247 | ABCC_cytochrome_bd | cI25403 | ATP-binding cassette domain of CyD, subfamily C | ABC-type molybdenum transport system, ATPase component/photorepair protein PhrA [Inorganic ion transport and metabolism] |
| non-specific | 3 | 52 | 0.00316 | COG1119 | ModF | cI28181 | ABC family protein | The Eye Pigment Precursor Transporter (EPP) Family protein |
| non-specific | 2 | 23 | 0.004193 | COG3840 | ThiQ | cI28181 | ABC family protein | ABC-type thiamine transport system, ATPase component [Coenzyme transport and metabolism] |
| non-specific | 1 | 19 | 0.004303 | TIGR03608 | L_ocin_972_ABC | cI28181 | putative bacteriocin export ABC transporter, lactococcin 972 group | ATP-binding cassette domain of the nitrate and sulfonate transporters |
| non-specific | 2 | 19 | 0.004448 | PRK01889 | PRK01889 | cI26332 | GTase Rga | Deoxynucleoside kinase |
| superfamily | 2 | 19 | 0.004448 | cI26332 | DUF258 superfamily | cI26334 | Protein of unknown function, DUF258 | ABC-type bacteriocin/lantibiotic exporters, contain an N-terminal double-glycine peptidase domain [Defense mechanisms] |
| non-specific | 1 | 19 | 0.004705 | COG0486 | MnmE | cI26334 | ATP-binding cassette transporter nucleotide-binding domain | ABC-type bacteriocin/lantibiotic exporters, contain an N-terminal double-glycine peptidase domain [Defense mechanisms] |
| non-specific | 2 | 22 | 0.005457 | COG0486 | MnmE | cI26334 | tRNA U34 5-carboxymethylaminomethyl modifying GTPase MnmE/TrmE [Translation, ribosomal structure and biogenesis] | ATP-binding cassette domain of methionine transporter |
| non-specific | 2 | 22 | 0.005561 | cd01854 | YjeQ_EngC | cI25401 | Ribosomal interacting GTase YjeQ/EngC, a circularly permuted subfamily of the Ras GTPases | ATP-binding cassette domain of the nitrate and sulfonate transporters |
| non-specific | 2 | 20 | 0.006201 | cd00267 | ABC_NrtD_SsuB_transporters | cI25403 | ATP-binding cassette domain of the nitrate and sulfonate transporters | ATP-binding cassette domain of methionine transporter |
| non-specific | 1 | 17 | 0.006699 | cd03258 | ABC_Methionine_transporter | cI25403 | ATP-binding cassette domain of methionine transporter | ATP-binding cassette domain of the nitrate and sulfonate transporters |
| non-specific | 1 | 19 | 0.006877 | PRK13548 | hmuV | cI28181 | Ribosomal interacting GTase YjeQ/EngC, a circularly permuted subfamily of the Ras GTPases | ATP-binding cassette domain of the nitrate and sulfonate transporters |
| non-specific | 2 | 19 | 0.006969 | cd01854 | YjeQ_EngC | cI25406 | Ribosomal interacting GTase YjeQ/EngC, a circularly permuted subfamily of the Ras GTPases | Circularly permuted YjeQ-related GTases |
| superfamily | 2 | 19 | 0.006969 | cI25406 | YjeQ_related_GTase superfamily | cI25403 | First domain of the ATP-binding cassette component of cohab transport system | First domain of the ATP-binding cassette component of cohab transport system |
| non-specific | 3 | 17 | 0.00716 | cd03225 | ABC_cobalt_CbiO_domain1 | cI26286 | type IV secretion/conjugal transfer ATPase, VirB4 family | Type IV secretion pathway, VirB4 component [Intracellular trafficking, secretion, and vesicular transport] |
| superfamily | 3 | 19 | 0.007294 | TIGR00929 | VirB4_CagE | cI26286 | Type IV secretion pathway, VirB4 component [Intracellular trafficking, secretion, and vesicular transport] | Type IV secretion pathway, VirB4 family |
| non-specific | 1 | 19 | 0.007436 | cd03229 | ABC_Class3 | cI25403 | ATP-binding cassette domain of the binding protein-dependent transport systems | ATP-binding cassette domain of the binding protein-dependent transport systems |
| Query | Hit type | ID region start | ID region end | E-Value | Accession | Short name | Superfamily | Definition |
|-------|----------|-----------------|---------------|---------|-----------|------------|-------------|------------|
| non-specific | 2 | 20 | 20 | 0.00811 | TIGR028668 | CydC | ci26602 | thiol reductant ABC exporter, CydC subunit |
| non-specific | 2 | 22 | 22 | 0.008138 | PRK05291 | trnE | ci26334 | tRNA modification GTase TrnE |
| non-specific | 1 | 21 | 21 | 0.009792 | cd03251 | ABCC_MbA | ci25403 | ATP-binding cassette domain of the bacterial lipid flipase and related proteins, subfamily C |
| specific | 10 | 199 | 199 | 6.37e-26 | COG0237 | CoaE | ci30785 | Dephospho-CoA kinase |
| superfamily | 10 | 199 | 199 | 4.84e-26 | c30785 | CoaE superfamily | - | Dephospho-CoA kinase |
| specific | 11 | 189 | 189 | 6.65e-25 | cd02022 | DPCK | ci17190 | Dephospho-CoA kinase |
| superfamily | 11 | 189 | 189 | 6.65e-25 | cl17190 | NK superfamily | - | Nucleoside/nucleotide kinase superfamily |
| non-specific | 21 | 201 | 201 | 4.13e-20 | PRK00081 | coaE | ci17190 | Dephospho-CoA kinase |
| non-specific | 11 | 199 | 199 | 3.87e-18 | TIGR00152 | TIGR00152 | ci17190 | Dephospho-CoA kinase |
| non-specific | 11 | 189 | 189 | 1.37e-11 | pfam01121 | CoaE | ci17190 | Dephospho-CoA kinase |
| non-specific | 10 | 199 | 199 | 1.22e-08 | PLN02422 | PLN02422 | ci17190 | Dephospho-CoA kinase |
| non-specific | 10 | 199 | 199 | 5.33e-06 | PRK14730 | coaE | ci17190 | Dephospho-CoA kinase |
| non-specific | 11 | 203 | 203 | 7.07e-06 | PRK14732 | coaE | ci17190 | Dephospho-CoA kinase |
| non-specific | 10 | 199 | 199 | 0.000192 | PRK01184 | PRK01184 | ci17190 | hypothetical protein |
| non-specific | 10 | 201 | 201 | 0.002715 | PRK14734 | coaE | ci17190 | Dephospho-CoA kinase |
| specific | 2 | 175 | 175 | 4.88e-34 | cd02022 | DPCK | ci17190 | Dephospho-CoA kinase |
| superfamily | 2 | 175 | 175 | 4.88e-34 | cl17190 | NK superfamily | - | Nucleoside/nucleotide kinase superfamily |
| non-specific | 1 | 168 | 168 | 3.69e-21 | PRK00081 | coaE | ci17190 | Dephospho-CoA kinase |
| specific | 1 | 155 | 155 | 8.39e-19 | COG0237 | CoaE | ci30785 | Dephospho-CoA kinase |
| superfamily | 1 | 155 | 155 | 8.39e-19 | c30785 | CoaE superfamily | - | Dephospho-CoA kinase |
| non-specific | 1 | 163 | 163 | 1.02e-16 | pfam01121 | CoaE | ci17190 | Dephospho-CoA kinase |
| non-specific | 2 | 170 | 170 | 1.28e-13 | TIGR00152 | TIGR00152 | ci17190 | Dephospho-CoA kinase |
| non-specific | 2 | 163 | 163 | 1.57e-10 | PRK14732 | coaE | ci17190 | Dephospho-CoA kinase |
| non-specific | 2 | 185 | 185 | 2.36e-10 | PRK14730 | coaE | ci17190 | Dephospho-CoA kinase |
| non-specific | 3 | 144 | 144 | 1.59e-08 | PRK14733 | coaE | ci17190 | Dephospho-CoA kinase |
| non-specific | 2 | 161 | 161 | 0.000358 | PRK14731 | coaE | ci17190 | Dephospho-CoA kinase |
| non-specific | 2 | 168 | 168 | 0.000801 | PLN02422 | PLN02422 | ci17190 | Dephospho-CoA kinase |
| superfamily | 1 | 119 | 119 | 5.92e-10 | cd02022 | CoaE | ci17190 | Dephospho-CoA kinase |
| superfamily | 1 | 119 | 119 | 5.92e-10 | cl17190 | NK superfamily | - | Nucleoside/nucleotide kinase superfamily |
| non-specific | 1 | 37 | 37 | 2.16e-08 | COG0237 | CoaE | ci30785 | Dephospho-CoA kinase |
| specific | 1 | 37 | 37 | 2.16e-08 | c30785 | CoaE superfamily | - | Dephospho-CoA kinase |
| non-specific | 2 | 106 | 106 | 4.00e-07 | PRK00081 | coaE | ci17190 | Dephospho-CoA kinase |
| non-specific | 2 | 174 | 174 | 0.000202 | TIGR00152 | TIGR00152 | ci17190 | Dephospho-CoA kinase |
| non-specific | 2 | 119 | 119 | 0.00902 | pfam01121 | CoaE | ci17190 | Dephospho-CoA kinase |
| non-specific | 1 | 187 | 187 | 2.08e-18 | COG0237 | CoaE | ci30785 | Dephospho-CoA kinase |
| superfamily | 1 | 187 | 187 | 2.08e-18 | c30785 | CoaE superfamily | - | Dephospho-CoA kinase |
| non-specific | 1 | 137 | 137 | 3.80e-13 | cd02022 | DPCK | ci17190 | Dephospho-CoA kinase |
| superfamily | 1 | 137 | 137 | 3.80e-13 | cl17190 | NK superfamily | - | Nucleoside/nucleotide kinase superfamily |
| non-specific | 2 | 137 | 137 | 7.85e-12 | TIGR00152 | TIGR00152 | ci17190 | Dephospho-CoA kinase |
| non-specific | 11 | 137 | 137 | 2.89e-06 | PRK00081 | coaE | ci17190 | Dephospho-CoA kinase |
| superfamily | 1 | 147 | 147 | 2.34e-16 | COG0237 | CoaE | ci30785 | Dephospho-CoA kinase |
| superfamily | 1 | 147 | 147 | 2.34e-16 | c30785 | CoaE superfamily | - | Dephospho-CoA kinase |
| Query | Hit type | ID | E-Value | Accession | Short name | Superfamily | Definition |
|-------|----------|----|---------|-----------|------------|-------------|------------|
|       | non-specific | 1 | 147 | 1.90e-15 | cd02022 | DPCK | e17190 | Dephospho-CoA kinase |
|       | superfamily | 1 | 147 | 1.90e-15 | c17190 | NK superfamily | - | Nucleoside/nucleotide kinase superfamily |
|       | non-specific | 2 | 172 | 3.00e-10 | TIGR00152 | TIGR00152 | e17190 | Dephospho-CoA kinase |
|       | non-specific | 2 | 147 | 9.86e-09 | PRK00081 | coaE | e17190 | Dephospho-CoA kinase |
|       | non-specific | 1 | 32 | 0.000576 | COG1936 | Fap7 | e17190 | Broad-specificity NMP kinase |
|       | non-specific | 2 | 147 | 0.006349 | pfam01121 | CoaE | e17190 | Dephospho-CoA kinase |
|       | non-specific | 1 | 136 | 4.12e-19 | COG0237 | CoaE | e30785 | Dephospho-CoA kinase |
|       | superfamily | 1 | 136 | 4.12e-19 | c130785 | CoaE superfamily | - | Dephospho-CoA kinase |
|       | non-specific | 1 | 131 | 3.33e-14 | cd02022 | DPCK | e17190 | Dephospho-CoA kinase |
|       | superfamily | 1 | 131 | 3.33e-14 | c17190 | NK superfamily | - | Nucleoside/nucleotide kinase superfamily |
|       | non-specific | 2 | 131 | 1.64e-09 | TIGR00152 | TIGR00152 | e17190 | Dephospho-CoA kinase |
|       | non-specific | 2 | 131 | 1.16e-05 | PRK00081 | coaE | e17190 | Dephospho-CoA kinase |
|       | M. molare | specific | 2 | 175 | 2.52e-36 | cd02022 | DPCK | e17190 | Dephospho-CoA kinase |
|       | superfamily | 2 | 175 | 2.52e-36 | c17190 | NK superfamily | - | Nucleoside/nucleotide kinase superfamily |
|       | non-specific | 1 | 170 | 4.86e-24 | PRK00081 | coaE | e17190 | Dephospho-CoA kinase |
|       | non-specific | 1 | 175 | 9.60e-21 | COG0237 | CoaE | e30785 | Dephospho-CoA kinase |
|       | superfamily | 1 | 175 | 9.60e-21 | c130785 | CoaE superfamily | - | Dephospho-CoA kinase |
|       | non-specific | 1 | 170 | 9.20e-20 | pfam01121 | CoaE | e17190 | Dephospho-CoA kinase |
|       | non-specific | 2 | 170 | 5.02e-15 | TIGR00152 | TIGR00152 | e17190 | Dephospho-CoA kinase |
|       | non-specific | 2 | 170 | 3.85e-12 | PRK14730 | coaE | e17190 | Dephospho-CoA kinase |
|       | specific | 2 | 170 | 5.65e-12 | PRK14732 | coaE | e17190 | Dephospho-CoA kinase |
|       | non-specific | 3 | 170 | 6.95e-09 | PRK14733 | coaE | e17190 | Dephospho-CoA kinase |
|       | non-specific | 2 | 170 | 1.76e-06 | PRK14731 | coaE | e17190 | Dephospho-CoA kinase |
|       | specific | 2 | 175 | 3.12e-05 | PLN02422 | PLN02422 | e17190 | Dephospho-CoA kinase |
|       | M. mycoides subsp. capri | specific | 6 | 179 | 5.87e-34 | cd02022 | DPCK | e17190 | Dephospho-CoA kinase |
|       | superfamily | 6 | 179 | 5.87e-34 | c17190 | NK superfamily | - | Nucleoside/nucleotide kinase superfamily |
|       | non-specific | 4 | 172 | 6.04e-21 | PRK00081 | coaE | e17190 | Dephospho-CoA kinase |
|       | non-specific | 4 | 159 | 7.48e-19 | COG0237 | CoaE | e30785 | Dephospho-CoA kinase |
|       | superfamily | 4 | 159 | 7.48e-19 | c130785 | CoaE superfamily | - | Dephospho-CoA kinase |
|       | non-specific | 5 | 167 | 9.70e-17 | pfam01121 | CoaE | e17190 | Dephospho-CoA kinase |
|       | non-specific | 6 | 174 | 9.44e-14 | TIGR00152 | TIGR00152 | e17190 | Dephospho-CoA kinase |
|       | superfamily | 6 | 167 | 9.65e-11 | PRK14732 | coaE | e17190 | Dephospho-CoA kinase |
|       | non-specific | 6 | 189 | 9.75e-11 | PRK14730 | coaE | e17190 | Dephospho-CoA kinase |
|       | non-specific | 7 | 148 | 3.64e-08 | PRK14735 | coaE | e17190 | Dephospho-CoA kinase |
|       | non-specific | 1 | 159 | 0.000422 | PRK14731 | coaE | e17190 | Dephospho-CoA kinase |
|       | non-specific | 6 | 172 | 0.001703 | PLN02422 | PLN02422 | e17190 | Dephospho-CoA kinase |
|       | non-specific | 1 | 135 | 8.34e-17 | COG0237 | CoaE | e30785 | Dephospho-CoA kinase |
|       | superfamily | 1 | 135 | 8.34e-17 | c130785 | CoaE superfamily | - | Dephospho-CoA kinase |
|       | non-specific | 1 | 135 | 3.58e-11 | cd02022 | DPCK | e17190 | Dephospho-CoA kinase |
|       | superfamily | 1 | 135 | 3.58e-11 | c17190 | NK superfamily | - | Nucleoside/nucleotide kinase superfamily |
|       | non-specific | 2 | 111 | 7.67e-09 | PRK00081 | coaE | e17190 | Dephospho-CoA kinase |
|       | non-specific | 2 | 159 | 3.30e-08 | TIGR00152 | TIGR00152 | e17190 | Dephospho-CoA kinase |
|       | non-specific | 2 | 129 | 1.34e-06 | pfam01121 | CoaE | e17190 | Dephospho-CoA kinase |
|       | M. opalescens | specific | 2 | 175 | 2.52e-36 | cd02022 | DPCK | e17190 | Dephospho-CoA kinase |
|       | superfamily | 2 | 175 | 2.52e-36 | c17190 | NK superfamily | - | Nucleoside/nucleotide kinase superfamily |
| Query                  | Hit type | ID region start | ID region end | E-Value   | Accession   | Short name | Superfamily | Definition                                                                 |
|-----------------------|----------|----------------|---------------|-----------|-------------|------------|-------------|---------------------------------------------------------------------------|
| M. ovipneumoniae      | non-specific | 2               | 33            | 0.002374  | cd01983     | Fer4_NiH   | cl28886     | The Fer4_NiH superfamily                                                 |
| M. ovipneumoniae      | superfamily | 2               | 33            | 0.002374  | cl28886     | Fer4_NiH superfamily         | -                                                                       |
| M. penetrans          | non-specific | 2               | 21            | 0.003859  | COG4598     | HisP       | cl28181     | ABC-type histidine transport system, ATPase component [Amino acid transport and metabolism] |
| M. penetrans          | superfamily | 2               | 21            | 0.003859  | cl28181     | AAA superfamily          | -                                                                       |
| M. penetrans          | non-specific | 2               | 135           | 0.007313  | PRK14730    | coaE       | cl17190     | Dephospho-CoA kinase                                                     |
| M. ovipneumoniae      | non-specific | 5               | 259           | 3.75e-35  | TIGR00099   | Cof-subfamily   | cl26787     | Haloacid dehalogenase superfamily                                        |
| M. ovipneumoniae      | superfamily | 5               | 259           | 3.75e-35  | c126787     | Hydrolase_3 superfamily       | -                                                                       |
| M. ovipneumoniae      | specific  | 1               | 266           | 3.19e-34  | COG0561     | Cof        | cl26787     | Hydroxymethylpyrimidine pyrophosphatase and other HAD family phosphatases [Coenzyme transport and metabolism, General function prediction only] |
| M. ovipneumoniae      | non-specific | 7               | 259           | 4.26e-34  | pfam08282   | Hydrolase_3     | cl26787     | Haloacid dehalogenase superfamily                                        |
| M. ovipneumoniae      | non-specific | 5               | 261           | 1.17e-27  | cd07516     | HAD_Pase   | cl21460     | phosphatase, similar to Escherichia coli CoA and Thermotoga maritima TM0651 |
| M. ovipneumoniae      | superfamily | 5               | 261           | 1.17e-27  | c121460     | HAD_like superfamily        | -                                                                       |
| M. ovipneumoniae      | non-specific | 4               | 262           | 2.92e-18  | cd07517     | HAD_HPP    | cl21460     | Haloacid Dehalogenase-like Hydrolases                                    |
| M. ovipneumoniae      | non-specific | 269             | 394           | 4.40e-12  | TIGR00237   | CoaE       | c130785     | Dephospho-CoA kinase                                                     |
| M. ovipneumoniae      | superfamily | 269             | 394           | 4.40e-12  | c130785     | CoaE superfamily     | -                                                                       |
| M. ovipneumoniae      | non-specific | 269             | 394           | 4.41e-09  | cd02022     | DPCK       | c17190      | Dephospho-CoA kinase                                                     |
| M. ovipneumoniae      | non-specific | 269             | 394           | 8.41e-09  | c17190      | NK superfamily     | -                                                                       |
| M. ovipneumoniae      | non-specific | 5               | 233           | 9.07e-09  | TIGR01484   | HAD-Sf-IIB  | cl26787     | Nucleoside/nucleotide kinase superfamily                                 |
| M. ovipneumoniae      | non-specific | 1               | 262           | 1.87e-08  | PRK01158    | PRK01158   | cl26787     | Phosphoglycollatophosphatase                                              |
| M. ovipneumoniae      | non-specific | 8               | 251           | 5.77e-08  | TIGR01482   | SPP_subfamily     | cl26787     | Sucrose-phosphate-phosphatase, TA0175-type                             |
| M. ovipneumoniae      | non-specific | 269             | 366           | 1.92e-07  | TIGR00152   | TIGR00152   | c17190      | Dephospho-CoA kinase                                                     |
| M. ovipneumoniae      | non-specific | 1               | 265           | 1.37e-06  | PRK10513    | PRK10513   | cl26787     | Sugar phosphatase                                                        |
| M. ovipneumoniae      | non-specific | 5               | 259           | 0.001224  | TIGR01487   | Pglycolate_arch     | c121460     | Trehalose:PPase                                                          |
| M. ovipneumoniae      | non-specific | 263             | 438           | 0.004457  | PRK14733    | coaE       | c17190      | Dephospho-CoA kinase                                                     |
| M. ovipneumoniae      | non-specific | 7               | 74            | 0.007687  | pfam02358   | Trehalose_PPase   | c121460     | Trehalose:PPase                                                          |
| M. penetrans          | superfamily | 14              | 143           | 1.58e-39  | cd02022     | DPCK       | c17190      | Dephospho-CoA kinase                                                     |
| M. penetrans          | superfamily | 13              | 143           | 1.53e-25  | COG0237     | CoaE       | c130785     | Dephospho-CoA kinase                                                     |
| M. penetrans          | specific  | 13              | 142           | 1.53e-25  | c130785     | CoaE superfamily     | -                                                                       |
| M. penetrans          | non-specific | 12              | 142           | 3.04e-24  | PRK00081    | coaE       | c17190      | Dephospho-CoA kinase                                                     |
| M. penetrans          | non-specific | 14              | 143           | 2.66e-19  | TIGR00152   | TIGR00152   | c17190      | Dephospho-CoA kinase                                                     |
| M. penetrans          | non-specific | 14              | 140           | 8.47e-15  | pfam01122   | CoaE       | c17190      | Dephospho-CoA kinase                                                     |
| M. penetrans          | non-specific | 14              | 203           | 2.35e-11  | PRK14731    | coaE       | c17190      | Dephospho-CoA kinase                                                     |
| M. penetrans          | non-specific | 15              | 142           | 1.05e-09  | PRK14730    | coaE       | c17190      | Dephospho-CoA kinase                                                     |
| M. penetrans          | non-specific | 13              | 106           | 4.78e-09  | PLN02422    | PLN02422   | c17190      | Dephospho-CoA kinase                                                     |
| M. penetrans          | non-specific | 14              | 203           | 1.78e-08  | PRK14732    | coaE       | c17190      | Dephospho-CoA kinase                                                     |
| Query                  | Hit type          | ID region start | ID region end | E-Value   | Accession       | Short name          | Superfamily         | Definition                                                                 |
|-----------------------|-------------------|-----------------|---------------|-----------|-----------------|---------------------|---------------------|---------------------------------------------------------------------------|
| non-specific          | 11 141            | PRK14733        | 5.77e-05      |           | coaE            | c117190             | Dephospho-CoA kinase    |                                                                           |
| non-specific          | 13 143            | PRK14734        | 0.000212      |           | coaE            | c117190             | Dephospho-CoA kinase    |                                                                           |
| non-specific          | 15 143            | pfam13238       | 0.000749      |           | AAA_18          | c121455             | P-loop containing Nucleoside Triphosphate Hydrolases                    |                                                                           |
| superfamily           | 15 143            | cl21455         | 0.000749      |           | P-loop_NTPase superfamily |                       | -                   |                                                                           |
| non-specific          | 13 30             | PRK00349        | 0.001651      |           | uvrA            | c126603             | excinuclease ABC subunit A                                            |                                                                           |
| superfamily           | 13 30             | cl26603         | 0.001651      |           | UvrA superfamily | -                   | Excinuclease UvrABC ATPase subunit [Replication, recombination and repair] |                                                                           |
| specific              | 4 194             | COG0237         | 9.22e-25      |           | CoaE            | cl30785             | Dephospho-CoA kinase                                               |                                                                           |
| superfamily           | 4 194             | cl30785         | 9.22e-25      |           | CoaE superfamily | -                   | Dephospho-CoA kinase                                               |                                                                           |
| superfamily           | 7 187             | TIGR00152       | 1.24e-22      |           | NK superfamily  | c117190             | Dephospho-CoA kinase                                               |                                                                           |
| specific              | 7 179             | cd02022         | 2.50e-22      |           | DPCK            | c117190             | Dephospho-CoA kinase                                               |                                                                           |
| non-specific          | 6 192             | PRK00081        | 1.75e-15      |           | coaE            | c117190             | Dephospho-CoA kinase                                               |                                                                           |
| superfamily           | 6 92              | pfam01121       | 3.16e-09      |           | CoaE            | c117190             | Dephospho-CoA kinase                                               |                                                                           |
| superfamily           | 7 92              | PRK14730        | 6.17e-07      |           | coaE            | c117190             | Dephospho-CoA kinase                                               |                                                                           |
| non-specific          | 7 92              | PRK14732        | 0.000103      |           | coaE            | c117190             | Dephospho-CoA kinase                                               |                                                                           |
| non-specific          | 7 92              | COG1136         | 0.0002        |           | LoID            | c128181             | ABC-type lipoprotein export system, ATPase component [Cell wall/membrane/envelope biogenesis] |                                                                           |
| superfamily           | 7 85              | PLN02422        | 0.000317      |           | AAA superfamily | -                   | ATPases associated with a variety of cellular activities             |                                                                           |
| non-specific          | 7 25              | cd01854         | 0.007071      |           | YjeQ_EngC       | cl25406             | Ribosomal interacting GTPase YjeQ_EngC, a circularly permuted subfamily of the Ras GTases |                                                                           |
| superfamily           | 7 25              | cl25406         | 0.007071      |           | YjeQ_related_GTPase superfamily | -                   | Circularly permuted YjeQ-related GTPases                             |                                                                           |
| non-specific          | 8 137             | pfam13238       | 0.000793      |           | AAA_18          | c121455             | P-loop containing Nucleoside Triphosphate Hydrolases                   |                                                                           |
| superfamily           | 8 137             | cl21455         | 0.000793      |           | P-loop_NTPase superfamily | -                   | -                   |                                                                           |
| non-specific          | 1 91              | PRK14731        | 0.00103       |           | coaE            | c117190             | Dephospho-CoA kinase                                               |                                                                           |
| non-specific          | 6 27              | COG1936         | 0.001255      |           | Fap7            | c117190             | Broad-specificity NMP kinase                                         |                                                                           |
| non-specific          | 6 33              | PRK04040        | 0.002034      |           | -               | c117190             | adenyate kinase                                                      |                                                                           |
| non-specific          | 7 92              | cd03255         | 0.002161      |           | ABC_MJ0796_LolCDE_FisE | c125403             | ATP-binding cassette domain of the transporters involved in export of lipoprotein and macrolide, and cell division protein |                                                                           |
| superfamily           | 7 92              | cl25403         | 0.002161      |           | ABC_ATPase superfamily | -                   | -                   |                                                                           |
| non-specific          | 1 28              | COG2019         | 0.003735      |           | AdkA            | c117190             | Archael adenyate kinase                                              |                                                                           |
| non-specific          | 6 35              | PRK03839        | 0.006283      |           | PRK03839        | c117190             | putative kinase                                                      |                                                                           |
| specific              | 2 183             | TIGR00152       | 1.28e-81      |           | TIGR00152       | c117190             | Dephospho-CoA kinase                                               |                                                                           |
| superfamily           | 2 183             | cl17190         | 1.28e-81      |           | NK superfamily  | -                   | Nucleoside/nucleotide kinase superfamily                             |                                                                           |
| specific              | 1 194             | COG0237         | 4.42e-48      |           | CoaE            | c130785             | Dephospho-CoA kinase                                               |                                                                           |
| superfamily           | 1 194             | cl30785         | 4.42e-48      |           | CoaE superfamily | -                   | Dephospho-CoA kinase                                               |                                                                           |
| specific              | 2 156             | cd02022         | 1.15e-39      |           | DPCK            | c117190             | Dephospho-CoA kinase                                               |                                                                           |

**M. pirum**

**M. pneumoniae**
| Query | Hit type | ID region start | ID region end | E-Value | Accession | Short name | Superfamily | Definition |
|-------|----------|-----------------|---------------|---------|-----------|------------|-------------|------------|
| non-specific | 3 | 156 | 1.67e-28 | PRK00081 | coaE | e17190 | Dephospho-CoA kinase |
| non-specific | 3 | 106 | 3.23e-14 | PRK14730 | coaE | e17190 | Dephospho-CoA kinase |
| non-specific | 1 | 156 | 3.67e-14 | pfam01121 | CoaE | e17190 | Dephospho-CoA kinase |
| non-specific | 2 | 156 | 6.80e-06 | PRK14732 | coaE | e17190 | Dephospho-CoA kinase |
| non-specific | 1 | 156 | 8.58e-05 | PRK14734 | coaE | e17190 | Dephospho-CoA kinase |
| non-specific | 2 | 185 | 0.000155 | PRK14731 | coaE | e17190 | Dephospho-CoA kinase |
| non-specific | 3 | 153 | 0.000692 | pfam13521 | AAA_28 | e121455 | AAA domain |
| superfamily | 3 | 153 | 0.000692 | pfam13521 | AAA_28 | e121455 | AAA domain |
| non-specific | 1 | 153 | 0.001474 | COG1428 | Dek | e17190 | Deoxyadenosine/deoxyxytidine kinase |
| non-specific | 5 | 90 | 0.003355 | PLN02422 | PLN02422 | e17190 | Dephospho-CoA kinase |
| non-specific | 1 | 28 | 0.003534 | PRK04182 | PRK04182 | e128332 | Cytidylate kinase |
| superfamily | 1 | 28 | 0.003534 | pfam01121 | CoaE superfamily | e128332 | Cytidylate kinase |
| non-specific | 3 | 35 | 0.000608 | cld01983 | Fer4 NiFH superfamily | e128886 | The Fer4 NiFH superfamily |
| superfamily | 3 | 35 | 0.000608 | pfam13521 | Fer4 NiFH superfamily | e128886 | The Fer4 NiFH superfamily |
| non-specific | 1 | 37 | 0.009106 | COG1102 | CmkB superfamily | e128332 | Cytidylate kinase |
| non-specific | 1 | 144 | 2.19e-18 | COG0237 | CoaE | e130785 | Dephospho-CoA kinase |
| superfamily | 1 | 144 | 2.19e-18 | pfam13521 | CoaE superfamily | e130785 | Dephospho-CoA kinase |
| superfamily | 1 | 148 | 2.85e-15 | cld02022 | DPCK | e17190 | Dephospho-CoA kinase |
| superfamily | 1 | 148 | 2.85e-15 | cld17190 | NK superfamily | e17190 | Nucleoside/nucleotide kinase superfamily |
| non-specific | 2 | 137 | 4.48e-10 | TIGR00152 | TIGR00152 | e17190 | Dephospho-CoA kinase |
| non-specific | 2 | 148 | 2.85e-05 | PRK00081 | coaE | e17190 | Dephospho-CoA kinase |
| specific | 1 | 172 | 1.38e-34 | COG0237 | CoaE | e130785 | Dephospho-CoA kinase |
| superfamily | 1 | 172 | 1.38e-34 | pfam13521 | CoaE superfamily | e130785 | Dephospho-CoA kinase |
| specific | 1 | 170 | 1.51e-29 | pfam13521 | CoaE | e17190 | Dephospho-CoA kinase |
| superfamily | 1 | 170 | 1.51e-29 | cld17190 | NK superfamily | e17190 | Nucleoside/nucleotide kinase superfamily |
| non-specific | 2 | 137 | 2.64e-20 | TIGR00152 | TIGR00152 | e17190 | Dephospho-CoA kinase |
| non-specific | 2 | 136 | 6.79e-12 | PRK00081 | coaE | e17190 | Dephospho-CoA kinase |
| non-specific | 2 | 143 | 9.80e-06 | pfam1121 | COG1102 | e17190 | Dephospho-CoA kinase |
| non-specific | 2 | 143 | 3.27e-05 | pfam13521 | AAA_18 | e121455 | AAA domain |
| superfamily | 2 | 143 | 3.27e-05 | pfam13521 | P-loop_NTPase superfamily | e121455 | AAA domain |
| non-specific | 1 | 78 | 0.000167 | COG1936 | Fap7 | e17190 | Broad-specificity NMP kinase |
| non-specific | 2 | 27 | 0.0002 | cld02034 | CooC | e128886 | The accessory protein CooC, which contains a nucleotide-binding domain (P-loop) near the N-terminus, participates in the maturation of the nickel center of carbon monoxide dehydrogenase (CODH). |
| superfamily | 2 | 27 | 0.0002 | cld02034 | RioM superfamily | e128886 | The accessory protein CooC, which contains a nucleotide-binding domain (P-loop) near the N-terminus, participates in the maturation of the nickel center of carbon monoxide dehydrogenase (CODH). |
| non-specific | 2 | 140 | 0.000148 | PRK14733 | coaE | e17190 | Dephospho-CoA kinase |
| non-specific | 2 | 171 | 0.002499 | COG1100 | Gem1 | e127030 | GTPase SAR1 family domain [General function prediction only] |
| superfamily | 2 | 171 | 0.002499 | pfam13521 | Ras superfamily | e127030 | Ras family |
| non-specific | 3 | 157 | 0.002851 | TIGR01054 | rgy | e127598 | reverse gyrase |
| Query          | Hit type | ID region start | ID region end | E-Value | Accession | Short name | Superfamily | Definition                                                                 |
|---------------|----------|----------------|---------------|---------|-----------|------------|-------------|-----------------------------------------------------------------------------|
| superfamily   | 3        | 157            |               | 0.002851| c127598   | TOP1Bc superfamily | -           | Bacterial DNA topoisomerases I ATP-binding domain                           |
| non-specific  | 2        | 146            |               | 0.003434| COG1102   | CmkB       | c128332     | Cytidylate kinase                                                           |
| superfamily   | 2        | 146            |               | 0.003434| c128332   | CmkB superfamily | -           | Cytidylate kinase                                                           |
| non-specific  | 2        | 30             |               | 0.004023| COG3640   | CooC       | c127521     | CO dehydrogenase nickel-insertion accessory protein CooC1 [Posttranslational modification, protein turnover, chaperones] |
| superfamily   | 2        | 30             |               | 0.004023| c127521   | ChIa superfamily | -           | CooQ/CobB/MinD/ParA nucleotide binding domain                               |
| non-specific  | 2        | 27             |               | 0.005486| cd01983   | Fer4_NifH superfamily | c128886     | The Fer4_NifH superfamily                                                 |
| specific      | 2        | 168            | 2.03e-25      |         | c02022    | DPCK       | c117190     | Dephospho-CoA kinase                                                       |
| superfamily   | 2        | 168            | 2.03e-25      |         | c117190   | NK superfamily | -           | Nucleoside/nucleotide kinase superfamily                                  |
| non-specific  | 1        | 144            | 6.61e-20      |         | PRK00081  | c0aE       | c117190     | Dephospho-CoA kinase                                                       |
| non-specific  | 1        | 144            | 1.37e-19      |         | pfam01121 | CooE       | c117190     | Dephospho-CoA kinase                                                       |
| non-specific  | 1        | 144            | 7.97e-17      |         | COG0237   | CooE       | c130783     | Dephospho-CoA kinase                                                       |
| superfamily   | 1        | 144            | 7.97e-17      |         | e130785   | CooE superfamily | -           | Dephospho-CoA kinase                                                       |
| non-specific  | 2        | 150            | 1.78e-15      | TIGR00152| TIGR00152 | c117190     | Dephospho-CoA kinase                                                       |
| non-specific  | 2        | 145            | 1.48e-08      | PRK14730 | c0aE       | c117190     | Dephospho-CoA kinase                                                       |
| non-specific  | 2        | 166            | 8.52e-08      | PRK14731 | c0aE       | c117190     | Dephospho-CoA kinase                                                       |
| non-specific  | 3        | 141            | 2.13e-06      | PRK14733 | c0aE       | c117190     | Dephospho-CoA kinase                                                       |
| non-specific  | 3        | 93             | 2.83e-05      | PRK14734 | c0aE       | c117190     | Dephospho-CoA kinase                                                       |
| non-specific  | 2        | 163            | 0.008238      | PRK14732 | c0aE       | c117190     | Dephospho-CoA kinase                                                       |
| non-specific  | 1        | 150            | 0.005854      | TIGR02173| c0aE       | c128332     | Dephospho-CoA kinase                                                       |
| superfamily   | 1        | 150            | 0.005854      | c128332  | CmkB superfamily | -           | Cytidylate kinase                                                          |
| non-specific  | 1        | 56             | 0.008825      | COG1102  | CmkB      | c128332     | Cytidylate kinase                                                          |
| non-specific  | 2        | 94             | 0.003407      | PLN02422 | PLN02422  | c117190     | Dephospho-CoA kinase                                                       |
| non-specific  | 10       | 86             | 0.003775      | pfam13207| AAA_17     | c121455     | AAA domain                                                                |
| superfamily   | 10       | 86             | 0.003775      | c121455  | P-loop_NTPase superfamily | -           | P-loop containing Nucleoside Triphosphate Hydrolases                      |
| specific      | 2        | 141            | 0.005687      | c02023   | UMPK      | c117190     | Uridine monophosphate kinase                                               |
| superfamily   | 2        | 141            | 0.006565      | TIGR00235| udk       | c117190     | Uridine kinase superfamily                                                 |
| non-specific  | 1        | 137            | 5.63e-19      | COG0237  | c0aE       | c130785     | Dephospho-CoA kinase                                                       |
| specific      | 1        | 137            | 5.63e-19      | c130785  | CmkB superfamily | -           | Dephospho-CoA kinase                                                       |
| non-specific  | 1        | 137            | 2.29e-16      | c02022   | DPCK      | c117190     | Dephospho-CoA kinase                                                       |
| superfamily   | 1        | 137            | 2.29e-16      | c117190  | NK superfamily | -           | Nucleoside/nucleotide kinase superfamily                                  |
| non-specific  | 2        | 146            | 5.49e-13      | TIGR00152| TIGR00152 | c117190     | Dephospho-CoA kinase                                                       |
| non-specific  | 2        | 137            | 1.57e-09      | PRK00081 | c0aE       | c117190     | Dephospho-CoA kinase                                                       |
| non-specific  | 2        | 137            | 5.44e-05      | pfam01121| c0aE       | c117190     | Dephospho-CoA kinase                                                       |
| non-specific  | 2        | 51             | 0.002071      | TIGR03375| type_I_sec_LssB | c126602     | type I secretion system ATPase, LssB family                               |
| superfamily   | 2        | 51             | 0.002071      | c126602  | SunT superfamily | -           | ABC-type bacteriocin/antibiotic exporters, contain an N-terminal double-glycine peptidase domain [Defense mechanisms] |

**M. putrefaciens**

**M. putrefaciens**

**M. simbae**

**M. simbae**
| Query              | Hit type | ID region start | ID region end | E-Value | Accession | Short name | Superfamily | Definition                                                                 |
|--------------------|----------|----------------|---------------|---------|-----------|------------|-------------|-----------------------------------------------------------------------------|
| M. sturni          | non-specific | 1              | 17            | 0.007807 | COG0488   | Uup        | cl28181     | ATPase components of ABC transporters with duplicated ATPase domains [General function prediction only] |
|                    | superfamily | 1              | 17            | 0.007807 | cl28181   | AAA superfamily | - | ATPases associated with a variety of cellular activities |
|                     |           | 1              | 129           | 6.98e-09 | cd02022   | DPCK       | cl17190     | - |
|                     |           | 1              | 129           | 6.98e-09 | cl17190   | - | Nucleoside/nucleotide kinase superfamily |
| non-specific        | 2         | 110            | 5.18e-05      | 0.000306 | PRK00081  | coaE       | cl17190     | Dephospho-CoA kinase |
| non-specific        | 2         | 128            | 0.000306      | 0.000306 | TIGR00152 | TIGR00152  | cl17190     | Dephospho-CoA kinase |
| M. synoviae        | non-specific | 1              | 141           | 1.74e-12 | COG0237   | CoaE       | cl30785     | Dephospho-CoA kinase |
|                     | superfamily | 1              | 141           | 1.74e-12 | cl30785   | CoaE superfamily | - | Dephospho-CoA kinase |
|                     |           | 1              | 147           | 2.92e-11 | cd02022   | DPCK       | cl17190     | Dephospho-CoA kinase |
|                     | non-specific | 2              | 166           | 1.06e-06 | TIGR00152 | TIGR00152  | cl17190     | Dephospho-CoA kinase |
|                     |           | 1              | 76            | 0.006477 | pfam05272 | VirE       | cl23993     | Virulence-associated protein E (these proteins contain a P-loop motif) |
|                     | superfamily | 1              | 76            | 0.006477 | cl23993   | VirE superfamily | - | Virulence-associated protein E (these proteins contain a P-loop motif) |
| M. testudinis       | specific  | 2              | 175           | 2.12e-33 | cd02022   | DPCK       | cl17190     | Dephospho-CoA kinase |
|                     | superfamily | 2              | 175           | 2.12e-33 | cl17190   | NK superfamily | - | Nucleoside/nucleotide kinase superfamily |
|                     | non-specific | 5              | 188           | 4.62e-32 | PRK00081  | coaE       | cl17190     | Dephospho-CoA kinase |
|                     | specific  | 1              | 193           | 1.37e-31 | COG0237   | CoaE       | cl30785     | Dephospho-CoA kinase |
|                     | superfamily | 1              | 193           | 1.37e-31 | cl30785   | CoaE superfamily | - | Dephospho-CoA kinase |
|                     | non-specific | 2              | 143           | 9.59e-29 | TIGR00152 | TIGR00152  | cl17190     | Dephospho-CoA kinase |
|                     | non-specific | 1              | 89            | 3.48e-16 | pfam01121 | CoaE       | cl17190     | Dephospho-CoA kinase |
|                     | non-specific | 2              | 191           | 6.50e-13 | PRK14732  | coaE       | cl17190     | Dephospho-CoA kinase |
|                     | non-specific | 5              | 175           | 1.07e-11 | PLN02422  | coaE       | cl17190     | Dephospho-CoA kinase |
|                     | non-specific | 2              | 187           | 4.17e-11 | PRK14731  | coaE       | cl17190     | Dephospho-CoA kinase |
|                     | non-specific | 7              | 89            | 8.21e-08 | PRK14730  | coaE       | cl17190     | Dephospho-CoA kinase |
|                     | non-specific | 1              | 89            | 3.35e-06 | PRK03333  | coaE       | cl30785     | Dephospho-CoA kinase |
|                     | non-specific | 1              | 89            | 0.00045  | PRK14734  | coaE       | cl17190     | Dephospho-CoA kinase |
|                     | non-specific | 2              | 15            | 0.001737 | pfam00349 | uvrA       | cl26603     | excinuclease UvrABC ATPassubunit [Replication, recombination and repair] |
|                     | superfamily | 2              | 15            | 0.001737 | cl26603   | UvrA superfamily | - | excinuclease UvrABC ATPassubunit [Replication, recombination and repair] |
|                     | non-specific | 1              | 175           | 0.002035 | PTZ00451  | PTZ00451   | cl17190     | Dephospho-CoA kinase |
|                     | non-specific | 2              | 19            | 0.003434 | PRK05416  | PRK05416   | cl23728     | glmZ(sRNA)-inactivating NTPass |
|                     | superfamily | 2              | 19            | 0.003434 | cl23728   | ATP_bind_2 superfamily | - | P-loop ATPase protein family |
|                     | non-specific | 2              | 21            | 0.007101 | COG0178   | UvrA       | cl26603     | excinuclease UvrABC ATPassubunit [Replication, recombination and repair] |
|                     |              |                |               |          |           |            |             | |
| M. yeatsii          | specific  | 2              | 169           | 2.21e-25 | cd02022   | DPCK       | cl17190     | Dephospho-CoA kinase |
|                     | superfamily | 2              | 169           | 2.21e-25 | cl17190   | NK superfamily | - | Nucleoside/nucleotide kinase superfamily |
| Query                | Hit type         | ID region start | ID region end | E-Value | Accession | Short name | E-value | Accession | Short name | Superfamily | Definition                      |
|---------------------|------------------|----------------|---------------|---------|-----------|------------|---------|-----------|------------|-------------|---------------------------------|
| non-specific        | 1                | 145            | 145           | 5.32e-18| PRK00081  | coaE       | c17190  | Dephospho-CoA kinase |
| non-specific        | 1                | 99             | 112           | 6.31e-18| pfam01121 | CoaE       | c17190  | Dephospho-CoA kinase |
| superfamily         | 1                | 176            | 176           | 6.42e-17| COG0237   | CoaE superfamily | c130785 | Dephospho-CoA kinase |
| non-specific        | 2                | 163            | 165           | 9.11e-14| TIGR00152 | TIGR00152  | c17190  | Dephospho-CoA kinase |
| non-specific        | 3                | 93             | 93            | 1.16e-08| PRK14734  | coaE       | c17190  | Dephospho-CoA kinase |
| non-specific        | 2                | 99             | 99            | 3.34e-08| PRK14730  | coaE       | c17190  | Dephospho-CoA kinase |
| non-specific        | 2                | 98             | 98            | 2.12e-07| PLN02422  | PLN02422   | c17190  | Dephospho-CoA kinase |
| non-specific        | 3                | 143            | 143           | 4.58e-07| PRK14733  | coaE       | c17190  | Dephospho-CoA kinase |
| non-specific        | 2                | 183            | 183           | 3.61e-06| PRK14732  | coaE       | c17190  | Dephospho-CoA kinase |
| non-specific        | 3                | 77             | 77            | 0.004789| PRK03333  | coaE       | c130785 | Dephospho-CoA kinase |

**Supplementary Table 14 DPCK InterPro results**

| Mycoplasma species | Amino acid region | Database   | Database ID            | Database signature description                  | ID region start | ID region end | InterPro ID | ID type       | Gene Ontology (GO) term        |
|--------------------|-------------------|------------|------------------------|-------------------------------------------------|----------------|---------------|-------------|---------------|-----------------------------|
| *M. sp. Ms02*      | 192               | Gene3D     | G3DSA:3.40.50.300      |                                                 | 1              | 144           | F           | GO:0004140; GO:0005524; GO:0015937 |
|                    |                   | Pfam       | PF01121                | Dephospho-CoA kinase                            | 1              | 127           | IPR0001977  | F             | GO:0004140; GO:0005524; GO:0015937 |
|                    |                   | SUPERFAMILY| SSF52540               |                                                 | 2              | 106           | IPR027417   | H             | GO:0004140; GO:0005524; GO:0015937 |
| *M. agalactiae*    | 190               | Gene3D     | G3DSA:3.40.50.300      |                                                 | 1              | 163           |             |               |                             |
|                    |                   | Pfam       | PF01121                | Dephospho-CoA kinase                            | 1              | 140           | IPR0001977  | F             | GO:0004140; GO:0005524; GO:0015937 |
|                    |                   | SUPERFAMILY| SSF52540               |                                                 | 2              | 137           | IPR027417   | H             | GO:0004140; GO:0005524; GO:0015937 |
| *M. alligatoris*   | 185               | Gene3D     | G3DSA:3.40.50.300      |                                                 | 1              | 183           |             |               |                             |
|                    |                   | SUPERFAMILY| SSF52540               |                                                 | 2              | 139           | IPR027417   | H             | GO:0004140; GO:0005524; GO:0015937 |
| *M. alvi*          | 196               | Gene3D     | G3DSA:3.40.50.300      |                                                 | 1              | 196           |             |               |                             |
|                    |                   | PANTHER    | PTHR10695:SF35         |                                                 | 2              | 186           |             |               |                             |
| Mycoplasma species | Amino acid region | Database | Database ID | Database signature description | ID region start | ID region end | InterPro ID | ID type | Gene Ontology (GO) term |
|-------------------|-------------------|----------|-------------|-------------------------------|----------------|--------------|-------------|---------|------------------------|
| **M. anatis** | 190 | Gene3D | G3DSA:3.40.50.300 | 1 187 | | | | | |
| | | Pfam | PF01121 | Dephospho-CoA kinase | 1 141 | IPR001977 | F | GO:0004140; GO:0005524; GO:0015937 |
| | | SUPERFAMILY | SSF52540 | Dephospho-CoA kinase | 2 137 | IPR027417 | H | GO:0004140; GO:0005524; GO:0015937 |
| **M. arginini** | 168 | Gene3D | G3DSA:3.40.50.300 | 1 167 | | | | | |
| | | Pfam | PF01121 | Dephospho-CoA kinase | 2 140 | IPR001977 | F | GO:0004140; GO:0005524; GO:0015937 |
| | | SUPERFAMILY | SSF52540 | Dephospho-CoA kinase | 2 124 | IPR027417 | H | GO:0004140; GO:0005524; GO:0015937 |
| **M. bovigenitalium** | 190 | Gene3D | G3DSA:3.40.50.300 | 1 190 | | | | | |
| | | Pfam | PF01121 | Dephospho-CoA kinase | 2 137 | IPR001977 | F | GO:0004140; GO:0005524; GO:0015937 |
| | | SUPERFAMILY | SSF52540 | Dephospho-CoA kinase | 2 181 | IPR027417 | H | GO:0004140; GO:0005524; GO:0015937 |
| **M. bovis** | 190 | CDD | cd02022 | DPCK | 1 146 | IPR001977 | F | GO:0004140; GO:0005524; GO:0015937 |
| | | Gene3D | G3DSA:3.40.50.300 | 1 159 | | | | | |
| | | Pfam | PF01121 | Dephospho-CoA kinase | 2 137 | IPR001977 | F | GO:0004140; GO:0005524; GO:0015937 |
| | | SUPERFAMILY | SSF52540 | Dephospho-CoA kinase | 2 181 | IPR027417 | H | GO:0004140; GO:0005524; GO:0015937 |
| **M. bovoculi** (HAD-DPCK) | 444 | Coils | Coil | 398 418 | | | | | |
| | | Gene3D | G3DSA:3.40.50.1000 | 1 261 | IPR023214 | H | | | |
| | | Pfam | PF08282 | haloacid dehalogenase-like hydrolase | 7 254 | | | | |
| Mycoplasma species                     | Amino acid region | Database          | Database ID   | Database signature description                        | ID region start | ID region end | InterPro ID      | ID type | Gene Ontology (GO term)                     |
|---------------------------------------|-------------------|-------------------|---------------|------------------------------------------------------|----------------|---------------|------------------|---------|--------------------------------------------|
| **M. buteonis**                       | 189               | Pfam              | PF01121       | Dephospho-CoA kinase                                  | 266            | 399           | IPR001977        | F       | GO:0004140; GO:0005524; GO:0015937         |
|                                      |                   | SUPERFAMILY       | SSF52540      |                                                      | 264            | 420           | IPR027417        | H       |                                            |
|                                      |                   | SUPERFAMILY       | SSF56784      |                                                      | 1              | 262           | IPR036412        | H       |                                            |
|                                      |                   | TIGRFAM           | TIGR01484     | HAD-SF-IIB: HAD hydrolase, family IIB                 | 7              | 218           | IPR006379        | F       |                                            |
| **M. californicum**                   | 190               | Pfam              | PF01121       | Dephospho-CoA kinase                                  | 1              | 146           | IPR001977        | F       | GO:0004140; GO:0005524; GO:0015937         |
|                                      |                   | Gene3D            | G3DSA:3.40.50.300 |                                              | 1              | 185           |                 |         |                                            |
|                                      |                   | SUPERFAMILY       | SSF52540      |                                                      | 2              | 179           | IPR027417        | H       |                                            |
|                                      |                   | Gene3D            | G3DSA:3.40.50.300 |                                              | 15             | 188           |                 |         |                                            |
| **M. canis**                          | 189               | Pfam              | PF01121       | Dephospho-CoA kinase                                  | 1              | 146           | IPR001977        | F       | GO:0004140; GO:0005524; GO:0015937         |
|                                      |                   | Gene3D            | G3DSA:3.40.50.300 |                                              | 1              | 178           | IPR027417        | H       |                                            |
|                                      |                   | SUPERFAMILY       | SSF52540      |                                                      | 2              | 141           |                 |         |                                            |
|                                      |                   | CDD               | cd02022       | DPCK                                                 | 6              | 179           | IPR001977        | F       | GO:0004140; GO:0005524; GO:0015937         |
|                                      |                   | Gene3D            | G3DSA:3.40.50.300 |                                              | 2              | 183           |                 |         |                                            |
|                                      |                   | Hamap             | MF_00376      | Dephospho-CoA kinase [coaE].                          | 4              | 188           | IPR001977        | F       | GO:0004140; GO:0005524; GO:0015937         |
|                                      |                   | PANTHER           | PTHR10695     |                                                      | 5              | 174           |                 |         |                                            |
| **M. capricolum**                     | 188               | Pfam              | PF01121       | Dephospho-CoA kinase                                  | 5              | 174           | IPR001977        | F       | GO:0004140; GO:0005524; GO:0015937         |
|                                      |                   | ProSiteProfiles   | PS51219       | Dephospho-CoA kinase (DPCK) domain profile,          | 6              | 188           | IPR001977        | F       | GO:0004140; GO:0005524; GO:0015937         |
|                                      |                   | SUPERFAMILY       | SSF52540      |                                                      | 4              | 174           | IPR027417        | H       |                                            |
|                                      |                   | TIGRFAM           | TIGR000152    | TIGR000152: depsho-pho-Co-A kinase                   | 6              | 178           | IPR001977        | F       | GO:0004140; GO:0005524; GO:0015937         |
| **M. capricolum subsp. capripneumoniae** | 184              | CDD               | cd02022       | DPCK                                                 | 2              | 175           | IPR001977        | F       | GO:0004140; GO:0005524; GO:0015937         |
|                                      |                   | Gene3D            | G3DSA:3.40.50.300 |                                              | 1              | 179           |                 |         |                                            |
|                                      |                   | PANTHER           | PTHR10695     |                                                      | 2              | 170           |                 |         |                                            |
|                                      |                   | PANTHER           | PTHR10695     |                                                      | 2              | 170           |                 |         |                                            |
|                                      |                   | Pfam              | PF01121       | Dephospho-CoA kinase                                  | 1              | 170           | IPR001977        | F       | GO:0004140; GO:0005524; GO:0015937         |
| **M. capricolum subsp. capripneumoniae** | 184              | CDD               | cd02022       | DPCK                                                 | 2              | 175           | IPR001977        | F       | GO:0004140; GO:0005524; GO:0015937         |
| **Mycoplasma species** | **Amino acid region** | **Database** | **Database ID** | **Database signature description** | **ID region start** | **ID region end** | **InterPro ID** | **ID type** | **Gene Ontology (GO) term** |
|------------------------|----------------------|--------------|----------------|----------------------------------|---------------------|------------------|----------------|-----------|-----------------------------|
| **M. collis** | 182 | ProSiteProfiles | PS51219 | Dephospho-CoA kinase (DPCK) domain profile. | 2 | 184 | IPR001977 | F | GO:0004140; GO:0005524; GO:0015937 |
| | | SUPERFAMILY | SSF52540 | | 1 | 170 | IPR027417 | H | |
| | | TIGRFAM | TIGR00152 | TIGR00152: dephospho-CoA kinase | 2 | 174 | IPR001977 | F | GO:0004140; GO:0005524; GO:0015937 |
| | | CDD | cd02022 | DPCK | 1 | 148 | IPR001977 | F | GO:0004140; GO:0005524; GO:0015937 |
| | | Gene3D | G3DSA:3.40.50.300 | | 1 | 155 | | |
| | | PANTHER | PTHR10695 | | 2 | 131 | | |
| | | PANTHER | PTHR10695:SF26 | | 2 | 131 | | |
| | | Pfam | PF01121 | Dephospho-CoA kinase | 1 | 100 | IPR001977 | F | GO:0004140; GO:0005524; GO:0015937 |
| **M. collis** | 182 | ProSiteProfiles | PS51219 | Dephospho-CoA kinase (DPCK) domain profile. | 1 | 92 | IPR001977 | F | GO:0004140; GO:0005524; GO:0015937 |
| | | SUPERFAMILY | SSF52540 | | 2 | 136 | IPR027417 | H | |
| | | TIGRFAM | TIGR00152 | TIGR00152: dephospho-CoA kinase | 1 | 150 | IPR001977 | F | GO:0004140; GO:0005524; GO:0015937 |
| | | CDD | cd02022 | DPCK | 1 | 137 | IPR001977 | F | GO:0004140; GO:0005524; GO:0015937 |
| | | Gene3D | G3DSA:3.40.50.300 | | 1 | 183 | | |
| | | Pfam | PF01121 | Dephospho-CoA kinase | 2 | 138 | IPR001977 | F | GO:0004140; GO:0005524; GO:0015937 |
| | | SUPERFAMILY | SSF52540 | | 2 | 137 | IPR027417 | H | |
| | | TIGRFAM | TIGR00152 | TIGR00152: dephospho-CoA kinase | 1 | 144 | IPR001977 | F | GO:0004140; GO:0005524; GO:0015937 |
| **M. columbinum** | 190 | Gene3D | G3DSA:3.40.50.300 | | 1 | 183 | | |
| | | Pfam | PF01121 | Dephospho-CoA kinase | 2 | 138 | IPR001977 | F | GO:0004140; GO:0005524; GO:0015937 |
| | | SUPERFAMILY | SSF52540 | | 2 | 137 | IPR027417 | H | |
| | | TIGRFAM | TIGR00152 | TIGR00152: dephospho-CoA kinase | 1 | 144 | IPR001977 | F | GO:0004140; GO:0005524; GO:0015937 |
| **M. columborale** | 185 | Gene3D | G3DSA:3.40.50.300 | | 1 | 181 | | |
| | | Pfam | PF01121 | Dephospho-CoA kinase | 2 | 135 | IPR001977 | F | GO:0004140; GO:0005524; GO:0015937 |
| **M. conjunctivae** | 445 | Gene3D | G3DSA:3.40.50.1000 | | 1 | 266 | IPR023214 | H | |
| | | Gene3D | G3DSA:3.40.50.300 | | 267 | 439 | | |
| | | PANTHER | PTHR10000:SF47 | | 341 | 412 | | |
| | | PANTHER | PTHR10000:SF47 | | 341 | 412 | | |
| | | SUPERFAMILY | SSF52540 | | 1 | 105 | IPR027417 | H | |
| Mycoplasma species | Amino acid region | Database | Database ID | Database signature description | ID region start | ID region end | InterPro ID | ID type | Gene Ontology (GO) term |
|-------------------|------------------|----------|-------------|-------------------------------|----------------|-------------|-------------|---------|------------------------|
| PANTHER           |                  | PTHR10000 | PF008282    | haloacid dehalogenase-like hydrolase | 4              | 262         |             |         |                        |
| Pfam              |                  | PF01121   |             | Dephospho-CoA kinase           | 7              | 257         |             |         |                        |
| SUPERFAMILY       | SSF52540         | 266       | 401         | IPR001977                     | F              |             | GO:0004140; GO:0005524; GO:0015937 |
| M. cricetuli      | 191              |           |             |                               |                |             |             |         |                        |
| Pfam              | G3DSA:3.40.50.300| 1         | 186         |                               |                |             |             |         |                        |
| SUPERFAMILY       | SSF52540         | 2         | 149         | IPR027417                     | H              |             | GO:0004140; GO:0005524; GO:0015937 |
| M. crocodyli      | 190              |           |             |                               |                |             |             |         |                        |
| Pfam              | PF01121          | 1         | 157         | IPR001977                     | F              |             | GO:0004140; GO:0005524; GO:0015937 |
| M. crocodyli      | 190              | ProSiteProfiles | PS51219 | Dephospho-CoA kinase (DPCK) domain profile. | 1              | 190         | IPR001977   | F       | GO:0004140; GO:0005524; GO:0015937 |
| SUPERFAMILY       | SSF52540         | 2         | 149         | IPR027417                     | H              |             | GO:0004140; GO:0005524; GO:0015937 |
| M. dispar (HAD-DPCK) | 447             |           |             |                               |                |             |             |         |                        |
| Pfam              | G3DSA:3.40.50.1000| 2         | 267         | IPR023214                     | H              |             | GO:0004140; GO:0005524; GO:0015937 |
| Pfam              | PF01121          | 1         | 267         | IPR023214                     | H              |             | GO:0004140; GO:0005524; GO:0015937 |
| Pfam              | PF01121          | 269       | 399         | IPR001977                     | F              |             | GO:0004140; GO:0005524; GO:0015937 |
| SUPERFAMILY       | SSF52540         | 266       | 401         | IPR027417                     | H              |             | GO:0004140; GO:0005524; GO:0015937 |
| M. felifaucium    | 190              |           |             |                               |                |             |             |         |                        |
| Pfam              | G3DSA:3.40.50.300| 1         | 137         | IPR001977                     | F              |             | GO:0004140; GO:0005524; GO:0015937 |
| SUPERFAMILY       | SSF52540         | 2         | 180         | IPR027417                     | H              |             | GO:0004140; GO:0005524; GO:0015937 |
| M. felis          | 184              |           |             |                               |                |             |             |         |                        |
| Pfam              | PF01121          | 4         | 118         | IPR001977                     | F              |             | GO:0004140; GO:0005524; GO:0015937 |
| SUPERFAMILY       | SSF52540         | 1         | 133         | IPR027417                     | H              |             | GO:0004140; GO:0005524; GO:0015937 |
| M. fermentans     | 190              | CDD       | cd02022     | DPCK                          | 1              | 146         | IPR001977   | F       | GO:0004140; GO:0005524; GO:0015937 |
| Mycoplasma species | Amino acid region | Database | Database ID | Database signature description | ID region start | ID region end | InterPro ID | ID type | Gene Ontology (GO) term |
|--------------------|------------------|----------|-------------|--------------------------------|----------------|--------------|-------------|--------|------------------------|
|                    |                  | Gene3D   | G3DSA:3.40.50.300 |                                |                |              |             |        |                        |
|                    |                  | PANTHER  | PTHR10695 |                                |                |              |             |        |                        |
|                    |                  | PANTHER  | PTHR10695:SF26 |                                |                |              |             |        |                        |
|                    |                  | Pfam     | PF01121 | Dephospho-CoA kinase | 1 146 | IPR001977 | F | GO-0004140; GO-0005524; GO-0015937 |
|                    |                  | ProSiteProfiles | PS51219 | Dephospho-CoA kinase (DPCK) domain profile. | 1 190 | IPR001977 | F | GO-0004140; GO-0005524; GO-0015937 |
|                    |                  | SUPERFAMILY | SSF52540 |                                | 2 142 | IPR027417 | H | GO-0004140; GO-0005524; GO-0015937 |
| M. flocculare (HAD-DPCK) | 447 | Gene3D | G3DSA:3.40.50.1000 |                                | 2 251 | IPR023214 | H |                        |
|                    |                  | PANTHER  | PTHR10000 |                                | 1 264 |              |             |        |                        |
|                    |                  | PANTHER  | PTHR10000:SF47 |                                | 1 264 |              |             |        |                        |
|                    |                  | SUPERFAMILY | SSF56784 | haloacid dehalogenase-like hydrolase | 3 263 | IPR036412 | H |                        |
|                    |                  | SUPERFAMILY | SSF52540 |                                | 268 402 | IPR027417 | H |                        |
|                    |                  | TIGRFAM  | TIGR00152 | HADSF-IIB: HAD hydrolase, family IIB | 7 229 | IPR006379 | F |                        |
|                    |                  | Gene3D   | G3DSA:3.40.50.300 |                                | 1 175 |              |             |        |                        |
| M. gallinarum       | 189              | Pfam     | PF01121 | Dephospho-CoA kinase | 1 151 | IPR001977 | F | GO-0004140; GO-0005524; GO-0015937 |
|                    |                  | SUPERFAMILY | SSF52540 |                                | 2 141 | IPR027417 | H | GO-0004140; GO-0005524; GO-0015937 |
|                    |                  | Gene3D   | G3DSA:3.40.50.300 |                                | 1 199 |              |             |        |                        |
| M. gallisepticum    | 200              | Hamap    | MF_00376 | Dephospho-CoA kinase [coaE] | 7 197 | IPR001977 | F | GO-0004140; GO-0005524; GO-0015937 |
|                    |                  | PANTHER  | PTHR10695:SF26 |                                | 8 190 |              |             |        |                        |
|                    |                  | PANTHER  | PTHR10695 |                                | 8 190 |              |             |        |                        |
|                    |                  | Pfam     | PF01121 | Dephospho-CoA kinase | 9 90 | IPR001977 | F | GO-0004140; GO-0005524; GO-0015937 |
|                    |                  | ProSiteProfiles | PS51219 | Dephospho-CoA kinase (DPCK) domain profile. | 9 200 | IPR001977 | F | GO-0004140; GO-0005524; GO-0015937 |
|                    |                  | SignalP_GRAM_P OSITIVE | SignalP-TM |                                | 1 12 |              |             |        |                        |
|                    |                  | SUPERFAMILY | SSF52540 |                                | 8 195 | IPR027417 | H | GO-0004140; GO-0005524; GO-0015937 |
| Mycoplasma species | Amino acid region | Database | Database ID | Database signature description | ID region start | ID region end | InterPro ID | ID type | Gene Ontology (GO) term |
|-------------------|------------------|----------|------------|-------------------------------|----------------|-------------|-------------|---------|------------------------|
| M. genitalium     | 198              | TIGRFAM  | TIGR00152  | TIGR00152: dephospho-CoA kinase | 9              | 188         | IPR001977   | F       | GO:0004140; GO:0005524; GO:0015937 |
|                   |                  | CDD      | cd02022    | DPCK                          | 2              | 169         | IPR001977   | F       | GO:0004140; GO:0005524; GO:0015937 |
|                   |                  | Gene3D   | G3DSA:3.40.50.300 |                  | 1              | 189         |             |         |                        |
|                   |                  | Hamap    | MF_00376   | Dephospho-CoA kinase [coaE]   | 1              | 188         | IPR001977   | F       | GO:0004140; GO:0005524; GO:0015937 |
|                   |                  | PANTHER  | PTHR10695:SF26 |                  | 2              | 132         |             |         |                        |
|                   |                  | PANTHER  | PTHR10695  |                  | 2              | 132         |             |         |                        |
|                   |                  | Pfam     | PF01121    | Dephospho-CoA kinase          | 1              | 155         | IPR001977   | F       | GO:0004140; GO:0005524; GO:0015937 |
|                   |                  | ProSiteProfiles | PS51219 | Dephospho-CoA kinase (DPCK) domain profile. | 2              | 90          | IPR001977   | F       | GO:0004140; GO:0005524; GO:0015937 |
|                   |                  | SUPERFAMILY | SSF52540 |                  | 1              | 186         | IPR027417   | H       |                        |
|                   |                  | TIGRFAM  | TIGR00152  | TIGR00152: dephospho-CoA kinase | 2              | 180         | IPR001977   | F       | GO:0004140; GO:0005524; GO:0015937 |
| M. hyopneumoniae (HAD-DPCK) | 446 | Gene3D | G3DSA:3.40.50.300 |                  | 269            | 429         |             |         |                        |
|                   |                  | Gene3D   | G3DSA:3.40.50.1000 |                  | 1              | 249         | IPR023214   | H       |                        |
|                   |                  | PANTHER  | PTHR10000  |                  | 1              | 266         |             |         |                        |
|                   |                  | PANTHER  | PTHR10000:SF47 |                  | 341            | 354         |             |         |                        |
|                   |                  | Pfam     | PF08282    | haloacid dehalogenase-like hydrolase | 7              | 258         |             |         |                        |
|                   |                  | Pfam     | PF01121    | Dephospho-CoA kinase          | 270            | 428         | IPR001977   | F       | GO:0004140; GO:0005524; GO:0015937 |
|                   |                  | SUPERFAMILY | SSF56784 |                  | 2              | 263         | IPR036412   | H       |                        |
|                   |                  | SUPERFAMILY | SSF52540 |                  | 269            | 402         | IPR027417   | H       |                        |
|                   |                  | TIGRFAM  | TIGR01484  | HAD-SF-IIB: HAD hydrolase, family IIB | 7              | 227         | IPR006379   | F       |                        |
| M. hyorhinis      | 195              | Gene3D   | G3DSA:3.40.50.300 |                  | 1              | 184         |             |         |                        |
|                   |                  | Pfam     | PF01121    | Dephospho-CoA kinase          | 12             | 154         | IPR001977   | F       | GO:0004140; GO:0005524; GO:0015937 |
|                   |                  | SUPERFAMILY | SSF52540 |                  | 5              | 158         | IPR027417   | H       |                        |
| M. imitans        | 196              | CDD      | cd02022    | DPCK                          | 9              | 182         | IPR001977   | F       | GO:0004140; GO:0005524; GO:0015937 |
|                   |                  | Gene3D   | G3DSA:3.40.50.300 |                  | 1              | 196         |             |         |                        |
| Mycoplasma species | Amino acid region | Database | Database ID | Database signature description | ID region start | ID region end | InterPro ID | ID type | Gene Ontology (GO) term |
|--------------------|------------------|----------|-------------|-------------------------------|----------------|--------------|-------------|--------|------------------------|
| M. imitans         | 196              | PANTHER  | PTHR10695:SF26 |  | 7 | 190 |  |  |  |
|                    |                  | PANTHER  | PTHR10695 |  | 7 | 190 |  |  |  |
|                    |                  | Pfam     | PF01121 | Dephospho-CoA kinase | 9 | 100 | IPR001977 | F | GO:0004140; GO:0005524; GO:0015937 |
|                    |                  | Phobius  | SIGNAL_PEPTIDE_C_REGION | C-terminal region of a signal peptide. | 14 | 18 |  |  |  |
|                    |                  | Phobius  | SIGNAL_PEPTIDE | Signal peptide region | 1 | 18 |  |  |  |
|                    |                  | Phobius  | NON_CYTOPLASMIC_DOMAIN | Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region. | 19 | 196 |  |  |  |
|                    |                  | Phobius  | SIGNAL_PEPTIDE_N_REGION | N-terminal region of a signal peptide. | 1 | 7 |  |  |  |
|                    |                  | Phobius  | SIGNAL_PEPTIDE_H_REGION | Hydrophobic region of a signal peptide. | 8 | 13 |  |  |  |
|                    | 196              | ProSiteProfiles | PS51219 | Dephospho-CoA kinase (DPCK) domain profile. | 9 | 196 | IPR001977 | F | GO:0004140; GO:0005524; GO:0015937 |
|                    |                  | SUPERFAMILY | SSSF52540 |  | 8 | 194 | IPR027417 | H |  |
|                    |                  | TIGRFAM  | TIGR00152 | TIGR00152: dephospho-CoA kinase | 9 | 189 | IPR001977 | F | GO:0004140; GO:0005524; GO:0015937 |
|                    |                  | Gene3D   | G3DSA:3.40.50.300 |  | 1 | 187 |  |  |  |
|                    | 190              | Pfam     | PF01121 | Dephospho-CoA kinase | 2 | 140 | IPR001977 | F | GO:0004140; GO:0005524; GO:0015937 |
|                    |                  | SUPERFAMILY | SSSF52540 |  | 2 | 137 | IPR027417 | H |  |
|                    |                  | CDD      | cd02022 | DPCK | 11 | 189 | IPR001977 | F | GO:0004140; GO:0005524; GO:0015937 |
|                    |                  | Gene3D   | G3DSA:3.40.50.300 |  | 1 | 203 |  |  |  |
|                    |                  | Hamap    | MF_00376 | Dephospho-CoA kinase [coaE] | 9 | 200 | IPR001977 | F | GO:0004140; GO:0005524; GO:0015937 |
|                    |                  | PANTHER  | PTHR10695 |  | 11 | 199 |  |  |  |
|                    |                  | PANTHER  | PTHR10695:SF35 |  | 11 | 199 |  |  |  |
|                    |                  | Pfam     | PF01121 | Dephospho-CoA kinase | 11 | 189 | IPR001977 | F | GO:0004140; GO:0005524; GO:0015937 |
|                    |                  | ProSiteProfiles | PS51219 | Dephospho-CoA kinase (DPCK) domain profile. | 11 | 203 | IPR001977 | F | GO:0004140; GO:0005524; GO:0015937 |
|                    |                  | SUPERFAMILY | SSSF52540 |  | 8 | 200 | IPR027417 | H |  |
|                    |                  | TIGRFAM  | TIGR00152 | TIGR00152: dephospho-CoA kinase | 11 | 195 | IPR001977 | F | GO:0004140; GO:0005524; GO:0015937 |
| Mycoplasma species | Amino acid region | Database | Database ID | Database signature description | ID region start | ID region end | InterPro ID | ID type | Gene Ontology (GO) term |
|--------------------|-------------------|----------|-------------|--------------------------------|----------------|--------------|-------------|--------|------------------------|
| M. leachii         | 185               | CDD      | cd02022     | DPCK                           | 2              | 175          | IPR001977   | F      | GO:0004140; GO:0005524; GO:0015937 |
|                    |                   | Gene3D   | G3DSA:3.40.50.300 |                           |                | 1            | 181          |        |                        |
|                    |                   | PANTHER  | PTHR10695:SF26 |                               | 2              | 159          |             |        |                        |
|                    |                   | Pfam     | PF01121     | Dephospho-CoA kinase           | 1              | 163          | IPR001977   | F      | GO:0004140; GO:0005524; GO:0015937 |
|                    |                   | ProSiteProfiles | PS51219 | Dephospho-CoA kinase (DPCK) domain profile, | 2              | 185          | IPR001977   | F      | GO:0004140; GO:0005524; GO:0015937 |
|                    |                   | SUPERFAMILY | SSF52540 |                                | 1              | 159          | IPR027417   | H      | GO:0004140; GO:0005524; GO:0015937 |
| M. leachii         | 185               | TIGRFAM  | TIGR00152   | TIGR00152: dephospho-CoA kinase | 2              | 163          | IPR001977   | F      | GO:0004140; GO:0005524; GO:0015937 |
| M. leonicaptivi    | 187               | Gene3D   | G3DSA:3.40.50.300 |                           | 1              | 183          |             |        |                        |
|                    |                   | PANTHER  | PTHR10695:SF26 |                               | 2              | 120          |             |        |                        |
|                    |                   | Pfam     | PF01121     | Dephospho-CoA kinase           | 1              | 120          | IPR001977   | F      | GO:0004140; GO:0005524; GO:0015937 |
|                    |                   | SUPERFAMILY | SSF52540 |                                | 2              | 116          | IPR027417   | H      | GO:0004140; GO:0005524; GO:0015937 |
| M. lipofaciens     | 190               | Gene3D   | G3DSA:3.40.50.300 |                           | 1              | 190          |             |        |                        |
|                    |                   | Pfam     | PF01121     | Dephospho-CoA kinase           | 2              | 137          | IPR001977   | F      | GO:0004140; GO:0005524; GO:0015937 |
|                    |                   | SUPERFAMILY | SSF52540 |                                | 2              | 124          | IPR027417   | H      | GO:0004140; GO:0005524; GO:0015937 |
| M. mobile          | 187               | Gene3D   | G3DSA:3.40.50.300 |                           | 1              | 186          |             |        |                        |
|                    |                   | Pfam     | PF01121     | Dephospho-CoA kinase           | 1              | 156          | IPR001977   | F      | GO:0004140; GO:0005524; GO:0015937 |
|                    |                   | SUPERFAMILY | SSF52540 |                                | 2              | 180          | IPR027417   | H      | GO:0004140; GO:0005524; GO:0015937 |
| M. molare          | 182               | Gene3D   | G3DSA:3.40.50.300 |                           | 1              | 177          |             |        |                        |
|                    |                   | Pfam     | PF01121     | Dephospho-CoA kinase           | 1              | 135          | IPR001977   | F      | GO:0004140; GO:0005524; GO:0015937 |
|                    |                   | ProSiteProfiles | PS51219 | Dephospho-CoA kinase (DPCK) domain profile, | 1              | 182          | IPR001977   | F      | GO:0004140; GO:0005524; GO:0015937 |
|                    |                   | SUPERFAMILY | SSF52540 |                                | 2              | 137          | IPR027417   | H      | GO:0004140; GO:0005524; GO:0015937 |
|                    |                   | TIGRFAM  | TIGR00152   | TIGR00152: dephospho-CoA kinase | 1              | 153          | IPR001977   | F      | GO:0004140; GO:0005524; GO:0015937 |
| Mycoplasma species | Amino acid region | Database | Database ID | Database signature description | ID region start | ID region end | InterPro ID | ID type | Gene Ontology (GO) term |
|--------------------|-------------------|----------|-------------|--------------------------------|----------------|--------------|-------------|---------|------------------------|
| *M. mycoides* subsp. *capri* | 185 | CDD | cd02022 | DPCK | 2 | 175 | IPR001977 | F | GO:0004140; GO:0005524; GO:0015937 |
| Gene3D | G3DSA:3.40.50.300 | 1 | 179 |
| PANTHER | PTHR10695 | 2 | 170 |
| Pfam | PF01121 | Dephospho-CoA kinase | 1 | 170 | IPR001977 | F | GO:0004140; GO:0005524; GO:0015937 |
| ProSiteProfiles | PS51219 | Dephospho-CoA kinase (DPCK) domain profile, | 2 | 185 | IPR001977 | F | GO:0004140; GO:0005524; GO:0015937 |
| SUPERFAMILY | SSF52540 | 1 | 170 | IPR027417 |
| *M. mycoides* subsp. *mycoides* | 189 | CDD | cd02022 | DPCK | 6 | 179 | IPR001977 | F | GO:0004140; GO:0005524; GO:0015937 |
| Gene3D | G3DSA:3.40.50.300 | 2 | 185 |
| Hamap | MF_00376 | Dephospho-CoA kinase [coaE]. | 4 | 188 | IPR001977 | F | GO:0004140; GO:0005524; GO:0015937 |
| PANTHER | PTHR10695 | 5 | 163 |
| PANTHER | PTHR10695:SF26 | 5 | 163 |
| Pfam | PF01121 | Dephospho-CoA kinase | 5 | 167 | IPR001977 | F | GO:0004140; GO:0005524; GO:0015937 |
| ProSiteProfiles | PS51219 | Dephospho-CoA kinase (DPCK) domain profile, | 6 | 189 | IPR001977 | F | GO:0004140; GO:0005524; GO:0015937 |
| SUPERFAMILY | SSF52540 | 4 | 163 | IPR027417 | H |
| *M. opalescens* | 187 | Gene3D | G3DSA:3.40.50.300 | 1 | 180 |
| Pfam | PF01121 | Dephospho-CoA kinase | 1 | 132 | IPR001977 | F | GO:0004140; GO:0005524; GO:0015937 |
| SUPERFAMILY | SSF52540 | 2 | 137 | IPR027417 | H |
| *M. ovipneumoniae* (HAD-DPCK) | 447 | Gene3D | G3DSA:3.40.50.1000 | 2 | 267 | IPR023214 | H |
| Gene3D | G3DSA:3.40.50.300 | 268 | 431 |
| PANTHER | PTHR10000 | 2 | 264 |
| Pfam | PF08282 | haloacid dehalogenase-like hydrolase | 7 | 259 |
| Mycoplasma species | Amino acid region | Database | Database ID | Database signature description | ID region start | ID region end | InterPro ID | ID type | Gene Ontology (GO) term |
|--------------------|------------------|----------|-------------|-------------------------------|----------------|--------------|-------------|---------|------------------------|
| *M. penetrans*     | 206              | Pfam     | PF01121     | Dephospho-CoA kinase          | 269            | 369          | IPR001977   | F       | GO:0004140; GO:0005524; GO:0015937 |
|                   |                  | SUPERFAMILY | SSF56784   |                               | 2              | 263          | IPR036412   | H       |                         |
|                   |                  | SUPERFAMILY | SSF52540   |                               | 266            | 410          | IPR027417   | H       |                         |
|                   |                  | TIGRFAM  | TIGR01484   | HAD-SF-IIB: HAD hydrolase, family IIB | 6              | 229          | IPR006379   | F       |                         |
|                   |                  | CDD      | cfd02022    | DPCK                          | 14             | 143          | IPR001977   | F       | GO:0004140; GO:0005524; GO:0015937 |
|                   |                  | Gene3D   | G3DA:3.40.50.300 |                    | 3              | 153          |             |         |                         |
|                   |                  | Hamap    | MF_00376    | Dephospho-CoA kinase [coaE]   | 12             | 206          | IPR001977   | F       | GO:0004140; GO:0005524; GO:0015937 |
|                   |                  | PANTHER  | PTHR10695:SF35 |                              | 14             | 200          |             |         |                         |
|                   |                  | PANTHER  | PTHR10695   |                              | 14             | 200          |             |         |                         |
|                   |                  | Pfam     | PF01121     | Dephospho-CoA kinase          | 14             | 144          | IPR001977   | F       | GO:0004140; GO:0005524; GO:0015937 |
|                   |                  | ProSiteProfiles | PS51219 | Dephospho-CoA kinase (DPCK) domain profile. | 14             | 206          | IPR001977   | F       | GO:0004140; GO:0005524; GO:0015937 |
|                   |                  | SUPERFAMILY | SSF52540   |                             | 13             | 201          | IPR027417   | H       |                         |
|                   |                  | TIGRFAM  | TIGR00152   | TIGR00152: dephospho-CoA kinase | 14             | 193          | IPR001977   | F       | GO:0004140; GO:0005524; GO:0015937 |
|                   |                  | CDD      | cfd02022    | DPCK                          | 7              | 179          | IPR001977   | F       | GO:0004140; GO:0005524; GO:0015937 |
|                   |                  | Gene3D   | G3DA:3.40.50.300 |                    | 1              | 194          |             |         |                         |
|                   |                  | PANTHER  | PTHR10695:SF26 |                              | 5              | 192          |             |         |                         |
|                   |                  | PANTHER  | PTHR10695   |                              | 5              | 192          |             |         |                         |
| *M. pirum*        | 194              | Pfam     | PF01121     | Dephospho-CoA kinase          | 6              | 138          | IPR001977   | F       | GO:0004140; GO:0005524; GO:0015937 |
|                   |                  | ProSiteProfiles | PS51219 | Dephospho-CoA kinase (DPCK) domain profile. | 7              | 194          | IPR001977   | F       | GO:0004140; GO:0005524; GO:0015937 |
|                   |                  | SUPERFAMILY | SSF52540   |                             | 6              | 192          | IPR027417   | H       |                         |
|                   |                  | TIGRFAM  | TIGR00152   | TIGR00152: dephospho-CoA kinase | 7              | 185          | IPR001977   | F       | GO:0004140; GO:0005524; GO:0015937 |
| *M. pneumoniae*   | 200              | CDD      | cfd02022    | DPCK                          | 2              | 156          | IPR001977   | F       | GO:0004140; GO:0005524; GO:0015937 |
| Mycoplasma species | Amino acid region | Database | Database ID | Database signature description | ID region start | ID region end | InterPro ID | ID type | Gene Ontology (GO) term |
|-------------------|-------------------|----------|-------------|--------------------------------|----------------|--------------|-------------|--------|------------------------|
| **M. pneumoniae** | 200               | Gene3D   | G3DSA:3.40.30.300 | 1 199 | GO:0004140; GO:0005524; GO:0015937 |
|                   |                   | Hamap    | MF_00376 | Dephospho-CoA kinase [coaE]. | 1 188 | IPR001977 | F | GO:0003460; GO:0005524; GO:0015937 |
|                   |                   | PANTHER  | PTHR10695 | 2 156 |  |
|                   |                   | Pfam     | PF01121 | Dephospho-CoA kinase | 1 156 | IPR001977 | F | GO:0003460; GO:0005524; GO:0015937 |
|                   |                   | ProSiteProfiles | PS51219 | Dephospho-CoA kinase (DPCK) domain profile, | 2 200 | IPR001977 | F | GO:0003460; GO:0005524; GO:0015937 |
|                   |                   | SUPERFAMILY | SSF52540 | 1 186 | IPR027417 | H |  |
| **M. primatum**  | 190               | Gene3D   | G3DSA:3.40.30.300 | 1 188 | GO:0004140; GO:0005524; GO:0015937 |
|                   |                   | Pfam     | PF01121 | Dephospho-CoA kinase | 1 137 | IPR001977 | F | GO:0003460; GO:0005524; GO:0015937 |
|                   |                   | SUPERFAMILY | SSF52540 | 2 188 | IPR027417 | H |  |
| **M. pulmonis**  | 172               | CDD      | cd02022 | DPCK | 1 170 | IPR001977 | F | GO:0003460; GO:0005524; GO:0015937 |
|                   |                   | Gene3D   | G3DSA:3.40.30.300 | 1 171 |  |
|                   |                   | Pfam     | PF01121 | Dephospho-CoA kinase | 1 143 | IPR001977 | F | GO:0003460; GO:0005524; GO:0015937 |
|                   |                   | ProSiteProfiles | PS51219 | Dephospho-CoA kinase (DPCK) domain profile, | 1 172 | IPR001977 | F | GO:0003460; GO:0005524; GO:0015937 |
|                   |                   | SUPERFAMILY | SSF52540 | 2 137 | IPR027417 | H |  |
| **M. putrefaciens** | 186              | TIGRFAM  | TIGR00152 | TIGR00152: dephospho-CoA kinase | 1 143 | IPR001977 | F | GO:0003460; GO:0005524; GO:0015937 |
|                   |                   | CDD      | cd02022 | DPCK | 1 168 | IPR001977 | F | GO:0003460; GO:0005524; GO:0015937 |
|                   |                   | Gene3D   | G3DSA:3.40.30.300 | 1 185 |  |
|                   |                   | PANTHER  | PTHR10695 | 2 149 |  |
|                   |                   | Pfam     | PF01121 | Dephospho-CoA kinase | 1 158 | IPR001977 | F | GO:0003460; GO:0005524; GO:0015937 |
| **Mycoplasma species** | **Amino acid region** | **Database** | **Database ID** | **Database signature description** | **ID region start** | **ID region end** | **InterPro ID** | **ID type** | **Gene Ontology (GO) term** |
|------------------------|-----------------------|--------------|----------------|-----------------------------------|-------------------|-----------------|-----------------|-------------|----------------------------|
| **M. simbae** 187      | ProSiteProfiles       | PS51219      | Dephospho-CoA kinase (DPCK) domain profile. | 2                   | 186               | IPR001977       | F             | GO:0004140; GO:0005524; GO:0015937 |
|                       | SUPERFAMILY           | SSF52540     |                | 1                   | 161               | IPR027417       | H             |                           |
|                       | TIGRFAM               | TIGR00152    | TIGR00152: dephospho-CoA kinase | 2                   | 162               | IPR001977       | F             | GO:0004140; GO:0005524; GO:0015937 |
| **M. simbae** 187      | Gene3D                | G3DSA:3.40.50.300 | 1                   | 187               |                 |                 |               |                           |
|                       | Pfam                  | PF01121      | Dephospho-CoA kinase | 1                   | 144               | IPR001977       | F             | GO:0004140; GO:0005524; GO:0015937 |
|                       | SUPERFAMILY           | SSF52540     |                | 2                   | 157               | IPR027417       | H             |                           |
| **M. sturni** 187      | TIGRFAM               | TIGR00152    | TIGR00152: dephospho-CoA kinase | 1                   | 149               | IPR001977       | F             | GO:0004140; GO:0005524; GO:0015937 |
|                       | Gene3D                | G3DSA:3.40.50.300 | 1                   | 187               |                 |                 |               |                           |
|                       | SUPERFAMILY           | SSF52540     |                | 2                   | 117               | IPR027417       | H             |                           |
| **M. synoviae** 168    | Gene3D                | G3DSA:3.40.50.300 | 1                   | 161               |                 |                 |               |                           |
|                       | SUPERFAMILY           | SSF52540     |                | 2                   | 124               | IPR027417       | H             |                           |
| **M. testudinis** 205  | CDD                   | cdr02022     | DPCK           | 2                   | 175               | IPR001977       | F             | GO:0004140; GO:0005524; GO:0015937 |
|                       | Gene3D                | G3DSA:3.40.50.300 | 1                   | 198               |                 |                 |               |                           |
|                       | PANTHER               | PTHR10695:SF35 | 2                   | 185               |                 |                 |               |                           |
|                       | PANTHER               | PTHR10695    |                | 2                   | 185               |                 |               |                           |
|                       | Pfam                  | PF01121      | Dephospho-CoA kinase | 1                   | 151               | IPR001977       | F             | GO:0004140; GO:0005524; GO:0015937 |
|                       | ProSiteProfiles       | PS51219      | Dephospho-CoA kinase (DPCK) domain profile. | 2                   | 201               | IPR001977       | F             | GO:0004140; GO:0005524; GO:0015937 |
|                       | SUPERFAMILY           | SSF52540     |                | 1                   | 188               | IPR027417       | H             |                           |
|                       | TIGRFAM               | TIGR00152    | TIGR00152: dephospho-CoA kinase | 2                   | 173               | IPR001977       | F             | GO:0004140; GO:0005524; GO:0015937 |
| **M. yeatsii** 187     | CDD                   | cdr02022     | DPCK           | 2                   | 169               | IPR001977       | F             | GO:0004140; GO:0005524; GO:0015937 |
|                       | Gene3D                | G3DSA:3.40.50.300 | 1                   | 187               |                 |                 |               |                           |
|                       | PANTHER               | PTHR10695    |                | 2                   | 115               |                 |               |                           |
|                       | PANTHER               | PTHR10695:SF26 | 2                   | 115               |                 |                 |               |                           |
|                       | Pfam                  | PF01121      | Dephospho-CoA kinase | 1                   | 163               | IPR001977       | F             | GO:0004140; GO:0005524; GO:0015937 |
| Mycoplasma species | Amino acid region | Database | Database ID | Database signature description | ID region start | ID region end | InterPro ID | ID type | Gene Ontology (GO) term |
|------------------|-------------------|----------|-------------|--------------------------------|----------------|--------------|-------------|---------|------------------------|
| ProSiteProfiles   |                   | PS51219  |             | Dephospho-CoA kinase (DPCK) domain profile. | 2              | 187          | IPR001977   | F       |                        |
| SUPERFAMILY       |                   | SSF52540 |             |                                | 1              | 163          | IPR027417   | H       | GO:0004140; GO:0005524; GO:00115937 |
| TIGRFAM          |                   | TIGR00152|             | TIGR00152: dephospho-CoA kinase | 2              | 167          | IPR001977   | F       | GO:0004140; GO:0005524; GO:00115937 |

1ID type abbreviations – H, Homologous superfamily; F, Family
2InterPro ID – IPR001977: Dephospho-CoA kinase; IPR036412: HAD-like superfamily; IPR023214: HAD superfamily; IPR006379: HAD-superfamily hydrolase, subfamily IIB
3GO term (Biological Process) – GO:0015937: Coenzyme A biosynthetic process
GO term (Molecular Function) – GO:0004140: Dephospho-CoA kinase activity; GO:0005524: ATP binding

**Supplementary Table 15 DPCK MEME + motif locations**

| Mycoplasma species                  | p-value   | Motif 1 | Motif 2 | Motif 3 | Motif 4 |
|-------------------------------------|-----------|---------|---------|---------|---------|
| M. sp. Ms02                         | 5.40e-39  | 1-21    | 23-42   | 58-73   | 90-121  |
| M. agalactiae                       | 1.11e-57  | 1-21    | 23-43   | 58-73   | 90-121  |
| M. alligatoris                      | 1.89e-43  | 1-21    | 23-43   | 53-68   | 85-116  |
| M. alvi                             | 7.76e-20  | 2-22    | 23-43   | 58-73   |         |
| M. anatis                           | 6.14e-43  | 1-21    | 23-43   | 58-73   | 90-121  |
| M. arginini                         | 5.90e-52  | 1-21    | 23-43   | 57-72   | 89-120  |
| M. bovigenitalium                   | 6.45e-45  | 1-21    | 23-43   | 58-73   | 90-121  |
| M. bovis                            | 2.31e-56  | 1-21    | 23-43   | 58-73   | 90-121  |
| M. bovoculi*                        | 5.64e-47  | 1-21    | 23-43   | 58-73   | 90-121  |
| M. buteonis                         | 2.98e-37  | 1-21    | 23-43   | 58-73   | 90-121  |
| M. californicum                     | 1.59e-43  | 1-21    | 23-43   | 58-73   | 90-121  |
| M. canis                            | 4.50e-39  | 1-21    | 23-43   | 57-72   | 89-120  |
| M. capricolum subsp. capricolum     | 1.88e-24  | 1-21    | 23-43   | 58-73   | 90-121  |
| M. capricolum subsp. capripneumoniae| 5.67e-25  | 1-21    | 23-43   | 58-73   | 90-121  |
| M. collis                           | 1.28e-53  | 1-21    | 23-43   | 58-73   | 90-121  |
| M. columbinum                       | 4.89e-51  | 1-21    | 23-43   | 58-73   | 90-121  |
| Mycoplasma species          | p-value | Motif 1 | Motif 2 | Motif 3 | Motif 4 |
|----------------------------|---------|---------|---------|---------|---------|
| *M. columbiale*            | 2.88e-38| 1-21    | 23-43   | 57-72   | 89-120  |
| *M. conjunctivae*          | 4.10e-51| 266-286 | 288-308 | 322-337 | 354-385 |
| *M. cricetuli*             | 8.29e-41| 1-21    | 23-43   | 57-72   | 89-120  |
| *M. crocodyli*             | 3.68e-47| 1-21    | 23-43   | 58-73   | 90-121  |
| *M. dispar*                | 2.73e-58| 268-288 | 290-310 | 324-339 | 356-387 |
| *M. felixfaucaium*         | 5.30e-54| 1-21    | 23-43   | 58-73   | 90-121  |
| *M. felis*                 | 4.01e-40| 3-23    | 25-45   | 60-75   | 92-123  |
| *M. fermentans*            | 1.28e-41| 1-21    | 23-43   | 58-73   | 90-121  |
| *M. flocculare*            | 3.42e-55| 267-287 | 289-309 | 323-338 | 355-386 |
| *M. gallinarum*            | 1.59e-45| 1-21    | 22-42   | 57-72   | 89-120  |
| *M. gallisepticum*         | 1.35e-26| 9-29    | 31-51   | 66-81   | -       |
| *M. genitalium*            | 2.60e-29| 2-22    | 25-45   | 60-75   | -       |
| *M. hyopneumoniae*         | 3.07e-57| 267-287 | 289-309 | 323-338 | 355-386 |
| *M. hyorhinis*             | 4.62e-51| 7-27    | 36-56   | 70-85   | 102-133 |
| *M. imitans*               | 9.80e-25| 9-29    | 31-51   | 66-81   | -       |
| *M. iners*                 | 2.08e-53| 1-21    | 23-43   | 58-73   | 90-121  |
| *M. iowae*                 | 1.92e-23| 11-31   | 33-53   | 68-83   | -       |
| *M. leachii*               | 3.03e-24| 2-22    | 26-46   | 59-74   | -       |
| *M. leonvicaptivi*         | 9.92e-43| 1-21    | 23-43   | 58-73   | 90-121  |
| *M. lipofaciens*           | 3.21e-47| 1-21    | 23-43   | 58-73   | 90-121  |
| *M. mobile*                | 7.43e-34| 1-21    | 23-43   | 58-73   | -       |
| *M. molare*                | 1.02e-55| 1-21    | 23-43   | 58-73   | 90-121  |
| *M. mycoides subsp. capri* | 8.30e-22| 2-22    | 26-46   | 59-74   | -       |
| *M. mycoides subsp. mycoides* | 1.38e-24 | 6-26    | 30-50   | 63-78   | -       |
| *M. opalescens*            | 7.78e-42| 1-21    | 23-43   | 58-73   | 90-121  |
| *M. ovipneumoniae*         | 4.21e-49| 268-288 | 290-310 | 324-339 | 356-387 |
| *M. penetrans*             | 2.96e-30| 14-34   | 36-56   | 71-86   | -       |
| *M. piriurn*                | 4.84e-25| 7-27    | 28-48   | 63-78   | -       |
| *M. pneumoniae*            | 1.92e-27| 2-22    | 25-45   | 133-148 | -       |
| *M. primatum*              | 2.97e-51| 1-21    | 23-43   | 58-73   | 90-121  |
| *M. pulmonis*              | 8.18e-55| 1-21    | 23-43   | 58-73   | 90-121  |
| *M. putrefaciens*          | 5.29e-22| 2-22    | 26-46   | 60-75   | -       |
| *M. simbae*                | 2.38e-48| 1-21    | 23-43   | 58-73   | 90-121  |
| *M. sturni*                | 2.80e-43| 1-21    | 23-43   | 58-73   | 90-121  |
| Mycoplasma species   | p-value     | Motif 1 | Motif 2 | Motif 3 | Motif 4 |
|----------------------|-------------|---------|---------|---------|---------|
| M. synoviae          | 5.90e-52    | 1-21    | 23-43   | 57-72   | 89-120  |
| M. testudinis         | 5.80e-27    | 2-22    | 24-44   | 59-74   | -       |
| M. yeatsii           | 2.57e-21    | 2-22    | 26-46   | 60-75   | -       |

*HAD-DPCK proteins