Phyre$^2$

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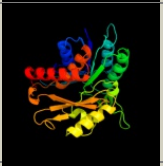
| Email | l.a.kelley@imperial.ac.uk |
| Description | P77150 |
| Date | Wed Jan 25 15:21:10 GMT 2012 |
| Unique Job ID | 19052f3ef6c8c02b |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | d1vi9a_ | Alignment |  | 100.0 | 97 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**PfkB-like kinase |
| 2 | d1lhpa_ | Alignment |  | 100.0 | 32 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**PfkB-like kinase |
| 3 | c3mbjA_ | Alignment |  | 100.0 | 22 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**putative phosphomethylpyrimidine kinase;<br>**PDBTitle:** crystal structure of a putative phosphomethylpyrimidine kinase2 (bt_4458) from bacteroides thetaiotaomicron vpi-5482 at 2.10 a3 resolution (rhombohedral form) |
| 4 | c2ddmA_ | Alignment |  | 100.0 | 30 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**pyridoxine kinase;<br>**PDBTitle:** crystal structure of pyridoxal kinase from the escherichia2 coli pdxk gene at 2.1 a resolution |
| 5 | c3ibqA_ | Alignment |  | 100.0 | 19 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**pyridoxal kinase;<br>**PDBTitle:** crystal structure of pyridoxal kinase from lactobacillus2 plantarum in complex with atp |
| 6 | c2i5bC_ | Alignment |  | 100.0 | 18 | **PDB header:**transferase<br>**Chain:** C: **PDB Molecule:**phosphomethylpyrimidine kinase;<br>**PDBTitle:** the crystal structure of an adp complex of bacillus2 subtilis pyridoxal kinase provides evidence for the3 parralel emergence of enzyme activity during evolution |
| 7 | c3rm5B_ | Alignment |  | 100.0 | 19 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**hydroxymethylpyrimidine/phosphomethylpyrimidine kinase<br>**PDBTitle:** structure of trifunctional thi20 from yeast |
| 8 | d1ub0a_ | Alignment |  | 100.0 | 26 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**Thiamin biosynthesis kinases |
| 9 | d1jxha_ | Alignment |  | 100.0 | 21 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**Thiamin biosynthesis kinases |
| 10 | d2abqa1 | Alignment |  | 99.9 | 21 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**Ribokinase-like |
| 11 | c2jg5B_ | Alignment |  | 99.9 | 18 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**fructose 1-phosphate kinase;<br>**PDBTitle:** crystal structure of a putative phosphofructokinase from2 staphylococcus aureus |

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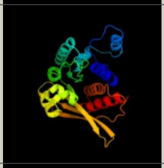
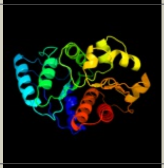
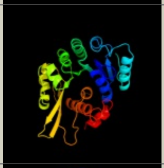
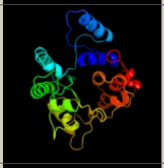
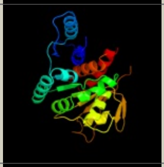
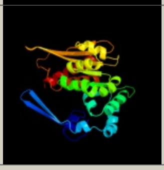
| 12 | d2afba1 | Alignment |  | 99.9 | 16 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**Ribokinase-like |
| 13 | c3cqdB_ | Alignment |  | 99.9 | 19 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**6-phosphofructokinase isozyme 2;<br>**PDBTitle:** structure of the tetrameric inhibited form of2 phosphofructokinase-2 from escherichia coli |
| 14 | d1rkda_ | Alignment |  | 99.9 | 24 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**Ribokinase-like |
| 15 | c2qcvA_ | Alignment |  | 99.8 | 18 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**putative 5-dehydro-2-deoxygluconokinase;<br>**PDBTitle:** crystal structure of a putative 5-dehydro-2-deoxygluconokinase (iolc)2 from bacillus halodurans c-125 at 1.90 a resolution |
| 16 | d2f02a1 | Alignment |  | 99.8 | 20 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**Ribokinase-like |
| 17 | c2nwhA_ | Alignment |  | 99.8 | 22 | **PDB header:**signaling protein,transferase<br>**Chain:** A: **PDB Molecule:**carbohydrate kinase;<br>**PDBTitle:** carbohydrate kinase from agrobacterium tumefaciens |
| 18 | c3pl2D_ | Alignment |  | 99.8 | 20 | **PDB header:**transferase<br>**Chain:** D: **PDB Molecule:**sugar kinase, ribokinase family;<br>**PDBTitle:** crystal structure of a 5-keto-2-deoxygluconokinase (ncgl0155, cgl0158)2 from corynebacterium glutamicum atcc 13032 kitasato at 1.89 a3 resolution |
| 19 | c3looC_ | Alignment |  | 99.8 | 20 | **PDB header:**transferase<br>**Chain:** C: **PDB Molecule:**anopheles gambiae adenosine kinase;<br>**PDBTitle:** crystal structure of anopheles gambiae adenosine kinase in complex2 with p1,p4-di(adenosine-5) tetraphosphate |
| 20 | c2xtbA_ | Alignment |  | 99.8 | 14 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**adenosine kinase;<br>**PDBTitle:** crystal structure of trypanosoma brucei rhodesiense2 adenosine kinase complexed with activator |
| 21 | c3kzhA_ | Alignment | not modelled | 99.8 | 16 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**probable sugar kinase;<br>**PDBTitle:** crystal structure of a putative sugar kinase from2 clostridium perfringens |
| 22 | c3iq0B_ | Alignment | not modelled | 99.8 | 17 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**putative ribokinase ii;<br>**PDBTitle:** crystal structure of a putative ribokinase ii in complex2 with atp and mg+2 from e.coli |
| 23 | c2jg1C_ | Alignment | not modelled | 99.8 | 16 | **PDB header:**transferase<br>**Chain:** C: **PDB Molecule:**tagatose-6-phosphate kinase;<br>**PDBTitle:** structure of staphylococcus aureus d-tagatose-6-phosphate2 kinase with cofactor and substrate |
| 24 | c2pkkA_ | Alignment | not modelled | 99.8 | 14 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**adenosine kinase;<br>**PDBTitle:** crystal structure of m tuberculosis adenosine kinase complexed with 2-2 fluro adenosine |
| 25 | d1v19a_ | Alignment | not modelled | 99.8 | 21 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**Ribokinase-like |
| 26 | c2qhpA_ | Alignment | not modelled | 99.8 | 15 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**fructokinase;<br>**PDBTitle:** crystal structure of fructokinase (np_810670.1) from bacteroides2 thetaiotaomicron vpi-5482 at 1.80 a resolution |
| 27 | c3ktnA_ | Alignment | not modelled | 99.8 | 15 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**carbohydrate kinase, pfkb family;<br>**PDBTitle:** crystal structure of a putative 2-keto-3-deoxygluconate2 kinase from enterococcus faecalis |
| 28 | c3lhxA_ | Alignment | not modelled | 99.8 | 19 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**ketodeoxygluconokinase;<br>**PDBTitle:** crystal structure of a ketodeoxygluconokinase (kdgk) from2 shigella flexneri |

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| 29 | d2fv7a1 | Alignment | not modelled | 99.8 | 20 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**Ribokinase-like |
| 30 | c2rbcA_ | Alignment | not modelled | 99.8 | 15 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**sugar kinase;<br>**PDBTitle:** crystal structure of a putative ribokinase from agrobacterium2 tumefaciens |
| 31 | c2c49A_ | Alignment | not modelled | 99.8 | 17 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**sugar kinase mj0406;<br>**PDBTitle:** crystal structure of methanocaldococcus jannaschii2 nucleoside kinase - an archaeal member of the ribokinase3 family |
| 32 | c3julA_ | Alignment | not modelled | 99.8 | 22 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**lin2199 protein;<br>**PDBTitle:** crystal structure of listeria innocua d-tagatose-6-phosphate2 kinase bound with substrate |
| 33 | d1bx4a_ | Alignment | not modelled | 99.8 | 14 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**Ribokinase-like |
| 34 | c3in1A_ | Alignment | not modelled | 99.8 | 17 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**uncharacterized sugar kinase ydjh;<br>**PDBTitle:** crystal structure of a putative ribokinase in complex with2 adp from e.coli |
| 35 | d2ajra1 | Alignment | not modelled | 99.8 | 16 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**Ribokinase-like |
| 36 | d1tyya_ | Alignment | not modelled | 99.8 | 17 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**Ribokinase-like |
| 37 | c3b1qD_ | Alignment | not modelled | 99.8 | 16 | **PDB header:**transferase<br>**Chain:** D: **PDB Molecule:**ribokinase, putative;<br>**PDBTitle:** structure of burkholderia thailandensis nucleoside kinase (bthnk) in2 complex with inosine |
| 38 | d1kyha_ | Alignment | not modelled | 99.7 | 16 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**YjeF C-terminal domain-like |
| 39 | c3dzvB_ | Alignment | not modelled | 99.7 | 17 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**4-methyl-5-(beta-hydroxyethyl)thiazole kinase;<br>**PDBTitle:** crystal structure of 4-methyl-5-(beta-hydroxyethyl)thiazole2 kinase (np_816404.1) from enterococcus faecalis v583 at3 2.57 a resolution |
| 40 | c1tz6B_ | Alignment | not modelled | 99.7 | 17 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**putative sugar kinase;<br>**PDBTitle:** crystal structure of aminoimidazole riboside kinase from2 salmonella enterica complexed with aminoimidazole riboside3 and atp analog |
| 41 | c2varB_ | Alignment | not modelled | 99.7 | 17 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**fructokinase;<br>**PDBTitle:** crystal structure of sulfolobus solfataricus 2-keto-3-2 deoxygluconate kinase complexed with 2-keto-3-3 deoxygluconate |
| 42 | d2ax3a1 | Alignment | not modelled | 99.7 | 14 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**YjeF C-terminal domain-like |
| 43 | c2absA_ | Alignment | not modelled | 99.7 | 13 | **PDB header:**signaling protein,transferase<br>**Chain:** A: **PDB Molecule:**adenosine kinase;<br>**PDBTitle:** crystal structure of t. gondii adenosine kinase complexed2 with amp-pcp |
| 44 | d2absa1 | Alignment | not modelled | 99.7 | 13 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**Ribokinase-like |
| 45 | d1vk4a_ | Alignment | not modelled | 99.7 | 15 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**Ribokinase-like |
| 46 | d1vm7a_ | Alignment | not modelled | 99.7 | 21 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**Ribokinase-like |
| 47 | c2r3bA_ | Alignment | not modelled | 99.7 | 18 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**yjef-related protein;<br>**PDBTitle:** crystal structure of a ribokinase-like superfamily protein (ef1790)2 from enterococcus faecalis v583 at 1.80 a resolution |
| 48 | c3go6B_ | Alignment | not modelled | 99.7 | 19 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**ribokinase rbsk;<br>**PDBTitle:** crystal structure of m. tuberculosis ribokinase (rv2436) in2 complex with ribose and amp-pnp |
| 49 | c3b3lC_ | Alignment | not modelled | 99.7 | 16 | **PDB header:**transferase<br>**Chain:** C: **PDB Molecule:**ketohexokinase;<br>**PDBTitle:** crystal structures of alternatively-spliced isoforms of human2 ketohexokinase |
| 50 | c3hj6B_ | Alignment | not modelled | 99.7 | 12 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**fructokinase;<br>**PDBTitle:** structure of halothermothrix orenii fructokinase (frk) |
| 51 | d2dcna1 | Alignment | not modelled | 99.7 | 12 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**Ribokinase-like |
| 52 | d1v8aa_ | Alignment | not modelled | 99.6 | 15 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**Thiamin biosynthesis kinases |
| 53 | c3lkiA_ | Alignment | not modelled | 99.6 | 21 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**fructokinase;<br>**PDBTitle:** crystal structure of fructokinase with bound atp from2 xylella fastidiosa |
| 54 | c3i3yB_ | Alignment | not modelled | 99.6 | 19 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**carbohydrate kinase;<br>**PDBTitle:** crystal structure of ribokinase in complex with d-ribose from2 klebsiella pneumoniae |

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| 55 | c3kd6B_ | Alignment | not modelled | 99.6 | 15 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**carbohydrate kinase, pfkb family;<br>**PDBTitle:** crystal structure of nucleoside kinase from chlorobium tepidum in2 complex with amp |
| 56 | c3bf5A_ | Alignment | not modelled | 99.6 | 17 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**ribokinase related protein;<br>**PDBTitle:** crystal structure of putative ribokinase (10640157) from thermoplasma2 acidophilum at 1.91 a resolution |
| 57 | c2ax3A_ | Alignment | not modelled | 99.6 | 15 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**hypothetical protein tm0922;<br>**PDBTitle:** crystal structure of a putative carbohydrate kinase (tm0922) from2 thermotoga maritima msb8 at 2.25 a resolution |
| 58 | c3gbuD_ | Alignment | not modelled | 99.6 | 17 | **PDB header:**transferase<br>**Chain:** D: **PDB Molecule:**uncharacterized sugar kinase ph1459;<br>**PDBTitle:** crystal structure of an uncharacterized sugar kinase ph1459 from2 pyrococcus horikoshii in complex with atp |
| 59 | c3bgkA_ | Alignment | not modelled | 99.6 | 18 | **PDB header:**unknown function<br>**Chain:** A: **PDB Molecule:**putative uncharacterized protein;<br>**PDBTitle:** the crystal structure of hypothetic protein smu.573 from2 streptococcus mutans |
| 60 | d1ekqa_ | Alignment | not modelled | 99.5 | 10 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**Thiamin biosynthesis kinases |
| 61 | c3nm3D_ | Alignment | not modelled | 99.4 | 12 | **PDB header:**transferase<br>**Chain:** D: **PDB Molecule:**thiamine biosynthetic bifunctional enzyme;<br>**PDBTitle:** the crystal structure of candida glabrata thi6, a bifunctional enzyme2 involved in thiamin biosyhthesis of eukaryotes |
| 62 | c3k5wA_ | Alignment | not modelled | 99.2 | 16 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**carbohydrate kinase;<br>**PDBTitle:** crystal structure of a carbohydrate kinase (yjef family)from2 helicobacter pylori |
| 63 | d1gc5a_ | Alignment | not modelled | 95.1 | 24 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**ADP-specific Phosphofructokinase/Glucokinase |
| 64 | d1u2xa_ | Alignment | not modelled | 94.7 | 24 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**ADP-specific Phosphofructokinase/Glucokinase |
| 65 | c3drwA_ | Alignment | not modelled | 94.3 | 23 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**adp-specific phosphofructokinase;<br>**PDBTitle:** crystal structure of a phosphofructokinase from pyrococcus2 horikoshii ot3 with amp |
| 66 | d1l2la_ | Alignment | not modelled | 88.3 | 23 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**ADP-specific Phosphofructokinase/Glucokinase |
| 67 | d1ua4a_ | Alignment | not modelled | 80.1 | 20 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**ADP-specific Phosphofructokinase/Glucokinase |
| 68 | c3g8cB_ | Alignment | not modelled | 80.0 | 15 | **PDB header:**ligase<br>**Chain:** B: **PDB Molecule:**biotin carboxylase;<br>**PDBTitle:** crystal structure of biotin carboxylase in complex with2 biotin, bicarbonate, adp and mg ion |
| 69 | c3sc6F_ | Alignment | not modelled | 76.3 | 13 | **PDB header:**oxidoreductase<br>**Chain:** F: **PDB Molecule:**dtdp-4-dehydrorhamnose reductase;<br>**PDBTitle:** 2.65 angstrom resolution crystal structure of dtdp-4-dehydrorhamnose2 reductase (rfbd) from bacillus anthracis str. ames in complex with3 nadp |
| 70 | c3ay3C_ | Alignment | not modelled | 74.8 | 19 | **PDB header:**oxidoreductase<br>**Chain:** C: **PDB Molecule:**nad-dependent epimerase/dehydratase;<br>**PDBTitle:** crystal structure of glucuronic acid dehydrogeanse from2 chromohalobacter salexigens |
| 71 | c2weuD_ | Alignment | not modelled | 74.5 | 23 | **PDB header:**antifungal protein<br>**Chain:** D: **PDB Molecule:**tryptophan 5-halogenase;<br>**PDBTitle:** crystal structure of tryptophan 5-halogenase (pyrh) complex2 with substrate tryptophan |
| 72 | c1ulzA_ | Alignment | not modelled | 73.1 | 15 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**pyruvate carboxylase n-terminal domain;<br>**PDBTitle:** crystal structure of the biotin carboxylase subunit of pyruvate2 carboxylase |
| 73 | c3dhnA_ | Alignment | not modelled | 70.6 | 19 | **PDB header:**isomerase, lyase<br>**Chain:** A: **PDB Molecule:**nad-dependent epimerase/dehydratase;<br>**PDBTitle:** crystal structure of the putative epimerase q89z24_bactn2 from bacteroides thetaiotaomicron. northeast structural3 genomics consortium target btr310. |
| 74 | c2gpwC_ | Alignment | not modelled | 69.6 | 15 | **PDB header:**ligase<br>**Chain:** C: **PDB Molecule:**biotin carboxylase;<br>**PDBTitle:** crystal structure of the biotin carboxylase subunit, f363a2 mutant, of acetyl-coa carboxylase from escherichia coli. |
| 75 | d2b7oa1 | Alignment | not modelled | 60.8 | 25 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Aldolase<br>**Family:**Class-II DAHP synthetase |
| 76 | c3d8xB_ | Alignment | not modelled | 56.2 | 19 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**thioredoxin reductase 1;<br>**PDBTitle:** crystal structure of saccharomyces cerevisiae nadph dependent2 thioredoxin reductase 1 |
| 77 | d1seza1 | Alignment | not modelled | 55.1 | 31 | **Fold:**FAD/NAD(P)-binding domain<br>**Superfamily:**FAD/NAD(P)-binding domain<br>**Family:**FAD-linked reductases, N-terminal domain |
| 78 | c2a87A_ | Alignment | not modelled | 54.5 | 23 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**thioredoxin reductase;<br>**PDBTitle:** crystal structure of m. tuberculosis thioredoxin reductase |
| 79 | c3gpiA_ | Alignment | not modelled | 54.2 | 27 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**nad-dependent epimerase/dehydratase;<br>**PDBTitle:** structure of putative nad-dependent epimerase/dehydratase2 from methylobacillus flagellatus |
|  |  |  |  |  |  | **Fold:**NAD(P)-binding Rossmann-fold domains |

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| 80 | d1f0ya2 | Alignment | not modelled | 54.1 | 23 | **Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain |
| 81 | d1qrda_ | Alignment | not modelled | 52.1 | 17 | **Fold:**Flavodoxin-like<br>**Superfamily:**Flavoproteins<br>**Family:**Quinone reductase |
| 82 | d2g0ta1 | Alignment | not modelled | 50.9 | 16 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**Nitrogenase iron protein-like |
| 83 | d2d1pb1 | Alignment | not modelled | 49.0 | 24 | **Fold:**DsrEFH-like<br>**Superfamily:**DsrEFH-like<br>**Family:**DsrEF-like |
| 84 | c3kd9B_ | Alignment | not modelled | 48.9 | 37 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**coenzyme a disulfide reductase;<br>**PDBTitle:** crystal structure of pyridine nucleotide disulfide oxidoreductase from2 pyrococcus horikoshii |
| 85 | c1y80A_ | Alignment | not modelled | 48.5 | 19 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**predicted cobalamin binding protein;<br>**PDBTitle:** structure of a corrinoid (factor iiim)-binding protein from2 moorella thermoacetica |
| 86 | c2dlnA_ | Alignment | not modelled | 45.9 | 23 | **PDB header:**ligase(peptidoglycan synthesis)<br>**Chain:** A: **PDB Molecule:**d-alanine--d-alanine ligase;<br>**PDBTitle:** vancomycin resistance: structure of d-alanine:d-alanine2 ligase at 2.3 angstroms resolution |
| 87 | c1apzB_ | Alignment | not modelled | 45.5 | 18 | **PDB header:**complex (hydrolase/peptide)<br>**Chain:** B: **PDB Molecule:**aspartylglucosaminidase;<br>**PDBTitle:** human aspartylglucosaminidase complex with reaction product |
| 88 | c3ab1B_ | Alignment | not modelled | 44.5 | 23 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**ferredoxin--nadp reductase;<br>**PDBTitle:** crystal structure of ferredoxin nadp+ oxidoreductase |
| 89 | c2q1wC_ | Alignment | not modelled | 44.5 | 23 | **PDB header:**sugar binding protein<br>**Chain:** C: **PDB Molecule:**putative nucleotide sugar epimerase/ dehydratase;<br>**PDBTitle:** crystal structure of the bordetella bronchiseptica enzyme wbmh in2 complex with nad+ |
| 90 | c3c1oA_ | Alignment | not modelled | 43.8 | 13 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**eugenol synthase;<br>**PDBTitle:** the multiple phenylpropene synthases in both clarkia2 breweri and petunia hybrida represent two distinct lineages |
| 91 | c3g5rA_ | Alignment | not modelled | 42.4 | 37 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**methylenetetrahydrofolate--trna-(uracil-5-)-<br>**PDBTitle:** crystal structure of thermus thermophilus trmfo in complex with2 tetrahydrofolate |
| 92 | d2gtad1 | Alignment | not modelled | 42.4 | 30 | **Fold:**all-alpha NTP pyrophosphatases<br>**Superfamily:**all-alpha NTP pyrophosphatases<br>**Family:**MazG-like |
| 93 | c3crcB_ | Alignment | not modelled | 41.5 | 19 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**protein mazg;<br>**PDBTitle:** crystal structure of escherichia coli mazg, the regulator2 of nutritional stress response |
| 94 | c2dzdB_ | Alignment | not modelled | 41.3 | 13 | **PDB header:**ligase<br>**Chain:** B: **PDB Molecule:**pyruvate carboxylase;<br>**PDBTitle:** crystal structure of the biotin carboxylase domain of2 pyruvate carboxylase |
| 95 | c2r60A_ | Alignment | not modelled | 39.7 | 16 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**glycosyl transferase, group 1;<br>**PDBTitle:** structure of apo sucrose phosphate synthase (sps) of2 halothermothrix orenii |
| 96 | c2gacD_ | Alignment | not modelled | 39.2 | 24 | **PDB header:**hydrolase<br>**Chain:** D: **PDB Molecule:**glycosylasparaginase;<br>**PDBTitle:** t152c mutant glycosylasparaginase from flavobacterium2 meningosepticum |
| 97 | d2gtaa1 | Alignment | not modelled | 38.4 | 30 | **Fold:**all-alpha NTP pyrophosphatases<br>**Superfamily:**all-alpha NTP pyrophosphatases<br>**Family:**MazG-like |
| 98 | c3p19A_ | Alignment | not modelled | 37.7 | 22 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**putative blue fluorescent protein;<br>**PDBTitle:** improved nadph-dependent blue fluorescent protein |
| 99 | c2q0lA_ | Alignment | not modelled | 37.3 | 33 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**thioredoxin reductase;<br>**PDBTitle:** helicobacter pylori thioredoxin reductase reduced by sodium dithionite2 in complex with nadp+ |
| 100 | c3kipU_ | Alignment | not modelled | 34.8 | 30 | **PDB header:**lyase<br>**Chain:** U: **PDB Molecule:**3-dehydroquinase, type ii;<br>**PDBTitle:** crystal structure of type-ii 3-dehydroquinase from c. albicans |
| 101 | c3ic9D_ | Alignment | not modelled | 33.7 | 19 | **PDB header:**oxidoreductase<br>**Chain:** D: **PDB Molecule:**dihydrolipoamide dehydrogenase;<br>**PDBTitle:** the structure of dihydrolipoamide dehydrogenase from colwellia2 psychrerythraea 34h. |
| 102 | c2eq8E_ | Alignment | not modelled | 33.3 | 33 | **PDB header:**oxidoreductase<br>**Chain:** E: **PDB Molecule:**pyruvate dehydrogenase complex, dihydrolipoamide<br>**PDBTitle:** crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdp |
| 103 | c3kpgA_ | Alignment | not modelled | 32.5 | 30 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**sulfide-quinone reductase, putative;<br>**PDBTitle:** crystal structure of sulfide:quinone oxidoreductase from2 acidithiobacillus ferrooxidans in complex with decylubiquinone |
| 104 | c3ouzA_ | Alignment | not modelled | 32.3 | 19 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**biotin carboxylase;<br>**PDBTitle:** crystal structure of biotin carboxylase-adp complex from campylobacter2 jejuni |
| 105 | c3rfxB_ | Alignment | not modelled | 32.1 | 16 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**uronate dehydrogenase; |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 105 | c3rfxB_ | | Alignment | not modelled | 32.1 | 16 | **PDBTitle:** crystal structure of uronate dehydrogenase from agrobacterium2 tumefaciens, y136a mutant complexed with nad |
| 106 | c2obnA_ | | Alignment | not modelled | 31.0 | 13 | **PDB header:**unknown function<br>**Chain:** A: **PDB Molecule:**hypothetical protein;<br>**PDBTitle:** crystal structure of a duf1611 family protein (ava_3511) from anabaena2 variabilis atcc 29413 at 2.30 a resolution |
| 107 | c3allA_ | | Alignment | not modelled | 29.6 | 23 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**2-methyl-3-hydroxypyridine-5-carboxylic acid oxygenase;<br>**PDBTitle:** crystal structure of 2-methyl-3-hydroxypyridine-5-carboxylic acid2 oxygenase, mutant y270a |
| 108 | c1xdiA_ | | Alignment | not modelled | 29.3 | 23 | **PDB header:**unknown function<br>**Chain:** A: **PDB Molecule:**rv3303c-lpda;<br>**PDBTitle:** crystal structure of lpda (rv3303c) from mycobacterium tuberculosis |
| 109 | d2hy5b1 | | Alignment | not modelled | 28.9 | 20 | **Fold:**DsrEFH-like<br>**Superfamily:**DsrEFH-like<br>**Family:**DsrEF-like |
| 110 | c2qzsA_ | | Alignment | not modelled | 28.7 | 19 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**glycogen synthase;<br>**PDBTitle:** crystal structure of wild-type e.coli gs in complex with adp2 and glucose(wtgsb) |
| 111 | d1bxka_ | | Alignment | not modelled | 28.1 | 16 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**Tyrosine-dependent oxidoreductases |
| 112 | d1oc2a_ | | Alignment | not modelled | 28.0 | 19 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**Tyrosine-dependent oxidoreductases |
| 113 | c3ezxA_ | | Alignment | not modelled | 27.4 | 17 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**monomethylamine corrinoid protein 1;<br>**PDBTitle:** structure of methanosarcina barkeri monomethylamine2 corrinoid protein |
| 114 | c2zktB_ | | Alignment | not modelled | 27.4 | 16 | **PDB header:**isomerase<br>**Chain:** B: **PDB Molecule:**2,3-bisphosphoglycerate-independent phosphoglycerate<br>**PDBTitle:** structure of ph0037 protein from pyrococcus horikoshii |
| 115 | c3ia7A_ | | Alignment | not modelled | 27.3 | 22 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**calg4;<br>**PDBTitle:** crystal structure of calg4, the calicheamicin glycosyltransferase |
| 116 | d1d4aa_ | | Alignment | not modelled | 27.2 | 17 | **Fold:**Flavodoxin-like<br>**Superfamily:**Flavoproteins<br>**Family:**Quinone reductase |
| 117 | c1ps9A_ | | Alignment | not modelled | 27.1 | 31 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**2,4-dienoyl-coa reductase;<br>**PDBTitle:** the crystal structure and reaction mechanism of e. coli 2,4-2 dienoyl coa reductase |
| 118 | c1v59B_ | | Alignment | not modelled | 25.6 | 30 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**dihydrolipoamide dehydrogenase;<br>**PDBTitle:** crystal structure of yeast lipoamide dehydrogenase2 complexed with nad+ |
| 119 | d1hdoa_ | | Alignment | not modelled | 25.2 | 22 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**Tyrosine-dependent oxidoreductases |
| 120 | c3u9sE_ | | Alignment | not modelled | 24.9 | 14 | **PDB header:**ligase<br>**Chain:** E: **PDB Molecule:**methylcrotonyl-coa carboxylase, alpha-subunit;<br>**PDBTitle:** crystal structure of p. aeruginosa 3-methylcrotonyl-coa carboxylase2 (mcc) 750 kd holoenzyme, coa complex |