# Phyre$^2$

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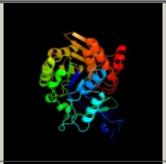
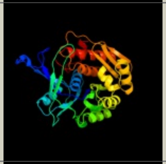
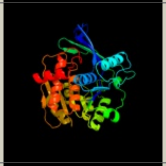
| Email | l.a.kelley@imperial.ac.uk |
| Description | P77493 |
| Date | Thu Jan 5 12:29:52 GMT 2012 |
| Unique Job ID | ea263e994e496873 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c3in1A_ | Alignment |  | 100.0 | 98 | **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 |
| 2 | c3iq0B_ | Alignment |  | 100.0 | 20 | **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 |
| 3 | c3pl2D_ | Alignment |  | 100.0 | 23 | **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 |
| 4 | c2pkkA_ | Alignment |  | 100.0 | 19 | **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 |
| 5 | c2rbcA_ | Alignment |  | 100.0 | 20 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**sugar kinase;<br>**PDBTitle:** crystal structure of a putative ribokinase from agrobacterium2 tumefaciens |
| 6 | c2qcvA_ | Alignment |  | 100.0 | 22 | **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 |
| 7 | c2varB_ | Alignment |  | 100.0 | 20 | **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 |
| 8 | d1rkda_ | Alignment |  | 100.0 | 27 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**Ribokinase-like |
| 9 | c3b1qD_ | Alignment |  | 100.0 | 19 | **PDB header:**transferase<br>**Chain:** D: **PDB Molecule:**ribokinase, putative;<br>**PDBTitle:** structure of burkholderia thailandensis nucleoside kinase (bthnk) in2 complex with inosine |
| 10 | c2c49A_ | Alignment |  | 100.0 | 21 | **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 |
| 11 | c3kzhA_ | Alignment |  | 100.0 | 23 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**probable sugar kinase;<br>**PDBTitle:** crystal structure of a putative sugar kinase from2 clostridium perfringens |

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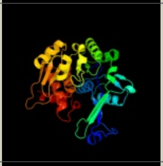
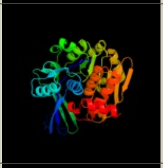
| 12 | d1v19a_ | Alignment |  | 100.0 | 25 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**Ribokinase-like |
| 13 | c2nwhA_ | Alignment |  | 100.0 | 25 | **PDB header:**signaling protein,transferase<br>**Chain:** A: **PDB Molecule:**carbohydrate kinase;<br>**PDBTitle:** carbohydrate kinase from agrobacterium tumefaciens |
| 14 | d2dcna1 | Alignment |  | 100.0 | 18 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**Ribokinase-like |
| 15 | d1vm7a_ | Alignment |  | 100.0 | 28 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**Ribokinase-like |
| 16 | d2fv7a1 | Alignment |  | 100.0 | 22 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**Ribokinase-like |
| 17 | c3go6B_ | Alignment |  | 100.0 | 18 | **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 |
| 18 | d1bx4a_ | Alignment |  | 100.0 | 19 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**Ribokinase-like |
| 19 | c3gbuD_ | Alignment |  | 100.0 | 22 | **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 |
| 20 | c3lkiA_ | Alignment |  | 100.0 | 18 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**fructokinase;<br>**PDBTitle:** crystal structure of fructokinase with bound atp from2 xylella fastidiosa |
| 21 | d1tyya_ | Alignment | not modelled | 100.0 | 22 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**Ribokinase-like |
| 22 | c2absA_ | Alignment | not modelled | 100.0 | 24 | **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 |
| 23 | d2absa1 | Alignment | not modelled | 100.0 | 24 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**Ribokinase-like |
| 24 | c3ktnA_ | Alignment | not modelled | 100.0 | 17 | **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 |
| 25 | d2afba1 | Alignment | not modelled | 100.0 | 17 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**Ribokinase-like |
| 26 | c3i3yB_ | Alignment | not modelled | 100.0 | 24 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**carbohydrate kinase;<br>**PDBTitle:** crystal structure of ribokinase in complex with d-ribose from2 klebsiella pneumoniae |
| 27 | c3cqdB_ | Alignment | not modelled | 100.0 | 17 | **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 |
| 28 | c3looC_ | Alignment | not modelled | 100.0 | 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 |
|  |  |  |  |  |  | **Fold:**Ribokinase-like |

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| 29 | d2f02a1 | Alignment | not modelled | 100.0 | 19 | **Superfamily:**Ribokinase-like<br>**Family:**Ribokinase-like |
| 30 | d2abqa1 | Alignment | not modelled | 100.0 | 22 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**Ribokinase-like |
| 31 | c2xtbA_ | Alignment | not modelled | 100.0 | 21 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**adenosine kinase;<br>**PDBTitle:** crystal structure of trypanosoma brucei rhodesiense2 adenosine kinase complexed with activator |
| 32 | c3kd6B_ | Alignment | not modelled | 100.0 | 23 | **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 |
| 33 | c2jg1C_ | Alignment | not modelled | 100.0 | 18 | **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 |
| 34 | c2jg5B_ | Alignment | not modelled | 100.0 | 15 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**fructose 1-phosphate kinase;<br>**PDBTitle:** crystal structure of a putative phosphofructokinase from2 staphylococcus aureus |
| 35 | c1tz6B_ | Alignment | not modelled | 100.0 | 22 | **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 |
| 36 | c3b3lC_ | Alignment | not modelled | 100.0 | 19 | **PDB header:**transferase<br>**Chain:** C: **PDB Molecule:**ketohexokinase;<br>**PDBTitle:** crystal structures of alternatively-spliced isoforms of human2 ketohexokinase |
| 37 | c3lhxA_ | Alignment | not modelled | 100.0 | 21 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**ketodeoxygluconokinase;<br>**PDBTitle:** crystal structure of a ketodeoxygluconokinase (kdgk) from2 shigella flexneri |
| 38 | c2qhpA_ | Alignment | not modelled | 100.0 | 18 | **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 |
| 39 | d2ajra1 | Alignment | not modelled | 100.0 | 15 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**Ribokinase-like |
| 40 | c3bf5A_ | Alignment | not modelled | 100.0 | 16 | **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 |
| 41 | c3julA_ | Alignment | not modelled | 100.0 | 17 | **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 |
| 42 | c3hj6B_ | Alignment | not modelled | 100.0 | 28 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**fructokinase;<br>**PDBTitle:** structure of halothermothrix orenii fructokinase (frk) |
| 43 | d1vk4a_ | Alignment | not modelled | 100.0 | 17 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**Ribokinase-like |
| 44 | c2ddmA_ | Alignment | not modelled | 99.8 | 19 | **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 |
| 45 | c3mbjA_ | Alignment | not modelled | 99.7 | 15 | **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) |
| 46 | c2i5bC_ | Alignment | not modelled | 99.6 | 16 | **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 |
| 47 | c3ibqA_ | Alignment | not modelled | 99.5 | 20 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**pyridoxal kinase;<br>**PDBTitle:** crystal structure of pyridoxal kinase from lactobacillus2 plantarum in complex with atp |
| 48 | d1vi9a_ | Alignment | not modelled | 99.5 | 16 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**PfkB-like kinase |
| 49 | d1ub0a_ | Alignment | not modelled | 99.5 | 19 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**Thiamin biosynthesis kinases |
| 50 | d1lhpa_ | Alignment | not modelled | 99.5 | 19 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**PfkB-like kinase |
| 51 | d1jxha_ | Alignment | not modelled | 99.3 | 17 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**Thiamin biosynthesis kinases |
| 52 | c3rm5B_ | Alignment | not modelled | 99.3 | 17 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**hydroxymethylpyrimidine/phosphomethylpyrimidine kinase<br>**PDBTitle:** structure of trifunctional thi20 from yeast |
| 53 | c3dzvB_ | Alignment | not modelled | 98.9 | 15 | **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 |

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| 54 | d1kyha_ | Alignment | not modelled | 98.8 | 17 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**YjeF C-terminal domain-like |
| 55 | d1v8aa_ | Alignment | not modelled | 98.6 | 16 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**Thiamin biosynthesis kinases |
| 56 | d1gc5a_ | Alignment | not modelled | 98.6 | 16 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**ADP-specific Phosphofructokinase/Glucokinase |
| 57 | d1l2la_ | Alignment | not modelled | 98.4 | 13 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**ADP-specific Phosphofructokinase/Glucokinase |
| 58 | d1ua4a_ | Alignment | not modelled | 98.4 | 14 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**ADP-specific Phosphofructokinase/Glucokinase |
| 59 | d1ekqa_ | Alignment | not modelled | 98.4 | 11 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**Thiamin biosynthesis kinases |
| 60 | c2r3bA_ | Alignment | not modelled | 98.3 | 15 | **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 |
| 61 | d2ax3a1 | Alignment | not modelled | 98.1 | 13 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**YjeF C-terminal domain-like |
| 62 | c3nm3D_ | Alignment | not modelled | 98.0 | 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 |
| 63 | d1u2xa_ | Alignment | not modelled | 97.8 | 18 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**ADP-specific Phosphofructokinase/Glucokinase |
| 64 | c3drwA_ | Alignment | not modelled | 97.8 | 16 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**adp-specific phosphofructokinase;<br>**PDBTitle:** crystal structure of a phosphofructokinase from pyrococcus2 horikoshii ot3 with amp |
| 65 | c3k5wA_ | Alignment | not modelled | 97.8 | 19 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**carbohydrate kinase;<br>**PDBTitle:** crystal structure of a carbohydrate kinase (yjef family)from2 helicobacter pylori |
| 66 | c2ax3A_ | Alignment | not modelled | 97.8 | 12 | **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 |
| 67 | c3bgkA_ | Alignment | not modelled | 97.5 | 13 | **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 |
| 68 | d3grsa1 | Alignment | not modelled | 87.0 | 28 | **Fold:**FAD/NAD(P)-binding domain<br>**Superfamily:**FAD/NAD(P)-binding domain<br>**Family:**FAD/NAD-linked reductases, N-terminal and central domains |
| 69 | c2zxiC_ | Alignment | not modelled | 86.0 | 38 | **PDB header:**fad-binding protein<br>**Chain:** C: **PDB Molecule:**trna uridine 5-carboxymethylaminomethyl<br>**PDBTitle:** structure of aquifex aeolicus gida in the form ii crystal |
| 70 | c2eq8E_ | Alignment | not modelled | 85.9 | 34 | **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 |
| 71 | c2xdoC_ | Alignment | not modelled | 85.6 | 19 | **PDB header:**oxidoreductase<br>**Chain:** C: **PDB Molecule:**tetx2 protein;<br>**PDBTitle:** structure of the tetracycline degrading monooxygenase tetx2 from2 bacteroides thetaiotaomicron |
| 72 | c1bwcA_ | Alignment | not modelled | 82.9 | 28 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**protein (glutathione reductase);<br>**PDBTitle:** structure of human glutathione reductase complexed with ajoene2 inhibitor and subversive substrate |
| 73 | c3fbsB_ | Alignment | not modelled | 79.4 | 29 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**oxidoreductase;<br>**PDBTitle:** the crystal structure of the oxidoreductase from agrobacterium2 tumefaciens |
| 74 | c2aczA_ | Alignment | not modelled | 76.4 | 44 | **PDB header:**oxidoreductase/electron transport<br>**Chain:** A: **PDB Molecule:**succinate dehydrogenase flavoprotein subunit;<br>**PDBTitle:** complex ii (succinate dehydrogenase) from e. coli with atpenin a52 inhibitor co-crystallized at the ubiquinone binding site |
| 75 | c2i0zA_ | Alignment | not modelled | 72.7 | 32 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**nad(fad)-utilizing dehydrogenases;<br>**PDBTitle:** crystal structure of a fad binding protein from bacillus2 cereus, a putative nad(fad)-utilizing dehydrogenases |
| 76 | c3ctyA_ | Alignment | not modelled | 72.2 | 35 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**thioredoxin reductase;<br>**PDBTitle:** crystal structure of t. acidophilum thioredoxin reductase |
| 77 | c3d8xB_ | Alignment | not modelled | 71.8 | 35 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**thioredoxin reductase 1;<br>**PDBTitle:** crystal structure of saccharomyces cerevisiae nadph dependent2 thioredoxin reductase 1 |
| 78 | d3lada1 | Alignment | not modelled | 69.2 | 48 | **Fold:**FAD/NAD(P)-binding domain<br>**Superfamily:**FAD/NAD(P)-binding domain<br>**Family:**FAD/NAD-linked reductases, N-terminal and central domains |
| 79 | c3ic9D_ | Alignment | not modelled | 68.6 | 28 | **PDB header:**oxidoreductase<br>**Chain:** D: **PDB Molecule:**dihydrolipoamide dehydrogenase; |

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| 79 | c3fc9D_ | Alignment | not modelled | 68.6 | 28 | **PDBTitle:** the structure of dihydrolipoamide dehydrogenase from colwellia2 psychrerythraea 34h. |
| 80 | c3i3lA_ | Alignment | not modelled | 68.3 | 25 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**alkylhalidase cmls;<br>**PDBTitle:** crystal structure of cmls, a flavin-dependent halogenase |
| 81 | c3l8kB_ | Alignment | not modelled | 67.6 | 32 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**dihydrolipoyl dehydrogenase;<br>**PDBTitle:** crystal structure of a dihydrolipoyl dehydrogenase from2 sulfolobus solfataricus |
| 82 | d1neka2 | Alignment | not modelled | 67.4 | 44 | **Fold:**FAD/NAD(P)-binding domain<br>**Superfamily:**FAD/NAD(P)-binding domain<br>**Family:**Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain |
| 83 | c1v59B_ | Alignment | not modelled | 64.9 | 31 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**dihydrolipoamide dehydrogenase;<br>**PDBTitle:** crystal structure of yeast lipoamide dehydrogenase2 complexed with nad+ |
| 84 | c2gqfA_ | Alignment | not modelled | 64.6 | 32 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**hypothetical protein hi0933;<br>**PDBTitle:** crystal structure of flavoprotein hi0933 from haemophilus influenzae2 rd |
| 85 | c3atrA_ | Alignment | not modelled | 63.9 | 38 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**conserved archaeal protein;<br>**PDBTitle:** geranylgeranyl reductase (ggr) from sulfolobus acidocaldarius co-2 crystallized with its ligand |
| 86 | d1dxla1 | Alignment | not modelled | 62.4 | 32 | **Fold:**FAD/NAD(P)-binding domain<br>**Superfamily:**FAD/NAD(P)-binding domain<br>**Family:**FAD/NAD-linked reductases, N-terminal and central domains |
| 87 | d1v59a1 | Alignment | not modelled | 61.9 | 32 | **Fold:**FAD/NAD(P)-binding domain<br>**Superfamily:**FAD/NAD(P)-binding domain<br>**Family:**FAD/NAD-linked reductases, N-terminal and central domains |
| 88 | c3f8rD_ | Alignment | not modelled | 61.2 | 35 | **PDB header:**oxidoreductase<br>**Chain:** D: **PDB Molecule:**thioredoxin reductase (trxb-3);<br>**PDBTitle:** crystal structure of sulfolobus solfataricus thioredoxin2 reductase b3 in complex with two nadp molecules |
| 89 | d1gesa1 | Alignment | not modelled | 59.7 | 29 | **Fold:**FAD/NAD(P)-binding domain<br>**Superfamily:**FAD/NAD(P)-binding domain<br>**Family:**FAD/NAD-linked reductases, N-terminal and central domains |
| 90 | c3rhaA_ | Alignment | not modelled | 59.6 | 38 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**putrescine oxidase;<br>**PDBTitle:** the crystal structure of oxidoreductase from arthrobacter aurescens |
| 91 | d1vdca1 | Alignment | not modelled | 58.9 | 29 | **Fold:**FAD/NAD(P)-binding domain<br>**Superfamily:**FAD/NAD(P)-binding domain<br>**Family:**FAD/NAD-linked reductases, N-terminal and central domains |
| 92 | d1ebda1 | Alignment | not modelled | 58.6 | 26 | **Fold:**FAD/NAD(P)-binding domain<br>**Superfamily:**FAD/NAD(P)-binding domain<br>**Family:**FAD/NAD-linked reductases, N-terminal and central domains |
| 93 | d1lpfa1 | Alignment | not modelled | 58.4 | 42 | **Fold:**FAD/NAD(P)-binding domain<br>**Superfamily:**FAD/NAD(P)-binding domain<br>**Family:**FAD/NAD-linked reductases, N-terminal and central domains |
| 94 | c2hqmB_ | Alignment | not modelled | 57.9 | 26 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**glutathione reductase;<br>**PDBTitle:** crystal structure of glutathione reductase glr1 from the yeast2 saccharomyces cerevisiae |
| 95 | c3crcB_ | Alignment | not modelled | 56.2 | 16 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**protein mazg;<br>**PDBTitle:** crystal structure of escherichia coli mazg, the regulator2 of nutritional stress response |
| 96 | d1h6va1 | Alignment | not modelled | 56.2 | 20 | **Fold:**FAD/NAD(P)-binding domain<br>**Superfamily:**FAD/NAD(P)-binding domain<br>**Family:**FAD/NAD-linked reductases, N-terminal and central domains |
| 97 | c1ojtA_ | Alignment | not modelled | 56.1 | 23 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**surface protein;<br>**PDBTitle:** structure of dihydrolipoamide dehydrogenase |
| 98 | c3dgzA_ | Alignment | not modelled | 55.9 | 26 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**thioredoxin reductase 2;<br>**PDBTitle:** crystal structure of mouse mitochondrial thioredoxin reductase, c-2 terminal 3-residue truncation |
| 99 | c1zkqA_ | Alignment | not modelled | 55.9 | 26 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**thioredoxin reductase 2, mitochondrial;<br>**PDBTitle:** crystal structure of mouse thioredoxin reductase type 2 |
| 100 | c1lvlA_ | Alignment | not modelled | 54.4 | 26 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**dihydrolipoamide dehydrogenase;<br>**PDBTitle:** the refined structure of pseudomonas putida lipoamide dehydrogenase2 complexed with nad+ at 2.45 angstroms resolution |
| 101 | c1ebdB_ | Alignment | not modelled | 54.2 | 26 | **PDB header:**complex (oxidoreductase/transferase)<br>**Chain:** B: **PDB Molecule:**dihydrolipoamide dehydrogenase;<br>**PDBTitle:** dihydrolipoamide dehydrogenase complexed with the binding2 domain of the dihydrolipoamide acetylase |
| 102 | d2i0za1 | Alignment | not modelled | 54.1 | 32 | **Fold:**FAD/NAD(P)-binding domain<br>**Superfamily:**FAD/NAD(P)-binding domain<br>**Family:**HI0933 N-terminal domain-like |
| 103 | c2r4jA_ | Alignment | not modelled | 53.9 | 25 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**aerobic glycerol-3-phosphate dehydrogenase;<br>**PDBTitle:** crystal structure of escherichia coli semet substituted2 glycerol-3-phosphate dehydrogenase in complex with dhap |
| 104 | c1geuA_ | Alignment | not modelled | 53.5 | 29 | **PDB header:**oxidoreductase(flavoenzyme)<br>**Chain:** A: **PDB Molecule:**glutathione reductase;<br>**PDBTitle:** anatomy of an engineered nad-binding site |

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| 105 | d1ryia1 | Alignment | not modelled | 52.3 | 25 | **Fold:**FAD/NAD(P)-binding domain<br>**Superfamily:**FAD/NAD(P)-binding domain<br>**Family:**FAD-linked reductases, N-terminal domain |
| 106 | c3g05B_ | Alignment | not modelled | 51.6 | 39 | **PDB header:**rna binding protein<br>**Chain:** B: **PDB Molecule:**trna uridine 5-carboxymethylaminomethyl modification enzyme<br>**PDBTitle:** crystal structure of n-terminal domain (2-550) of e.coli mnmg |
| 107 | c1yq4A_ | Alignment | not modelled | 49.6 | 36 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**succinate dehydrogenase flavoprotein subunit;<br>**PDBTitle:** avian respiratory complex ii with 3-nitropropionate and ubiquinone |
| 108 | c1qo8A_ | Alignment | not modelled | 48.8 | 29 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**flavocytochrome c3 fumarate reductase;<br>**PDBTitle:** the structure of the open conformation of a flavocytochrome2 c3 fumarate reductase |
| 109 | c1ryiB_ | Alignment | not modelled | 48.0 | 25 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**glycine oxidase;<br>**PDBTitle:** structure of glycine oxidase with bound inhibitor glycolate |
| 110 | c2r9zB_ | Alignment | not modelled | 47.7 | 32 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**glutathione amide reductase;<br>**PDBTitle:** glutathione amide reductase from chromatium gracile |
| 111 | c3lzxB_ | Alignment | not modelled | 45.9 | 19 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**ferredoxin--nadp reductase 2;<br>**PDBTitle:** crystal structure of ferredoxin-nadp+ oxidoreductase from bacillus2 subtilis (form ii) |
| 112 | c3o0hA_ | Alignment | not modelled | 45.8 | 39 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**glutathione reductase;<br>**PDBTitle:** crystal structure of glutathione reductase from bartonella henselae |
| 113 | c2bs3A_ | Alignment | not modelled | 45.8 | 25 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**quinol-fumarate reductase flavoprotein subunit a;<br>**PDBTitle:** glu c180 -> gln variant quinol:fumarate reductase from2 wolinella succinogenes |
| 114 | c1vdcA_ | Alignment | not modelled | 45.7 | 28 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**nadph dependent thioredoxin reductase;<br>**PDBTitle:** structure of nadph dependent thioredoxin reductase |
| 115 | c1f6mF_ | Alignment | not modelled | 45.6 | 23 | **PDB header:**oxidoreductase<br>**Chain:** F: **PDB Molecule:**thioredoxin reductase;<br>**PDBTitle:** crystal structure of a complex between thioredoxin2 reductase, thioredoxin, and the nadp+ analog, aadp+ |
| 116 | d1kf6a2 | Alignment | not modelled | 45.2 | 34 | **Fold:**FAD/NAD(P)-binding domain<br>**Superfamily:**FAD/NAD(P)-binding domain<br>**Family:**Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain |
| 117 | c1kf6A_ | Alignment | not modelled | 43.8 | 35 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**fumarate reductase flavoprotein;<br>**PDBTitle:** e. coli quinol-fumarate reductase with bound inhibitor hqno |
| 118 | c2a87A_ | Alignment | not modelled | 43.3 | 33 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**thioredoxin reductase;<br>**PDBTitle:** crystal structure of m. tuberculosis thioredoxin reductase |
| 119 | c3allA_ | Alignment | not modelled | 43.3 | 16 | **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 |
| 120 | d1k0ia1 | Alignment | not modelled | 42.7 | 29 | **Fold:**FAD/NAD(P)-binding domain<br>**Superfamily:**FAD/NAD(P)-binding domain<br>**Family:**FAD-linked reductases, N-terminal domain |