



















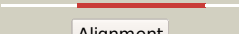



# Phyre2

|               |                                 |
|---------------|---------------------------------|
| Email         | mdejesus@rockefeller.edu        |
| Description   | RVBD2964_(purU)_3316539_3317471 |
| Date          | Thu Aug 8 16:20:12 BST 2019     |
| Unique Job ID | 1aa288ec1dbea846                |

Detailed template information

| #  | Template                | Alignment Coverage   | 3D Model  | Confidence | % i.d. | Template Information  |
|----|-------------------------|--|---|------------|--------|---|
| 1  | <a href="#">c3w7bB_</a> | <br>Alignment   |    | 100.0      | 58     | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> formyltetrahydrofolate deformylase;<br><b>PDBTitle:</b> crystal structure of formyltetrahydrofolate deformylase from thermus2 thermophilus hb8  |
| 2  | <a href="#">c3o1lB_</a> | <br>Alignment   |    | 100.0      | 45     | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> formyltetrahydrofolate deformylase;<br><b>PDBTitle:</b> crystal structure of a formyltetrahydrofolate deformylase (pspto_4314)2 from pseudomonas syringae pv. tomato str. dc3000 at 2.20 a resolution |
| 3  | <a href="#">c3obiC_</a> | <br>Alignment   |    | 100.0      | 45     | <b>PDB header:</b> hydrolase<br><b>Chain:</b> C: <b>PDB Molecule:</b> formyltetrahydrofolate deformylase;<br><b>PDBTitle:</b> crystal structure of a formyltetrahydrofolate deformylase (np_949368)2 from rhodopseudomonas palustris cga009 at 1.95 a resolution            |
| 4  | <a href="#">c3louB_</a> | <br>Alignment   |    | 100.0      | 43     | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> formyltetrahydrofolate deformylase;<br><b>PDBTitle:</b> crystal structure of formyltetrahydrofolate deformylase (yp_105254.1)2 from burkholderia mallei atcc 23344 at 1.90 a resolution               |
| 5  | <a href="#">c3n0vD_</a> | <br>Alignment |  | 100.0      | 36     | <b>PDB header:</b> hydrolase<br><b>Chain:</b> D: <b>PDB Molecule:</b> formyltetrahydrofolate deformylase;<br><b>PDBTitle:</b> crystal structure of a formyltetrahydrofolate deformylase (pp_0327)2 from pseudomonas putida kt2440 at 2.25 a resolution                      |
| 6  | <a href="#">c3nrbd_</a> | <br>Alignment |  | 100.0      | 46     | <b>PDB header:</b> hydrolase<br><b>Chain:</b> D: <b>PDB Molecule:</b> formyltetrahydrofolate deformylase;<br><b>PDBTitle:</b> crystal structure of a formyltetrahydrofolate deformylase (puru,2 pp_1943) from pseudomonas putida kt2440 at 2.05 a resolution                |
| 7  | <a href="#">c3aufA_</a> | <br>Alignment |  | 100.0      | 31     | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> glycinamide ribonucleotide transformylase 1;<br><b>PDBTitle:</b> crystal structure of glycinamide ribonucleotide transformylase 1 from2 symbiobacterium toebii                                      |
| 8  | <a href="#">c2ywrA_</a> | <br>Alignment |  | 100.0      | 32     | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylglycinamide formyltransferase;<br><b>PDBTitle:</b> crystal structure of gar transformylase from aquifex aeolicus  |
| 9  | <a href="#">d1jkxa_</a> | <br>Alignment |  | 100.0      | 27     | <b>Fold:</b> Formyltransferase<br><b>Superfamily:</b> Formyltransferase<br><b>Family:</b> Formyltransferase   |
| 10 | <a href="#">c3p9xB_</a> | <br>Alignment |  | 100.0      | 30     | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> phosphoribosylglycinamide formyltransferase;<br><b>PDBTitle:</b> crystal structure of phosphoribosylglycinamide formyltransferase from2 bacillus halodurans   |
| 11 | <a href="#">c3tqrA_</a> | <br>Alignment |  | 100.0      | 27     | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylglycinamide formyltransferase;<br><b>PDBTitle:</b> structure of the phosphoribosylglycinamide formyltransferase (purn) in2 complex with ches from coxiella burnetii                   |

|    |                         |           |              |       |    |   |
|----|-------------------------|-----------|--------------|-------|----|---|
| 12 | <a href="#">c3av3A_</a> | Alignment |              | 100.0 | 28 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylglycinamide formyltransferase;<br><b>PDBTitle:</b> crystal structure of glycinamide ribonucleotide transformylase 1 from2 geobacillus kaustophilus  |
| 13 | <a href="#">d1meoa_</a> | Alignment |              | 100.0 | 29 | <b>Fold:</b> Formyltransferase<br><b>Superfamily:</b> Formyltransferase<br><b>Family:</b> Formyltransferase   |
| 14 | <a href="#">c3dcjA_</a> | Alignment |              | 100.0 | 29 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> probable 5'-phosphoribosylglycinamide formyltransferase<br><b>PDBTitle:</b> crystal structure of glycinamide formyltransferase (purn) from2 mycobacterium tuberculosis in complex with 5-methyl-5,6,7,8-3 tetrahydrofolic acid derivative |
| 15 | <a href="#">c3kcgA_</a> | Alignment |              | 100.0 | 30 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylglycinamide formyltransferase;<br><b>PDBTitle:</b> crystal structure of phosphoribosylglycinamide formyltransferase from2 anaplasma phagocytophilum   |
| 16 | <a href="#">c4ds3A_</a> | Alignment |              | 100.0 | 28 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylglycinamide formyltransferase;<br><b>PDBTitle:</b> crystal structure of phosphoribosylglycinamide formyltransferase from2 brucella melitensis   |
| 17 | <a href="#">c4s1nA_</a> | Alignment |              | 100.0 | 27 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylglycinamide formyltransferase;<br><b>PDBTitle:</b> the crystal structure of phosphoribosylglycinamide formyltransferase2 from streptococcus pneumoniae tigr4  |
| 18 | <a href="#">c5cjjA_</a> | Alignment |              | 100.0 | 28 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylglycinamide formyltransferase;<br><b>PDBTitle:</b> the crystal structure of phosphoribosylglycinamide formyltransferase2 from campylobacter jejuni subsp. jejuni nctc 11168   |
| 19 | <a href="#">d1fmta2</a> | Alignment |              | 100.0 | 22 | <b>Fold:</b> Formyltransferase<br><b>Superfamily:</b> Formyltransferase<br><b>Family:</b> Formyltransferase   |
| 20 | <a href="#">d1s3ia2</a> | Alignment |              | 100.0 | 21 | <b>Fold:</b> Formyltransferase<br><b>Superfamily:</b> Formyltransferase<br><b>Family:</b> Formyltransferase   |
| 21 | <a href="#">c1z7eC_</a> | Alignment | not modelled | 100.0 | 16 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> C: <b>PDB Molecule:</b> protein arna;<br><b>PDBTitle:</b> crystal structure of full length arna   |
| 22 | <a href="#">c1fmtA_</a> | Alignment | not modelled | 100.0 | 22 | <b>PDB header:</b> formyltransferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> methionyl-trna fmet formyltransferase;<br><b>PDBTitle:</b> methionyl-trnafmet formyltransferase from escherichia coli   |
| 23 | <a href="#">d2blna2</a> | Alignment | not modelled | 100.0 | 16 | <b>Fold:</b> Formyltransferase<br><b>Superfamily:</b> Formyltransferase<br><b>Family:</b> Formyltransferase   |
| 24 | <a href="#">c3tqgA_</a> | Alignment | not modelled | 100.0 | 24 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> methionyl-trna formyltransferase;<br><b>PDBTitle:</b> structure of the methionyl-trna formyltransferase (fmt) from coxiella2 burnetii   |
| 25 | <a href="#">d2bw0a2</a> | Alignment | not modelled | 100.0 | 20 | <b>Fold:</b> Formyltransferase<br><b>Superfamily:</b> Formyltransferase<br><b>Family:</b> Formyltransferase   |
| 26 | <a href="#">c3rfoA_</a> | Alignment | not modelled | 100.0 | 25 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> methionyl-trna formyltransferase;<br><b>PDBTitle:</b> crystal structure of methionyl-trna formyltransferase from bacillus2 anthracis  |
| 27 | <a href="#">c1yrwA_</a> | Alignment | not modelled | 100.0 | 16 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> protein arna;<br><b>PDBTitle:</b> crystal structure of e.coli arna transformylase domain  |
| 28 | <a href="#">c5uaiA_</a> | Alignment | not modelled | 100.0 | 25 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> methionyl-trna formyltransferase;<br><b>PDBTitle:</b> crystal structure of methionyl-trna formyltransferase from pseudomonas2 aeruginosa  |
| 29 | <a href="#">c1s3iA_</a> | Alignment | not modelled | 100.0 | 21 | <b>PDB header:</b> hydrolase, oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 10-formyltetrahydrofolate dehydrogenase;<br><b>PDBTitle:</b> crystal structure of the n terminal hydrolase domain of  |

|    |                         |           |              |       |    |  |
|----|-------------------------|-----------|--------------|-------|----|--|
|    |                         |           |              |       |    | 10-2 formyltetrahydrofolate dehydrogenase  |
| 30 | <a href="#">c3q0IA</a>  | Alignment | not modelled | 100.0 | 22 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> methionyl-trna formyltransferase;<br><b>PDBTitle:</b> methionyl-trna formyltransferase from vibrio cholerae  |
| 31 | <a href="#">c4nv1D</a>  | Alignment | not modelled | 100.0 | 18 | <b>PDB header:</b> transferase<br><b>Chain:</b> D: <b>PDB Molecule:</b> formyltransferase;<br><b>PDBTitle:</b> crystal structure of a 4-n formyltransferase from francisella2 tularensis   |
| 32 | <a href="#">c4pzuF</a>  | Alignment | not modelled | 100.0 | 20 | <b>PDB header:</b> transferase<br><b>Chain:</b> F: <b>PDB Molecule:</b> uncharacterized protein rv3404c/mt3512;<br><b>PDBTitle:</b> crystal structure of a putative uncharacterize protein rv3404c and2 likely sugar n-formyltransferase from mycobacterium tuberculosis       |
| 33 | <a href="#">c6nbpA</a>  | Alignment | not modelled | 100.0 | 19 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> n-formyltransferase;<br><b>PDBTitle:</b> crystal structure of a sugar n-formyltransferase from the plant2 pathogen pantoea ananatis  |
| 34 | <a href="#">c5vytD</a>  | Alignment | not modelled | 100.0 | 19 | <b>PDB header:</b> transferase<br><b>Chain:</b> D: <b>PDB Molecule:</b> gdp-mannose 4,6-dehydratase / gdp-4-amino-4,6-dideoxy-d-<br><b>PDBTitle:</b> crystal structure of the wbkc n-formyltransferase (f142a variant) from2 brucella melitensis                               |
| 35 | <a href="#">c4yfvA</a>  | Alignment | not modelled | 100.0 | 19 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> viof;<br><b>PDBTitle:</b> x-ray structure of the 4-n-formyltransferase viof from providencia2 alcalifaciens o30  |
| 36 | <a href="#">c6ci2A</a>  | Alignment | not modelled | 100.0 | 21 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> formyltransferase psej;<br><b>PDBTitle:</b> crystal structure of the formyltransferase psej from anoxybacillus2 kamchatkensis  |
| 37 | <a href="#">c5uimB</a>  | Alignment | not modelled | 100.0 | 15 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> formyltransferase;<br><b>PDBTitle:</b> x-ray structure of the fdtf n-formyltransferase from salmonella2 enteric o60 in complex with folinic acid and tdp-qui3n   |
| 38 | <a href="#">c4lxuB</a>  | Alignment | not modelled | 100.0 | 20 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> wlard, a sugar 3n-formyl transferase;<br><b>PDBTitle:</b> dtdp-fuc3n and 5-n-formyl-thf  |
| 39 | <a href="#">d1zgha2</a> | Alignment | not modelled | 100.0 | 16 | <b>Fold:</b> Formyltransferase<br><b>Superfamily:</b> Formyltransferase<br><b>Family:</b> Formyltransferase  |
| 40 | <a href="#">c1zghA</a>  | Alignment | not modelled | 100.0 | 15 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> methionyl-trna formyltransferase;<br><b>PDBTitle:</b> methionyl-trna formyltransferase from clostridium thermocellum   |
| 41 | <a href="#">c4xd0A</a>  | Alignment | not modelled | 99.8  | 16 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> tdp-3-aminoquinovose-n-formyltransferase;<br><b>PDBTitle:</b> x-ray structure of the n-formyltransferase qdft from providencia2 alcalifaciens  |
| 42 | <a href="#">d1zpvA1</a> | Alignment | not modelled | 99.6  | 21 | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> ACT-like<br><b>Family:</b> SPO238-like   |
| 43 | <a href="#">c1u8sB</a>  | Alignment | not modelled | 99.4  | 12 | <b>PDB header:</b> transcription<br><b>Chain:</b> B: <b>PDB Molecule:</b> glycine cleavage system transcriptional<br><b>PDBTitle:</b> crystal structure of putative glycine cleavage system2 transcriptional repressor   |
| 44 | <a href="#">d1u8sa1</a> | Alignment | not modelled | 99.4  | 17 | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> ACT-like<br><b>Family:</b> Glycine cleavage system transcriptional repressor   |
| 45 | <a href="#">d1u8sa2</a> | Alignment | not modelled | 99.2  | 14 | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> ACT-like<br><b>Family:</b> Glycine cleavage system transcriptional repressor   |
| 46 | <a href="#">c2nyiB</a>  | Alignment | not modelled | 99.0  | 18 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> B: <b>PDB Molecule:</b> unknown protein;<br><b>PDBTitle:</b> crystal structure of an unknown protein from galdieria sulphuraria  |
| 47 | <a href="#">c6culG</a>  | Alignment | not modelled | 98.2  | 26 | <b>PDB header:</b> transferase<br><b>Chain:</b> G: <b>PDB Molecule:</b> pyoverdine synthetase f;<br><b>PDBTitle:</b> pvdf of pyoverdin biosynthesis is a structurally unique n10-2 formyltetrahydrofolate-dependent formyltransferase  |
| 48 | <a href="#">c3p96A</a>  | Alignment | not modelled | 97.8  | 19 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> phosphoserine phosphatase serb;<br><b>PDBTitle:</b> crystal structure of phosphoserine phosphatase serb from mycobacterium2 avium, native form   |
| 49 | <a href="#">c3ibwA</a>  | Alignment | not modelled | 97.1  | 11 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> gtp pyrophosphokinase;<br><b>PDBTitle:</b> crystal structure of the act domain from gtp pyrophosphokinase of2 chlorobium tepidum. northeast structural genomics consortium target3 ctr148a             |
| 50 | <a href="#">d1ygya3</a> | Alignment | not modelled | 97.0  | 22 | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> ACT-like<br><b>Family:</b> Phosphoglycerate dehydrogenase, regulatory (C-terminal) domain  |
| 51 | <a href="#">d1sc6a3</a> | Alignment | not modelled | 97.0  | 18 | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> ACT-like<br><b>Family:</b> Phosphoglycerate dehydrogenase, regulatory (C-terminal) domain  |
| 52 | <a href="#">c1ygyA</a>  | Alignment | not modelled | 96.7  | 21 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> d-3-phosphoglycerate dehydrogenase;<br><b>PDBTitle:</b> crystal structure of d-3-phosphoglycerate dehydrogenase from2 mycobacterium tuberculosis  |
| 53 | <a href="#">c5uscB</a>  | Alignment | not modelled | 96.1  | 22 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> prephenate dehydrogenase;<br><b>PDBTitle:</b> crystal structure of prephenate dehydrogenase tyra from bacillus2 anthracis in complex with nad and l-tyrosine   |
| 54 | <a href="#">c1y7pB</a>  | Alignment | not modelled | 95.8  | 19 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein af1403;<br><b>PDBTitle:</b> 1.9 a crystal structure of a protein of unknown function2 af1403 from archaeoglobus fulgidus, probable metabolic3 regulator |

|    |                         |           |              |      |    |   |
|----|-------------------------|-----------|--------------|------|----|---|
| 55 | <a href="#">d1ru8a_</a> | Alignment | not modelled | 95.6 | 19 | <b>Fold:</b> Adenine nucleotide alpha hydrolase-like<br><b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like<br><b>Family:</b> N-type ATP pyrophosphatases  |
| 56 | <a href="#">c2lvwA_</a> | Alignment | not modelled | 95.2 | 14 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> acetolactate synthase isozyme 1 small subunit;<br><b>PDBTitle:</b> solution nmr studies of the dimeric regulatory subunit ilvN of the 2 e.coli acetohydroxyacid synthase i (ahas i)               |
| 57 | <a href="#">c2fgcA_</a> | Alignment | not modelled | 94.9 | 24 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> acetolactate synthase, small subunit;<br><b>PDBTitle:</b> crystal structure of acetolactate synthase- small subunit from 2 thermotoga maritima  |
| 58 | <a href="#">d2fgca2</a> | Alignment | not modelled | 94.8 | 24 | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> ACT-like<br><b>Family:</b> ilvH-like  |
| 59 | <a href="#">c2pc6C_</a> | Alignment | not modelled | 94.8 | 14 | <b>PDB header:</b> lyase<br><b>Chain:</b> C: <b>PDB Molecule:</b> probable acetolactate synthase isozyme iii (small subunit);<br><b>PDBTitle:</b> crystal structure of putative acetolactate synthase- small subunit2 from nitrosomonas europaea                          |
| 60 | <a href="#">c3a14B_</a> | Alignment | not modelled | 94.5 | 17 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> 1-deoxy-d-xylulose 5-phosphate reductoisomerase;<br><b>PDBTitle:</b> crystal structure of dxr from thermotoga maritima, in complex with 2 nadph  |
| 61 | <a href="#">c2f1fA_</a> | Alignment | not modelled | 94.2 | 13 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> acetolactate synthase isozyme iii small subunit;<br><b>PDBTitle:</b> crystal structure of the regulatory subunit of acetohydroxyacid2 synthase isozyme iii from e. coli                           |
| 62 | <a href="#">d2pc6a2</a> | Alignment | not modelled | 93.9 | 22 | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> ACT-like<br><b>Family:</b> ilvH-like  |
| 63 | <a href="#">c1ni5A_</a> | Alignment | not modelled | 93.7 | 15 | <b>PDB header:</b> cell cycle<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative cell cycle protein mesj;<br><b>PDBTitle:</b> structure of the mesj pp-atpase from escherichia coli  |
| 64 | <a href="#">d2f1fa1</a> | Alignment | not modelled | 93.5 | 21 | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> ACT-like<br><b>Family:</b> ilvH-like  |
| 65 | <a href="#">c6dzsD_</a> | Alignment | not modelled | 93.5 | 26 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> D: <b>PDB Molecule:</b> homoserine dehydrogenase;<br><b>PDBTitle:</b> mycobacterial homoserine dehydrogenase thra in complex with nadp   |
| 66 | <a href="#">d1f0ka_</a> | Alignment | not modelled | 93.1 | 16 | <b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase<br><b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase<br><b>Family:</b> Peptidoglycan biosynthesis glycosyltransferase MurG   |
| 67 | <a href="#">d1r0ka2</a> | Alignment | not modelled | 93.0 | 16 | <b>Fold:</b> NAD(P)-binding Rossmann-fold domains<br><b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains<br><b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain  |
| 68 | <a href="#">d1xi8a3</a> | Alignment | not modelled | 92.8 | 22 | <b>Fold:</b> Molybdenum cofactor biosynthesis proteins<br><b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins<br><b>Family:</b> MoeA central domain-like  |
| 69 | <a href="#">c2e21A_</a> | Alignment | not modelled | 92.5 | 19 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> trna(ile)-lysine synthase;<br><b>PDBTitle:</b> crystal structure of tils in a complex with amppnp from aquifex2 aeolicus.  |
| 70 | <a href="#">d2d13a1</a> | Alignment | not modelled | 91.9 | 27 | <b>Fold:</b> Adenine nucleotide alpha hydrolase-like<br><b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like<br><b>Family:</b> N-type ATP pyrophosphatases  |
| 71 | <a href="#">c2f06B_</a> | Alignment | not modelled | 91.6 | 18 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> B: <b>PDB Molecule:</b> conserved hypothetical protein;<br><b>PDBTitle:</b> crystal structure of protein bt0572 from bacteroides thetaiotaomicron   |
| 72 | <a href="#">c1ofgF_</a> | Alignment | not modelled | 91.6 | 13 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> F: <b>PDB Molecule:</b> glucose-fructose oxidoreductase;<br><b>PDBTitle:</b> glucose-fructose oxidoreductase   |
| 73 | <a href="#">c1h6dL_</a> | Alignment | not modelled | 91.5 | 13 | <b>PDB header:</b> protein translocation<br><b>Chain:</b> L: <b>PDB Molecule:</b> precursor form of glucose-fructose oxidoreductase2 from zymomonas mobilis complexed with glycerol   |
| 74 | <a href="#">d2f06a2</a> | Alignment | not modelled | 91.0 | 23 | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> ACT-like<br><b>Family:</b> BT0572-like  |
| 75 | <a href="#">c3luyA_</a> | Alignment | not modelled | 90.7 | 16 | <b>PDB header:</b> isomerase<br><b>Chain:</b> A: <b>PDB Molecule:</b> probable chorismate mutase;<br><b>PDBTitle:</b> putative chorismate mutase from bifidobacterium adolescentis  |
| 76 | <a href="#">c5g2rA_</a> | Alignment | not modelled | 90.3 | 21 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> molybdopterin biosynthesis protein cnx1;<br><b>PDBTitle:</b> crystal structure of the mo-insertase domain cnx1e from 2 arabidopsis thaliana   |
| 77 | <a href="#">d1ni5a1</a> | Alignment | not modelled | 90.1 | 17 | <b>Fold:</b> Adenine nucleotide alpha hydrolase-like<br><b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like<br><b>Family:</b> PP-loop ATPase   |
| 78 | <a href="#">d1wu2a3</a> | Alignment | not modelled | 90.0 | 16 | <b>Fold:</b> Molybdenum cofactor biosynthesis proteins<br><b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins<br><b>Family:</b> MoeA central domain-like  |
| 79 | <a href="#">c2jcyA_</a> | Alignment | not modelled | 89.4 | 22 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 1-deoxy-d-xylulose 5-phosphate reductoisomerase;<br><b>PDBTitle:</b> x-ray structure of mutant 1-deoxy-d-xylulose 5-phosphate2 reductoisomerase, dxr, rv2870c, from mycobacterium tuberculosis |

|     |                         |           |              |      |    |   |
|-----|-------------------------|-----------|--------------|------|----|---|
| 80  | <a href="#">d2ftsa3</a> | Alignment | not modelled | 89.4 | 22 | <b>Fold:</b> Molybdenum cofactor biosynthesis proteins<br><b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins<br><b>Family:</b> MoeA central domain-like  |
| 81  | <a href="#">c3a2kB</a>  | Alignment | not modelled | 88.3 | 15 | <b>PDB header:</b> ligase/rna<br><b>Chain:</b> B: <b>PDB Molecule:</b> trna(ile)-lysine synthase;<br><b>PDBTitle:</b> crystal structure of tils complexed with trna   |
| 82  | <a href="#">c2qmxB</a>  | Alignment | not modelled | 88.2 | 12 | <b>PDB header:</b> ligase<br><b>Chain:</b> B: <b>PDB Molecule:</b> prephenate dehydratase;<br><b>PDBTitle:</b> the crystal structure of l-phe inhibited prephenate dehydratase from2 chlorobium tepidum tIs   |
| 83  | <a href="#">c3mtjA</a>  | Alignment | not modelled | 88.1 | 20 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> homoserine dehydrogenase;<br><b>PDBTitle:</b> the crystal structure of a homoserine dehydrogenase from thiobacillus2 denitrificans to 2.15a  |
| 84  | <a href="#">c3s2uA</a>  | Alignment | not modelled | 88.1 | 17 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylglucosamine--n-acetylmuramyl-(pentapeptide)<br><b>PDBTitle:</b> crystal structure of the pseudomonas aeruginosa murg:udp-glcnaC2 substrate complex  |
| 85  | <a href="#">d2f06a1</a> | Alignment | not modelled | 87.8 | 22 | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> ACT-like<br><b>Family:</b> BT0572-like  |
| 86  | <a href="#">d1wy5a1</a> | Alignment | not modelled | 87.3 | 18 | <b>Fold:</b> Adenine nucleotide alpha hydrolase-like<br><b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like<br><b>Family:</b> PP-loop ATPase   |
| 87  | <a href="#">c2nqqA</a>  | Alignment | not modelled | 87.1 | 21 | <b>PDB header:</b> biosynthetic protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> molybdopterin biosynthesis protein moea;<br><b>PDBTitle:</b> moea r137q  |
| 88  | <a href="#">c1r0lD</a>  | Alignment | not modelled | 86.7 | 25 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> D: <b>PDB Molecule:</b> 1-deoxy-d-xylulose 5-phosphate reductoisomerase;<br><b>PDBTitle:</b> 1-deoxy-d-xylulose 5-phosphate reductoisomerase from zymomonas mobilis2 in complex with nadph   |
| 89  | <a href="#">c5udwB</a>  | Alignment | not modelled | 86.5 | 11 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> lactate racemization operon protein lare;<br><b>PDBTitle:</b> lare, a sulfur transferase involved in synthesis of the cofactor for2 lactate racemase, in complex with nickel                                  |
| 90  | <a href="#">c2fu3A</a>  | Alignment | not modelled | 85.9 | 21 | <b>PDB header:</b> biosynthetic protein/structural protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> gephyrin;<br><b>PDBTitle:</b> crystal structure of gephyrin e-domain  |
| 91  | <a href="#">c2hmaA</a>  | Alignment | not modelled | 85.7 | 20 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> probable trna (5-methylaminomethyl-2-thiouridylate)-<br><b>PDBTitle:</b> the crystal structure of trna (5-methylaminomethyl-2-thiouridylate)-2 methyltransferase trmu from streptococcus pneumoniae           |
| 92  | <a href="#">c4gmfD</a>  | Alignment | not modelled | 85.2 | 18 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> D: <b>PDB Molecule:</b> yersiniabactin biosynthetic protein ybtu;<br><b>PDBTitle:</b> apo structure of a thiazolinyI imine reductase from yersinia2 enterocolitica (irp3)  |
| 93  | <a href="#">d1phza1</a> | Alignment | not modelled | 85.0 | 10 | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> ACT-like<br><b>Family:</b> Phenylalanine metabolism regulatory domain   |
| 94  | <a href="#">c3e9mC</a>  | Alignment | not modelled | 84.8 | 10 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> C: <b>PDB Molecule:</b> oxidoreductase, gfo/idh/moca family;<br><b>PDBTitle:</b> crystal structure of an oxidoreductase from enterococcus2 faecalis  |
| 95  | <a href="#">c5b3uB</a>  | Alignment | not modelled | 84.6 | 28 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> biliverdin reductase;<br><b>PDBTitle:</b> crystal structure of biliverdin reductase in complex with nadp+ from2 synechocystis sp. pcc 6803  |
| 96  | <a href="#">c1uz5A</a>  | Alignment | not modelled | 84.2 | 16 | <b>PDB header:</b> molybdopterin biosynthesis<br><b>Chain:</b> A: <b>PDB Molecule:</b> 402aa long hypothetical molybdopterin<br><b>PDBTitle:</b> the crystal structure of molybdopterin biosynthesis moea2 protein from pyrococcus horikosii  |
| 97  | <a href="#">c2derA</a>  | Alignment | not modelled | 84.1 | 15 | <b>PDB header:</b> transferase/rna<br><b>Chain:</b> A: <b>PDB Molecule:</b> trna-specific 2-thiouridylase mnma;<br><b>PDBTitle:</b> cocrystal structure of an rna sulfuration enzyme mnma and2 trna-glu in the initial trna binding state   |
| 98  | <a href="#">c3l76B</a>  | Alignment | not modelled | 83.7 | 33 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> aspartokinase;<br><b>PDBTitle:</b> crystal structure of aspartate kinase from synechocystis   |
| 99  | <a href="#">c3bl5E</a>  | Alignment | not modelled | 83.4 | 16 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> E: <b>PDB Molecule:</b> queuosine biosynthesis protein quec;<br><b>PDBTitle:</b> crystal structure of quec from bacillus subtilis: an enzyme2 involved in preq1 biosynthesis  |
| 100 | <a href="#">c4oh7B</a>  | Alignment | not modelled | 81.7 | 13 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> ornithine carbamoyltransferase;<br><b>PDBTitle:</b> crystal structure of ornithine carbamoyltransferase from brucella2 melitensis   |
| 101 | <a href="#">d1uz5a3</a> | Alignment | not modelled | 81.2 | 22 | <b>Fold:</b> Molybdenum cofactor biosynthesis proteins<br><b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins<br><b>Family:</b> MoeA central domain-like  |
| 102 | <a href="#">d2hmfa3</a> | Alignment | not modelled | 79.4 | 17 | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> ACT-like<br><b>Family:</b> Aspartokinase allosteric domain-like   |
| 103 | <a href="#">c2nvwB</a>  | Alignment | not modelled | 79.3 | 8  | <b>PDB header:</b> transcription<br><b>Chain:</b> B: <b>PDB Molecule:</b> galactose/lactose metabolism regulatory protein<br><b>PDBTitle:</b> crystal scture of transcriptional regulator gal80p from2 kluveromymes lactis  |
| 104 | <a href="#">c2q8nB</a>  | Alignment | not modelled | 78.3 | 10 | <b>PDB header:</b> isomerase<br><b>Chain:</b> B: <b>PDB Molecule:</b> glucose-6-phosphate isomerase;<br><b>PDBTitle:</b> crystal structure of glucose-6-phosphate isomerase (ec 5.3.1.9)2 (tm1385) from thermotoga maritima at 1.82 a resolution<br><b>PDB header:</b> oxidoreductase |

|     |                         |           |              |      |    |  |
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| 105 | <a href="#">c5i78A_</a> | Alignment | not modelled | 76.9 | 15 | <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-aminoadipic semialdehyde synthase, mitochondrial;<br><b>PDBTitle:</b> crystal structure of human aminoadipate semialdehyde synthase,2 saccharopine dehydrogenase domain (in nad+ bound form)     |
| 106 | <a href="#">d1q0qa2</a> | Alignment | not modelled | 76.5 | 15 | <b>Fold:</b> NAD(P)-binding Rossmann-fold domains<br><b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains<br><b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain   |
| 107 | <a href="#">c3s1tB_</a> | Alignment | not modelled | 76.4 | 15 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> aspartokinase;<br><b>PDBTitle:</b> structure of the regulatory domain of aspartokinase (rv3709c; ak-beta)2 in complex with threonine from mycobacterium tuberculosis |
| 108 | <a href="#">d2nvwa1</a> | Alignment | not modelled | 76.0 | 10 | <b>Fold:</b> NAD(P)-binding Rossmann-fold domains<br><b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains<br><b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain   |
| 109 | <a href="#">d1jsca3</a> | Alignment | not modelled | 75.9 | 19 | <b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding)<br><b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding)<br><b>Family:</b> Pyruvate oxidase and decarboxylase PP module   |
| 110 | <a href="#">c3u3xj_</a> | Alignment | not modelled | 75.9 | 22 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> J: <b>PDB Molecule:</b> oxidoreductase;<br><b>PDBTitle:</b> crystal structure of a putative oxidoreductase from sinorhizobium2 meliloti 1021  |
| 111 | <a href="#">c4gqaC_</a> | Alignment | not modelled | 75.6 | 13 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> C: <b>PDB Molecule:</b> nad binding oxidoreductase;<br><b>PDBTitle:</b> crystal structure of nad binding oxidoreductase from klebsiella2 pneumoniae                                       |
| 112 | <a href="#">c3q2kB_</a> | Alignment | not modelled | 74.9 | 14 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> oxidoreductase;<br><b>PDBTitle:</b> crystal structure of the wlbA dehydrogenase from bordetella pertussis2 in complex with nadh and udp-glcnaC                    |
| 113 | <a href="#">c3rbvA_</a> | Alignment | not modelled | 74.8 | 21 | <b>PDB header:</b> sugar binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> sugar 3-ketoreductase;<br><b>PDBTitle:</b> crystal structure of kjd10, a 3-ketoreductase from actinomadura2 kijaniata in complex with nadp                 |
| 114 | <a href="#">c5fa0B_</a> | Alignment | not modelled | 74.3 | 26 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> putative n-acetyl glucosaminyl transferase;<br><b>PDBTitle:</b> the structure of the beta-3-deoxy-d-manno-oct-2-ulosonic acid2 transferase domain from wbbb          |
| 115 | <a href="#">c1ybaC_</a> | Alignment | not modelled | 74.2 | 30 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> C: <b>PDB Molecule:</b> d-3-phosphoglycerate dehydrogenase;<br><b>PDBTitle:</b> the active form of phosphoglycerate dehydrogenase   |
| 116 | <a href="#">c4ycsC_</a> | Alignment | not modelled | 73.2 | 13 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized protein;<br><b>PDBTitle:</b> crystal structure of putative lipoprotein from peptoclostridium2 difficile 630 (fragment)                                 |
| 117 | <a href="#">c3gd5D_</a> | Alignment | not modelled | 73.2 | 19 | <b>PDB header:</b> transferase<br><b>Chain:</b> D: <b>PDB Molecule:</b> ornithine carbamoyltransferase;<br><b>PDBTitle:</b> crystal structure of ornithine carbamoyltransferase from gloebacter2 violaceus                                   |
| 118 | <a href="#">d1j8yf2</a> | Alignment | not modelled | 73.0 | 15 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> Nitrogenase iron protein-like  |
| 119 | <a href="#">c1xeaD_</a> | Alignment | not modelled | 72.7 | 14 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> D: <b>PDB Molecule:</b> oxidoreductase, gfo/idh/moca family;<br><b>PDBTitle:</b> crystal structure of a gfo/idh/moca family oxidoreductase2 from vibrio cholerae                          |
| 120 | <a href="#">d1mvla_</a> | Alignment | not modelled | 70.9 | 19 | <b>Fold:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD<br><b>Superfamily:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD<br><b>Family:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD       |