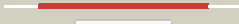



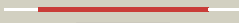



















# Phyre2

|               |                                 |
|---------------|---------------------------------|
| Email         | mdejesus@rockefeller.edu        |
| Description   | RVBD1611_(trpC)_1810247_1811065 |
| Date          | Fri Aug 2 13:30:20 BST 2019     |
| Unique Job ID | 3412228383bdfa4f                |

Detailed template information

| #  | Template                | Alignment Coverage  | 3D Model  | Confidence | % i.d. | Template Information   |
|----|-------------------------|---|---|------------|--------|--|
| 1  | <a href="#">c1piiA_</a> |  Alignment   |    | 100.0      | 35     | <b>PDB header:</b> bifunctional(isomerase and synthase)<br><b>Chain:</b> A: <b>PDB Molecule:</b> n-(5'phosphoribosyl)anthranilate isomerase;<br><b>PDBTitle:</b> three-dimensional structure of the bifunctional enzyme2 phosphoribosylanthranilate isomerase: indoleglycerolphosphate3 synthase from escherichia coli refined at 2.0 angstroms resolution |
| 2  | <a href="#">d1pia2</a>  |  Alignment   |    | 100.0      | 35     | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Ribulose-phosphate binding barrel<br><b>Family:</b> Tryptophan biosynthesis enzymes  |
| 3  | <a href="#">c3qjaA_</a> |  Alignment   |    | 100.0      | 97     | <b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> indole-3-glycerol phosphate synthase;<br><b>PDBTitle:</b> crystal structure of the mycobacterium tuberculosis indole-3-glycerol2 phosphate synthase (trpc) in apo form   |
| 4  | <a href="#">c6bmaA_</a> |  Alignment   |   | 100.0      | 37     | <b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> indole-3-glycerol phosphate synthase;<br><b>PDBTitle:</b> the crystal structure of indole-3-glycerol phosphate synthase from2 campylobacter jejuni subsp. jejuni nctc 11168  |
| 5  | <a href="#">c3tsmB_</a> |  Alignment |  | 100.0      | 39     | <b>PDB header:</b> lyase<br><b>Chain:</b> B: <b>PDB Molecule:</b> indole-3-glycerol phosphate synthase;<br><b>PDBTitle:</b> crystal structure of indole-3-glycerol phosphate synthase from2 brucella melitensis  |
| 6  | <a href="#">d1vc4a_</a> |  Alignment |  | 100.0      | 44     | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Ribulose-phosphate binding barrel<br><b>Family:</b> Tryptophan biosynthesis enzymes  |
| 7  | <a href="#">d1i4na_</a> |  Alignment |  | 100.0      | 29     | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Ribulose-phosphate binding barrel<br><b>Family:</b> Tryptophan biosynthesis enzymes  |
| 8  | <a href="#">d1a53a_</a> |  Alignment |  | 100.0      | 33     | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Ribulose-phosphate binding barrel<br><b>Family:</b> Tryptophan biosynthesis enzymes  |
| 9  | <a href="#">d1j5ta_</a> |  Alignment |  | 100.0      | 30     | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Ribulose-phosphate binding barrel<br><b>Family:</b> Tryptophan biosynthesis enzymes  |
| 10 | <a href="#">c2c3zA_</a> |  Alignment |  | 100.0      | 35     | <b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> indole-3-glycerol phosphate synthase;<br><b>PDBTitle:</b> crystal structure of a truncated variant of indole-3-2 glycerol phosphate synthase from sulfolobus solfataricus  |
| 11 | <a href="#">d1znn1</a>  |  Alignment |  | 100.0      | 23     | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Ribulose-phosphate binding barrel<br><b>Family:</b> PdxS-like  |

|    |                         |           |              |       |    |  |
|----|-------------------------|-----------|--------------|-------|----|--|
| 12 | <a href="#">c1znnF_</a> | Alignment |              | 100.0 | 23 | <b>PDB header:</b> biosynthetic protein<br><b>Chain:</b> F; <b>PDB Molecule:</b> plp synthase;<br><b>PDBTitle:</b> structure of the synthase subunit of plp synthase   |
| 13 | <a href="#">d1qopa_</a> | Alignment |              | 100.0 | 14 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Ribulose-phoshate binding barrel<br><b>Family:</b> Tryptophan biosynthesis enzymes   |
| 14 | <a href="#">c5tchG_</a> | Alignment |              | 100.0 | 21 | <b>PDB header:</b> lyase<br><b>Chain:</b> G; <b>PDB Molecule:</b> tryptophan synthase alpha chain;<br><b>PDBTitle:</b> crystal structure of tryptophan synthase from m. tuberculosis -2 ligand-free form, trpa-g66v mutant                                 |
| 15 | <a href="#">c3igsB_</a> | Alignment |              | 100.0 | 19 | <b>PDB header:</b> isomerase<br><b>Chain:</b> B; <b>PDB Molecule:</b> n-acetylmannosamine-6-phosphate 2-epimerase 2;<br><b>PDBTitle:</b> structure of the salmonella enterica n-acetylmannosamine-6-phosphate2 2-epimerase                                 |
| 16 | <a href="#">c3q58A_</a> | Alignment |              | 100.0 | 20 | <b>PDB header:</b> isomerase<br><b>Chain:</b> A; <b>PDB Molecule:</b> n-acetylmannosamine-6-phosphate 2-epimerase;<br><b>PDBTitle:</b> structure of n-acetylmannosamine-6-phosphate epimerase from salmonella2 enterica                                    |
| 17 | <a href="#">c5k9xA_</a> | Alignment |              | 100.0 | 15 | <b>PDB header:</b> lyase<br><b>Chain:</b> A; <b>PDB Molecule:</b> tryptophan synthase alpha chain;<br><b>PDBTitle:</b> crystal structure of tryptophan synthase alpha chain from legionella2 pneumophila subsp. pneumophila                                |
| 18 | <a href="#">c3vndD_</a> | Alignment |              | 100.0 | 15 | <b>PDB header:</b> lyase<br><b>Chain:</b> D; <b>PDB Molecule:</b> tryptophan synthase alpha chain;<br><b>PDBTitle:</b> crystal structure of tryptophan synthase alpha-subunit from the2 psychrophile shewanella frigidimarina k14-2                        |
| 19 | <a href="#">c5kzmA_</a> | Alignment |              | 100.0 | 14 | <b>PDB header:</b> lyase<br><b>Chain:</b> A; <b>PDB Molecule:</b> tryptophan synthase alpha chain;<br><b>PDBTitle:</b> crystal structure of tryptophan synthase alpha-beta chain complex from2 francisella tularensis                                      |
| 20 | <a href="#">c3navB_</a> | Alignment |              | 100.0 | 13 | <b>PDB header:</b> lyase<br><b>Chain:</b> B; <b>PDB Molecule:</b> tryptophan synthase alpha chain;<br><b>PDBTitle:</b> crystal structure of an alpha subunit of tryptophan synthase from2 vibrio cholerae o1 biovar el tor str. n16961                     |
| 21 | <a href="#">c2ekcA_</a> | Alignment | not modelled | 100.0 | 15 | <b>PDB header:</b> lyase<br><b>Chain:</b> A; <b>PDB Molecule:</b> tryptophan synthase alpha chain;<br><b>PDBTitle:</b> structural study of project id aq_1548 from aquifex aeolicus vf5  |
| 22 | <a href="#">d1ujpa_</a> | Alignment | not modelled | 100.0 | 15 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Ribulose-phoshate binding barrel<br><b>Family:</b> Tryptophan biosynthesis enzymes   |
| 23 | <a href="#">c5ey5A_</a> | Alignment | not modelled | 100.0 | 18 | <b>PDB header:</b> lyase<br><b>Chain:</b> A; <b>PDB Molecule:</b> lbcats-a;<br><b>PDBTitle:</b> lbcats   |
| 24 | <a href="#">c5kinC_</a> | Alignment | not modelled | 100.0 | 15 | <b>PDB header:</b> lyase<br><b>Chain:</b> C; <b>PDB Molecule:</b> tryptophan synthase alpha chain;<br><b>PDBTitle:</b> crystal structure of tryptophan synthase alpha beta complex from2 streptococcus pneumoniae  |
| 25 | <a href="#">c4x2rA_</a> | Alignment | not modelled | 100.0 | 23 | <b>PDB header:</b> isomerase<br><b>Chain:</b> A; <b>PDB Molecule:</b> 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)]<br><b>PDBTitle:</b> crystal structure of pria from actinomyces urogenitalis   |
| 26 | <a href="#">c2h6rG_</a> | Alignment | not modelled | 100.0 | 15 | <b>PDB header:</b> isomerase<br><b>Chain:</b> G; <b>PDB Molecule:</b> triosephosphate isomerase;<br><b>PDBTitle:</b> crystal structure of triosephosphate isomerase (tim) from2 methanocaldococcus jannaschii  |
| 27 | <a href="#">d1xya1</a>  | Alignment | not modelled | 100.0 | 18 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Ribulose-phoshate binding barrel<br><b>Family:</b> NanE-like   |
| 28 | <a href="#">c5zjnB_</a> | Alignment | not modelled | 100.0 | 17 | <b>PDB header:</b> isomerase<br><b>Chain:</b> B; <b>PDB Molecule:</b> putative n-acetylmannosamine-6-phosphate 2-epimerase;<br><b>PDBTitle:</b> structure of n-acetylmannosamine-6-phosphate-2-epimerase from vibrio2 cholerae with n-acetylmannosamine-6- |

|    |                         |           |              |       |   |
|----|-------------------------|-----------|--------------|-------|---|
|    |                         |           |              |       | phosphate   |
| 29 | <a href="#">d1w0ma_</a> | Alignment | not modelled | 100.0 | 22<br><b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Triosephosphate isomerase (TIM)<br><b>Family:</b> Triosephosphate isomerase (TIM)   |
| 30 | <a href="#">c5cssA</a>  | Alignment | not modelled | 100.0 | 22<br><b>PDB header:</b> isomerase<br><b>Chain:</b> A: <b>PDB Molecule:</b> triosephosphate isomerase;<br><b>PDBTitle:</b> crystal structure of triosephosphate isomerase from thermoplasma2 acidophilum with glycerol 3-phosphate  |
| 31 | <a href="#">d1rd5a_</a> | Alignment | not modelled | 100.0 | 16<br><b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Ribulose-phosphate binding barrel<br><b>Family:</b> Tryptophan biosynthesis enzymes   |
| 32 | <a href="#">c5zknA</a>  | Alignment | not modelled | 100.0 | 18<br><b>PDB header:</b> isomerase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative n-acetylmannosamine-6-phosphate 2-epimerase;<br><b>PDBTitle:</b> structure of n-acetylmannosamine-6-phosphate 2-epimerase from2 fusobacterium nucleatum                                      |
| 33 | <a href="#">c4utwB</a>  | Alignment | not modelled | 100.0 | 16<br><b>PDB header:</b> isomerase<br><b>Chain:</b> B: <b>PDB Molecule:</b> putative n-acetylmannosamine-6-phosphate 2-epimerase;<br><b>PDBTitle:</b> structural characterisation of nane, mannac6p c2 epimerase,2 from clostridium perfringens                                   |
| 34 | <a href="#">c4axkB</a>  | Alignment | not modelled | 100.0 | 21<br><b>PDB header:</b> isomerase<br><b>Chain:</b> B: <b>PDB Molecule:</b> 1-(5-phosphoribosyl)-5-[(5'-phosphoribosylamino)<br><b>PDBTitle:</b> crystal structure of subhisa from the thermophile corynebacterium2 efficiens   |
| 35 | <a href="#">d1rpxa_</a> | Alignment | not modelled | 99.9  | 18<br><b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Ribulose-phosphate binding barrel<br><b>Family:</b> D-ribulose-5-phosphate 3-epimerase  |
| 36 | <a href="#">d1h5ya_</a> | Alignment | not modelled | 99.9  | 26<br><b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Ribulose-phosphate binding barrel<br><b>Family:</b> Histidine biosynthesis enzymes  |
| 37 | <a href="#">d1geqa_</a> | Alignment | not modelled | 99.9  | 16<br><b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Ribulose-phosphate binding barrel<br><b>Family:</b> Tryptophan biosynthesis enzymes   |
| 38 | <a href="#">d1y0ea_</a> | Alignment | not modelled | 99.9  | 19<br><b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Ribulose-phosphate binding barrel<br><b>Family:</b> NanE-like   |
| 39 | <a href="#">c4qj1A</a>  | Alignment | not modelled | 99.9  | 18<br><b>PDB header:</b> isomerase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)<br><b>PDBTitle:</b> crystal structure of 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)2 methylideneamino] imidazole-4-carboxamide isomerase (hisa). |
| 40 | <a href="#">c5aheA</a>  | Alignment | not modelled | 99.9  | 20<br><b>PDB header:</b> isomerase<br><b>Chain:</b> A: <b>PDB Molecule:</b><br><b>PDBTitle:</b> crystal structure of salmonella enterica hisa   |
| 41 | <a href="#">d1ka9f_</a> | Alignment | not modelled | 99.9  | 25<br><b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Ribulose-phosphate binding barrel<br><b>Family:</b> Histidine biosynthesis enzymes  |
| 42 | <a href="#">c4wd0A</a>  | Alignment | not modelled | 99.9  | 18<br><b>PDB header:</b> isomerase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)<br><b>PDBTitle:</b> crystal structure of hisap form arthrobacter aurescens  |
| 43 | <a href="#">d1tqja_</a> | Alignment | not modelled | 99.9  | 17<br><b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Ribulose-phosphate binding barrel<br><b>Family:</b> D-ribulose-5-phosphate 3-epimerase  |
| 44 | <a href="#">d1thfd_</a> | Alignment | not modelled | 99.9  | 21<br><b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Ribulose-phosphate binding barrel<br><b>Family:</b> Histidine biosynthesis enzymes  |
| 45 | <a href="#">d1hg3a_</a> | Alignment | not modelled | 99.9  | 19<br><b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Triosephosphate isomerase (TIM)<br><b>Family:</b> Triosephosphate isomerase (TIM)   |
| 46 | <a href="#">c2y85D</a>  | Alignment | not modelled | 99.9  | 22<br><b>PDB header:</b> isomerase<br><b>Chain:</b> D: <b>PDB Molecule:</b> phosphoribosyl isomerase a;<br><b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis phosphoribosyl2 isomerase with bound rcdrp  |
| 47 | <a href="#">c3thaB</a>  | Alignment | not modelled | 99.9  | 16<br><b>PDB header:</b> lyase<br><b>Chain:</b> B: <b>PDB Molecule:</b> tryptophan synthase alpha chain;<br><b>PDBTitle:</b> tryptophan synthase subunit alpha from campylobacter jejuni.   |
| 48 | <a href="#">c3tdnB</a>  | Alignment | not modelled | 99.9  | 20<br><b>PDB header:</b> de novo protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> f1r symmetric alpha-beta tim barrel;<br><b>PDBTitle:</b> computationally designed two-fold symmetric tim-barrel protein, f1r  |
| 49 | <a href="#">c2v82A</a>  | Alignment | not modelled | 99.9  | 20<br><b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 2-dehydro-3-deoxy-6-phosphogalactonate aldolase;<br><b>PDBTitle:</b> kdpgal complexed to kdpgal   |
| 50 | <a href="#">d2flia1</a> | Alignment | not modelled | 99.9  | 21<br><b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Ribulose-phosphate binding barrel<br><b>Family:</b> D-ribulose-5-phosphate 3-epimerase  |
| 51 | <a href="#">c5umfB</a>  | Alignment | not modelled | 99.9  | 16<br><b>PDB header:</b> isomerase<br><b>Chain:</b> B: <b>PDB Molecule:</b> ribulose-phosphate 3-epimerase;<br><b>PDBTitle:</b> crystal structure of a ribulose-phosphate 3-epimerase from neisseria2 gonorrhoeae with bound phosphate  |
| 52 | <a href="#">d1vzwa1</a> | Alignment | not modelled | 99.9  | 21<br><b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Ribulose-phosphate binding barrel<br><b>Family:</b> Histidine biosynthesis enzymes  |
| 53 | <a href="#">c4e38A</a>  | Alignment | not modelled | 99.9  | 12<br><b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> keto-hydroxyglutarate-aldolase/keto-deoxy-phosphogluconate<br><b>PDBTitle:</b> crystal structure of probable keto-hydroxyglutarate-aldolase from2 vibionales bacterium swat-3 (target efi-502156)         |

|    |                         |           |              |      |    |  |
|----|-------------------------|-----------|--------------|------|----|--|
| 54 | <a href="#">d1h1ya_</a> | Alignment | not modelled | 99.9 | 16 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Ribulose-phosphate binding barrel<br><b>Family:</b> D-ribulose-5-phosphate 3-epimerase   |
| 55 | <a href="#">c6oviA_</a> | Alignment | not modelled | 99.9 | 18 | <b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> keto-deoxy-phosphogluconate aldolase;<br><b>PDBTitle:</b> crystal structure of kdpG aldolase from legionella pneumophila with 2 pyruvate captured at low pH as a covalent carbinolamine intermediate                           |
| 56 | <a href="#">c1jvnB_</a> | Alignment | not modelled | 99.9 | 21 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional histidine biosynthesis protein hishf;<br><b>PDBTitle:</b> crystal structure of imidazole glycerol phosphate synthase: a tunnel through a (beta/alpha) <sub>8</sub> barrel joins two active sites            |
| 57 | <a href="#">c3inpA_</a> | Alignment | not modelled | 99.9 | 14 | <b>PDB header:</b> isomerase<br><b>Chain:</b> A: <b>PDB Molecule:</b> d-ribulose-phosphate 3-epimerase;<br><b>PDBTitle:</b> 2.05 angstrom resolution crystal structure of d-ribulose-phosphate 3-2 epimerase from francisella tularensis.  |
| 58 | <a href="#">d1jvna1</a> | Alignment | not modelled | 99.9 | 22 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Ribulose-phosphate binding barrel<br><b>Family:</b> Histidine biosynthesis enzymes   |
| 59 | <a href="#">c3qc3B_</a> | Alignment | not modelled | 99.9 | 15 | <b>PDB header:</b> isomerase<br><b>Chain:</b> B: <b>PDB Molecule:</b> d-ribulose-5-phosphate-3-epimerase;<br><b>PDBTitle:</b> crystal structure of a d-ribulose-5-phosphate-3-epimerase (np_954699) <sub>2</sub> from homo sapiens at 2.20 a resolution  |
| 60 | <a href="#">c5n2pA_</a> | Alignment | not modelled | 99.9 | 13 | <b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> tryptophan synthase alpha chain;<br><b>PDBTitle:</b> sulfolobus solfataricus tryptophan synthase a   |
| 61 | <a href="#">d1tqxa_</a> | Alignment | not modelled | 99.9 | 11 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Ribulose-phosphate binding barrel<br><b>Family:</b> D-ribulose-5-phosphate 3-epimerase   |
| 62 | <a href="#">d1vhca_</a> | Alignment | not modelled | 99.9 | 15 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Aldolase<br><b>Family:</b> Class I aldolase  |
| 63 | <a href="#">d1wbha1</a> | Alignment | not modelled | 99.9 | 20 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Aldolase<br><b>Family:</b> Class I aldolase  |
| 64 | <a href="#">c2w6rA_</a> | Alignment | not modelled | 99.9 | 19 | <b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> imidazole glycerol phosphate synthase subunit<br><b>PDBTitle:</b> crystal structure of an artificial (ba) <sub>8</sub> -barrel protein <sub>2</sub> designed from identical half barrels                                       |
| 65 | <a href="#">c4nu7C_</a> | Alignment | not modelled | 99.9 | 16 | <b>PDB header:</b> isomerase<br><b>Chain:</b> C: <b>PDB Molecule:</b> ribulose-phosphate 3-epimerase;<br><b>PDBTitle:</b> 2.05 angstrom crystal structure of ribulose-phosphate 3-epimerase from <i>Toxoplasma gondii</i> .  |
| 66 | <a href="#">d2tpsa_</a> | Alignment | not modelled | 99.9 | 21 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Thiamin phosphate synthase<br><b>Family:</b> Thiamin phosphate synthase  |
| 67 | <a href="#">d1xcfa_</a> | Alignment | not modelled | 99.9 | 14 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Ribulose-phosphate binding barrel<br><b>Family:</b> Tryptophan biosynthesis enzymes  |
| 68 | <a href="#">d1wa3a1</a> | Alignment | not modelled | 99.9 | 18 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Aldolase<br><b>Family:</b> Class I aldolase  |
| 69 | <a href="#">c4qccA_</a> | Alignment | not modelled | 99.8 | 21 | <b>PDB header:</b> structural protein, lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 2-dehydro-3-deoxy-6-phosphogalactonate aldolase, peptidyl-<br><b>PDBTitle:</b> structure of a cube-shaped, highly porous protein cage designed by <sub>2</sub> fusing symmetric oligomeric domains         |
| 70 | <a href="#">d1qo2a_</a> | Alignment | not modelled | 99.8 | 18 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Ribulose-phosphate binding barrel<br><b>Family:</b> Histidine biosynthesis enzymes   |
| 71 | <a href="#">c4bk9B_</a> | Alignment | not modelled | 99.8 | 17 | <b>PDB header:</b> lyase<br><b>Chain:</b> B: <b>PDB Molecule:</b> 2-dehydro-3-deoxyphosphogluconate aldolase/4-hydroxy-2-oxo<br><b>PDBTitle:</b> crystal structure of 2-keto-3-deoxy-6-phospho-gluconate aldolase from <i>Zymomonas mobilis</i> atcc 29191                                       |
| 72 | <a href="#">c5b69A_</a> | Alignment | not modelled | 99.8 | 16 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> geranylgeranyl glyceryl phosphate synthase;<br><b>PDBTitle:</b> crystal structure of geranylgeranyl glyceryl phosphate synthase <sub>2</sub> complexed with an g-1-p from thermoplasma acidophilum                       |
| 73 | <a href="#">d1xi3a_</a> | Alignment | not modelled | 99.8 | 17 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Thiamin phosphate synthase<br><b>Family:</b> Thiamin phosphate synthase  |
| 74 | <a href="#">c4ml9A_</a> | Alignment | not modelled | 99.8 | 15 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein;<br><b>PDBTitle:</b> crystal structure of uncharacterized tim barrel protein with the <sub>2</sub> conserved phosphate binding site from <i>Seibaldella termitidis</i> |
| 75 | <a href="#">d1mxsa_</a> | Alignment | not modelled | 99.8 | 17 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Aldolase<br><b>Family:</b> Class I aldolase  |
| 76 | <a href="#">c6nkeA_</a> | Alignment | not modelled | 99.8 | 18 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> geranylgeranyl glyceryl phosphate synthase;<br><b>PDBTitle:</b> wild-type gggps from thermoplasma volcanium  |
| 77 | <a href="#">c4jeiA_</a> | Alignment | not modelled | 99.8 | 11 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> geranylgeranyl glyceryl phosphate synthase;<br><b>PDBTitle:</b> gggps from flavobacterium johnsoniae   |
| 78 | <a href="#">c3o63B_</a> | Alignment | not modelled | 99.8 | 23 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> probable thiamine-phosphate pyrophosphorylase;<br><b>PDBTitle:</b> crystal structure of thiamin phosphate synthase from  |

|     |                         |           |              |      |    |   |
|-----|-------------------------|-----------|--------------|------|----|---|
|     |                         |           |              |      |    | mycobacterium2 tuberculosis   |
| 79  | <a href="#">c4n6eA_</a> | Alignment | not modelled | 99.8 | 17 | <b>PDB header:</b> lyase/biosynthetic protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative thiosugar synthase;<br><b>PDBTitle:</b> crystal structure of amycolatopsis orientalis bexx/cyso complex   |
| 80  | <a href="#">c3ct7E_</a> | Alignment | not modelled | 99.8 | 16 | <b>PDB header:</b> isomerase<br><b>Chain:</b> E: <b>PDB Molecule:</b> d-allulose-6-phosphate 3-epimerase;<br><b>PDBTitle:</b> crystal structure of d-allulose 6-phosphate 3-epimerase2 from escherichia coli k-12   |
| 81  | <a href="#">c1yadD_</a> | Alignment | not modelled | 99.7 | 16 | <b>PDB header:</b> transcription<br><b>Chain:</b> D: <b>PDB Molecule:</b> regulatory protein teni;<br><b>PDBTitle:</b> structure of teni from bacillus subtilis   |
| 82  | <a href="#">c2agkA_</a> | Alignment | not modelled | 99.7 | 13 | <b>PDB header:</b> isomerase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)<br><b>PDBTitle:</b> structure of s. cerevisiae his6 protein   |
| 83  | <a href="#">c3vkbA_</a> | Alignment | not modelled | 99.7 | 23 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> moeo5;<br><b>PDBTitle:</b> crystal structure of moeo5 soaked with fspp overnight  |
| 84  | <a href="#">c4adsF_</a> | Alignment | not modelled | 99.7 | 23 | <b>PDB header:</b> transferase/transferase<br><b>Chain:</b> F: <b>PDB Molecule:</b> pyridoxine biosynthetic enzyme pdx1 homologue, putative;<br><b>PDBTitle:</b> crystal structure of plasmodial plp synthase complex   |
| 85  | <a href="#">c2zbtB_</a> | Alignment | not modelled | 99.7 | 23 | <b>PDB header:</b> lyase<br><b>Chain:</b> B: <b>PDB Molecule:</b> pyridoxal biosynthesis lyase pdxs;<br><b>PDBTitle:</b> crystal structure of pyridoxine biosynthesis protein from thermus2 thermophilus hb8  |
| 86  | <a href="#">c5z9yB_</a> | Alignment | not modelled | 99.7 | 19 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> thiazole synthase;<br><b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis thiazole synthase2 (thig) complexed with dxp   |
| 87  | <a href="#">d1viza_</a> | Alignment | not modelled | 99.7 | 11 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> FMN-linked oxidoreductases<br><b>Family:</b> FMN-linked oxidoreductases   |
| 88  | <a href="#">c3labA_</a> | Alignment | not modelled | 99.7 | 16 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative kdpg (2-keto-3-deoxy-6-phosphogluconate) aldolase;<br><b>PDBTitle:</b> crystal structure of a putative kdpg (2-keto-3-deoxy-6-2 phosphogluconate) aldolase from oleispira antarctica |
| 89  | <a href="#">c3femB_</a> | Alignment | not modelled | 99.7 | 23 | <b>PDB header:</b> biosynthetic protein, transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> pyridoxine biosynthesis protein snz1;<br><b>PDBTitle:</b> structure of the synthase subunit pdx1.1 (snz1) of plp synthase from2 saccharomyces cerevisiae  |
| 90  | <a href="#">c3f4wA_</a> | Alignment | not modelled | 99.7 | 14 | <b>PDB header:</b> synthase, lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative hexulose 6 phosphate synthase;<br><b>PDBTitle:</b> the 1.65a crystal structure of 3-hexulose-6-phosphate2 synthase from salmonella typhimurium   |
| 91  | <a href="#">c2nv2U_</a> | Alignment | not modelled | 99.7 | 24 | <b>PDB header:</b> lyase/transferase<br><b>Chain:</b> U: <b>PDB Molecule:</b> pyridoxal biosynthesis lyase pdxs;<br><b>PDBTitle:</b> structure of the plp synthase complex pdx1/2 (yaad/e) from bacillus2 subtilis  |
| 92  | <a href="#">c2yzzB_</a> | Alignment | not modelled | 99.7 | 23 | <b>PDB header:</b> lyase<br><b>Chain:</b> B: <b>PDB Molecule:</b> pyridoxal biosynthesis lyase pdxs;<br><b>PDBTitle:</b> crystal structure of pyridoxine biosynthesis protein from2 methanocaldococcus jannaschii   |
| 93  | <a href="#">c4firB_</a> | Alignment | not modelled | 99.7 | 23 | <b>PDB header:</b> lyase<br><b>Chain:</b> B: <b>PDB Molecule:</b> pyridoxal biosynthesis lyase pdxs;<br><b>PDBTitle:</b> crystal structure of pyridoxal biosynthesis lyase pdxs from pyrococcus   |
| 94  | <a href="#">c2htmB_</a> | Alignment | not modelled | 99.7 | 18 | <b>PDB header:</b> biosynthetic protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> thiazole biosynthesis protein thig;<br><b>PDBTitle:</b> crystal structure of ttha0676 from thermus thermophilus hb8  |
| 95  | <a href="#">c3nm3D_</a> | Alignment | not modelled | 99.7 | 13 | <b>PDB header:</b> transferase<br><b>Chain:</b> D: <b>PDB Molecule:</b> thiamine biosynthetic bifunctional enzyme;<br><b>PDBTitle:</b> the crystal structure of candida glabrata th16, a bifunctional enzyme2 involved in thiamin biosynthesis of eukaryotes                                    |
| 96  | <a href="#">d1q6oa_</a> | Alignment | not modelled | 99.7 | 12 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Ribulose-phosphate binding barrel<br><b>Family:</b> Decarboxylase   |
| 97  | <a href="#">c6hyeF_</a> | Alignment | not modelled | 99.6 | 25 | <b>PDB header:</b> plant protein<br><b>Chain:</b> F: <b>PDB Molecule:</b> pyridoxal 5'-phosphate synthase subunit pdx1.3;<br><b>PDBTitle:</b> pdx1.2/pdx1.3 complex (pdx1.3:k97a)   |
| 98  | <a href="#">c3ajxA_</a> | Alignment | not modelled | 99.6 | 20 | <b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 3-hexulose-6-phosphate synthase;<br><b>PDBTitle:</b> crystal structure of 3-hexulose-6-phosphate synthase   |
| 99  | <a href="#">c6hxgE_</a> | Alignment | not modelled | 99.6 | 25 | <b>PDB header:</b> plant protein<br><b>Chain:</b> E: <b>PDB Molecule:</b> pyridoxal 5'-phosphate synthase-like subunit pdx1.2;<br><b>PDBTitle:</b> pdx1.2/pdx1.3 complex (intermediate)   |
| 100 | <a href="#">c4naeA_</a> | Alignment | not modelled | 99.6 | 13 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> heptaprenylglyceryl phosphate synthase;<br><b>PDBTitle:</b> pcrb from geobacillus kaustophilus, with bound g1p  |
| 101 | <a href="#">c1zfiA_</a> | Alignment | not modelled | 99.6 | 19 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> inosine monophosphate dehydrogenase;<br><b>PDBTitle:</b> inosine monophosphate dehydrogenase (impdh; ec 1.1.1.205) from2 streptococcus pyogenes  |
| 102 | <a href="#">c2yw3E_</a> | Alignment | not modelled | 99.6 | 22 | <b>PDB header:</b> lyase<br><b>Chain:</b> E: <b>PDB Molecule:</b> 4-hydroxy-2-oxoglutarate aldolase/2-dehydro-3-<br><b>PDBTitle:</b> crystal structure analysis of the 4-hydroxy-2-oxoglutarate aldolase/2-2 dehydro-3-deoxyphosphogluconate aldolase from thb1                                 |
| 103 | <a href="#">d1xm3a_</a> | Alignment | not modelled | 99.6 | 17 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> ThiG-like<br><b>Family:</b> ThiG-like   |
|     |                         |           |              |      |    | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> inosine-5'-monophosphate   |

|     |                         |           |              |      |    |  |
|-----|-------------------------|-----------|--------------|------|----|--|
| 104 | <a href="#">c4z87B_</a> | Alignment | not modelled | 99.6 | 14 | dehydrogenase;<br><b>PDBTitle:</b> structure of the imp dehydrogenase from ashbya gossypii bound to gdp  |
| 105 | <a href="#">c4dqwb_</a> | Alignment | not modelled | 99.6 | 19 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> inosine-5'-monophosphate dehydrogenase;<br><b>PDBTitle:</b> crystal structure analysis of pa3770  |
| 106 | <a href="#">d1wv2a_</a> | Alignment | not modelled | 99.6 | 15 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> ThiG-like<br><b>Family:</b> ThiG-like  |
| 107 | <a href="#">c2z6jB_</a> | Alignment | not modelled | 99.6 | 17 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> trans-2-enoyl-acyl reductase ii;<br><b>PDBTitle:</b> crystal structure of s. pneumoniae enoyl-acyl carrier2 protein reductase (fabk) in complex with an inhibitor             |
| 108 | <a href="#">c3khjE_</a> | Alignment | not modelled | 99.5 | 20 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> E: <b>PDB Molecule:</b> inosine-5-monophosphate dehydrogenase;<br><b>PDBTitle:</b> c. parvum inosine monophosphate dehydrogenase bound by inhibitor c64   |
| 109 | <a href="#">c3tsdA_</a> | Alignment | not modelled | 99.5 | 19 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> inosine-5'-monophosphate dehydrogenase;<br><b>PDBTitle:</b> crystal structure of inosine-5'-monophosphate dehydrogenase from2 bacillus anthracis str. ames complexed with xmp |
| 110 | <a href="#">c3ffsc_</a> | Alignment | not modelled | 99.5 | 22 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> C: <b>PDB Molecule:</b> inosine-5-monophosphate dehydrogenase;<br><b>PDBTitle:</b> the crystal structure of cryptosporidium parvum inosine-5'-2 monophosphate dehydrogenase                           |
| 111 | <a href="#">c4iqjB_</a> | Alignment | not modelled | 99.5 | 15 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> enoyl-(acyl-carrier-protein) reductase ii;<br><b>PDBTitle:</b> crystal structure of porphyromonas gingivalis enoyl-acyl reductase ii2 (fabk) with cofactors nadph and fmn     |
| 112 | <a href="#">c4fxsA_</a> | Alignment | not modelled | 99.5 | 15 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> inosine-5'-monophosphate dehydrogenase;<br><b>PDBTitle:</b> inosine 5'-monophosphate dehydrogenase from vibrio cholerae complexed2 with imp and mycophenolic acid             |
| 113 | <a href="#">c5x8oA_</a> | Alignment | not modelled | 99.5 | 20 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> inosine-5'-monophosphate dehydrogenase;<br><b>PDBTitle:</b> crystal structure of gmp reductase from trypanosoma brucei with2 guanosine 5'-triphosphate                        |
| 114 | <a href="#">d1ojxa_</a> | Alignment | not modelled | 99.5 | 19 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Aldolase<br><b>Family:</b> Class I aldolase  |
| 115 | <a href="#">c3w01A_</a> | Alignment | not modelled | 99.5 | 11 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> heptaprenylglyceryl phosphate synthase;<br><b>PDBTitle:</b> crystal structure of pcrb complexed with peg from staphylococcus2 aureus subsp. aureus mu3                           |
| 116 | <a href="#">c3bo9B_</a> | Alignment | not modelled | 99.5 | 15 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> putative nitroalkan dioxygenase;<br><b>PDBTitle:</b> crystal structure of putative nitroalkan dioxygenase (tm0800) from2 thermotoga maritima at 2.71 a resolution             |
| 117 | <a href="#">d2f6ua1</a> | Alignment | not modelled | 99.5 | 9  | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> FMN-linked oxidoreductases<br><b>Family:</b> FMN-linked oxidoreductases  |
| 118 | <a href="#">c2gjlA_</a> | Alignment | not modelled | 99.5 | 16 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein pa1024;<br><b>PDBTitle:</b> crystal structure of 2-nitropropane dioxygenase  |
| 119 | <a href="#">c3exsB_</a> | Alignment | not modelled | 99.5 | 13 | <b>PDB header:</b> lyase<br><b>Chain:</b> B: <b>PDB Molecule:</b> rrmpd (hexulose-6-phosphate synthase);<br><b>PDBTitle:</b> crystal structure of kgpdc from streptococcus mutans in2 complex with d-r5p   |
| 120 | <a href="#">c2qjhH_</a> | Alignment | not modelled | 99.4 | 19 | <b>PDB header:</b> lyase<br><b>Chain:</b> H: <b>PDB Molecule:</b> putative aldolase mj0400;<br><b>PDBTitle:</b> m. jannaschii adh synthase covalently bound to2 dihydroxyacetone phosphate   |