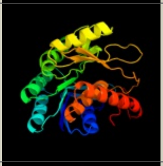
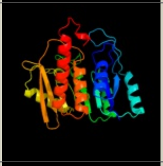
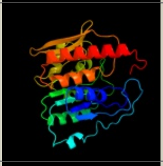
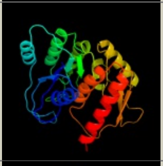
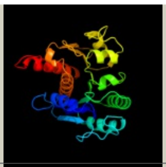
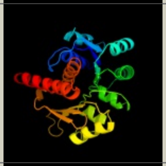
Phyre2

| | |
|---|---|
| Email | l.a.kelley@imperial.ac.uk |
| Description | P76422 |
| Date | Thu Jan 5 12:22:56 GMT 2012 |
| Unique Job ID | 1d59ec61e7df1579 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | d1jxha_ | Alignment |  | 100.0 | 86 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**Thiamin biosynthesis kinases |
| 2 | c3rm5B_ | Alignment |  | 100.0 | 32 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**hydroxymethylpyrimidine/phosphomethylpyrimidine kinase<br>**PDBTitle:** structure of trifunctional thi20 from yeast |
| 3 | c2i5bC_ | Alignment |  | 100.0 | 36 | **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 |
| 4 | d1ub0a_ | Alignment |  | 100.0 | 52 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**Thiamin biosynthesis kinases |
| 5 | c3mbjA_ | Alignment |  | 100.0 | 16 | **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) |
| 6 | 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 |
| 7 | d1vi9a_ | Alignment |  | 100.0 | 16 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**PfkB-like kinase |
| 8 | d1lhpa_ | Alignment |  | 100.0 | 20 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**PfkB-like kinase |
| 9 | c2ddmA_ | Alignment |  | 100.0 | 17 | **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 |
| 10 | d1kyha_ | Alignment |  | 100.0 | 16 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**YjeF C-terminal domain-like |
| 11 | c2r3bA_ | Alignment |  | 100.0 | 19 | **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 |

| | | | | | | |
|---|---|---|---|---|---|---|
| 12 | d2ax3a1 | Alignment |  | 100.0 | 17 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**YjeF C-terminal domain-like |
| 13 | c2ax3A_ | Alignment |  | 100.0 | 17 | **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 |
| 14 | c3bgkA_ | Alignment |  | 100.0 | 16 | **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 |
| 15 | c3k5wA_ | Alignment |  | 100.0 | 17 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**carbohydrate kinase;<br>**PDBTitle:** crystal structure of a carbohydrate kinase (yjef family)from2 helicobacter pylori |
| 16 | c3dzvB_ | Alignment |  | 99.8 | 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 |
| 17 | d1v8aa_ | Alignment |  | 99.8 | 18 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**Thiamin biosynthesis kinases |
| 18 | d1ekqa_ | Alignment |  | 99.8 | 15 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**Thiamin biosynthesis kinases |
| 19 | c2jg1C_ | Alignment |  | 99.8 | 21 | **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 |
| 20 | d2abqa1 | Alignment |  | 99.8 | 20 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**Ribokinase-like |
| 21 | c3kzhA_ | Alignment | not modelled | 99.7 | 20 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**probable sugar kinase;<br>**PDBTitle:** crystal structure of a putative sugar kinase from2 clostridium perfringens |
| 22 | c2jg5B_ | Alignment | not modelled | 99.7 | 20 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**fructose 1-phosphate kinase;<br>**PDBTitle:** crystal structure of a putative phosphofructokinase from2 staphylococcus aureus |
| 23 | c3cqdB_ | Alignment | not modelled | 99.7 | 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 |
| 24 | c3nm3D_ | Alignment | not modelled | 99.7 | 13 | **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 |
| 25 | c2nwhA_ | Alignment | not modelled | 99.7 | 21 | **PDB header:**signaling protein,transferase<br>**Chain:** A: **PDB Molecule:**carbohydrate kinase;<br>**PDBTitle:** carbohydrate kinase from agrobacterium tumefaciens |
| 26 | d2f02a1 | Alignment | not modelled | 99.6 | 19 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**Ribokinase-like |
| 27 | c3looC_ | Alignment | not modelled | 99.6 | 15 | **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 |
| 28 | c2qhpA_ | Alignment | not modelled | 99.6 | 13 | **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 |
| 29 | d1rkda_ | Alignment | not modelled | 99.6 | 23 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**Ribokinase-like |
| 30 | d1bx4a_ | Alignment | not modelled | 99.6 | 13 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**Ribokinase-like |
| 31 | c2xtbA_ | Alignment | not modelled | 99.6 | 11 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**adenosine kinase;<br>**PDBTitle:** crystal structure of trypanosoma brucei rhodesiense2 adenosine kinase complexed with activator |
| 32 | c2qcvA_ | Alignment | not modelled | 99.6 | 16 | **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 |
| 33 | c3pl2D_ | Alignment | not modelled | 99.6 | 15 | **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 |
| 34 | d1vm7a_ | Alignment | not modelled | 99.5 | 17 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**Ribokinase-like |
| 35 | d1v19a_ | Alignment | not modelled | 99.5 | 23 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**Ribokinase-like |
| 36 | c3i3yB_ | Alignment | not modelled | 99.5 | 21 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**carbohydrate kinase;<br>**PDBTitle:** crystal structure of ribokinase in complex with d-ribose from2 klebsiella pneumoniae |
| 37 | c3julA_ | Alignment | not modelled | 99.5 | 19 | **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 |
| 38 | d2afba1 | Alignment | not modelled | 99.5 | 10 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**Ribokinase-like |
| 39 | c3go6B_ | Alignment | not modelled | 99.5 | 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 |
| 40 | c2c49A_ | Alignment | not modelled | 99.5 | 12 | **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 |
| 41 | c3iq0B_ | Alignment | not modelled | 99.5 | 16 | **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 |
| 42 | d2absa1 | Alignment | not modelled | 99.5 | 14 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**Ribokinase-like |
| 43 | c2absA_ | Alignment | not modelled | 99.5 | 14 | **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 | c3ktnA_ | Alignment | not modelled | 99.5 | 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 |
| 45 | c2pkkA_ | Alignment | not modelled | 99.5 | 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 |
| 46 | c3b1qD_ | Alignment | not modelled | 99.5 | 20 | **PDB header:**transferase<br>**Chain:** D: **PDB Molecule:**ribokinase, putative;<br>**PDBTitle:** structure of burkholderia thailandensis nucleoside kinase (bthnk) in2 complex with inosine |
| 47 | c2varB_ | Alignment | not modelled | 99.4 | 13 | **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 |
| 48 | c3in1A_ | Alignment | not modelled | 99.4 | 18 | **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 |
| 49 | d1tyya_ | Alignment | not modelled | 99.4 | 21 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**Ribokinase-like |
| 50 | d2ajra1 | Alignment | not modelled | 99.4 | 11 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**Ribokinase-like |
| 51 | c2rbcA_ | Alignment | not modelled | 99.4 | 12 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**sugar kinase;<br>**PDBTitle:** crystal structure of a putative ribokinase from agrobacterium2 tumefaciens |
| 52 | d1vk4a_ | Alignment | not modelled | 99.4 | 18 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**Ribokinase-like |
| 53 | d2fv7a1 | Alignment | not modelled | 99.4 | 18 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**Ribokinase-like |
| | | | | | | **Fold:**Ribokinase-like |

| | | | | | | |
|---|---|---|---|---|---|---|
| 54 | d2dcna1 | Alignment | not modelled | 99.3 | 9 | **Superfamily:**Ribokinase-like<br>**Family:**Ribokinase-like |
| 55 | c3lhxA_ | Alignment | not modelled | 99.3 | 14 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**ketodeoxygluconokinase;<br>**PDBTitle:** crystal structure of a ketodeoxygluconokinase (kdgk) from2 shigella flexneri |
| 56 | c3bf5A_ | Alignment | not modelled | 99.2 | 13 | **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 | c1tz6B_ | Alignment | not modelled | 99.2 | 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 |
| 58 | c3gbuD_ | Alignment | not modelled | 99.2 | 8 | **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 | c3hj6B_ | Alignment | not modelled | 99.2 | 13 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**fructokinase;<br>**PDBTitle:** structure of halothermothrix orenii fructokinase (frk) |
| 60 | c3kd6B_ | Alignment | not modelled | 99.2 | 21 | **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 |
| 61 | c3b3lC_ | Alignment | not modelled | 99.2 | 14 | **PDB header:**transferase<br>**Chain:** C: **PDB Molecule:**ketohexokinase;<br>**PDBTitle:** crystal structures of alternatively-spliced isoforms of human2 ketohexokinase |
| 62 | c3lkiA_ | Alignment | not modelled | 99.1 | 20 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**fructokinase;<br>**PDBTitle:** crystal structure of fructokinase with bound atp from2 xylella fastidiosa |
| 63 | d2nu7b1 | Alignment | not modelled | 71.3 | 14 | **Fold:**Flavodoxin-like<br>**Superfamily:**Succinyl-CoA synthetase domains<br>**Family:**Succinyl-CoA synthetase domains |
| 64 | d1a9xa4 | Alignment | not modelled | 67.2 | 13 | **Fold:**PreATP-grasp domain<br>**Superfamily:**PreATP-grasp domain<br>**Family:**BC N-terminal domain-like |
| 65 | d1a9xa3 | Alignment | not modelled | 40.3 | 18 | **Fold:**PreATP-grasp domain<br>**Superfamily:**PreATP-grasp domain<br>**Family:**BC N-terminal domain-like |
| 66 | c2hunB_ | Alignment | not modelled | 36.5 | 17 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**336aa long hypothetical dtdp-glucose 4,6-dehydratase;<br>**PDBTitle:** crystal structure of hypothetical protein ph0414 from pyrococcus2 horikoshii ot3 |
| 67 | d1a2za_ | Alignment | not modelled | 32.3 | 15 | **Fold:**Phosphorylase/hydrolase-like<br>**Superfamily:**Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase)<br>**Family:**Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase) |
| 68 | c1zxxA_ | Alignment | not modelled | 28.0 | 32 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**6-phosphofructokinase;<br>**PDBTitle:** the crystal structure of phosphofructokinase from lactobacillus2 delbrueckii |
| 69 | c3i3lA_ | Alignment | not modelled | 26.6 | 34 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**alkylhalidase cmls;<br>**PDBTitle:** crystal structure of cmls, a flavin-dependent halogenase |
| 70 | d1su0b_ | Alignment | not modelled | 25.3 | 19 | **Fold:**SufE/NifU<br>**Superfamily:**SufE/NifU<br>**Family:**NifU/IscU domain |
| 71 | d4pfka_ | Alignment | not modelled | 25.0 | 32 | **Fold:**Phosphofructokinase<br>**Superfamily:**Phosphofructokinase<br>**Family:**Phosphofructokinase |
| 72 | c3lwbA_ | Alignment | not modelled | 24.4 | 17 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**d-alanine--d-alanine ligase;<br>**PDBTitle:** crystal structure of apo d-alanine:d-alanine ligase (ddl) from2 mycobacterium tuberculosis |
| 73 | d1iu8a_ | Alignment | not modelled | 23.8 | 24 | **Fold:**Phosphorylase/hydrolase-like<br>**Superfamily:**Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase)<br>**Family:**Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase) |
| 74 | c3d3kD_ | Alignment | not modelled | 22.4 | 14 | **PDB header:**protein binding<br>**Chain:** D: **PDB Molecule:**enhancer of mrna-decapping protein 3;<br>**PDBTitle:** crystal structure of human edc3p |
| 75 | c2ys6A_ | Alignment | not modelled | 20.5 | 16 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**phosphoribosylglycinamide synthetase;<br>**PDBTitle:** crystal structure of gar synthetase from geobacillus kaustophilus |
| 76 | d1eucb1 | Alignment | not modelled | 19.7 | 14 | **Fold:**Flavodoxin-like<br>**Superfamily:**Succinyl-CoA synthetase domains<br>**Family:**Succinyl-CoA synthetase domains |
| 77 | c2gacD_ | Alignment | not modelled | 18.9 | 12 | **PDB header:**hydrolase<br>**Chain:** D: **PDB Molecule:**glycosylasparaginase;<br>**PDBTitle:** t152c mutant glycosylasparaginase from flavobacterium2 meningosepticum |
| 78 | c3d3jA_ | Alignment | not modelled | 18.6 | 16 | **PDB header:**protein binding<br>**Chain:** A: **PDB Molecule:**enhancer of mrna-decapping protein 3;<br>**PDBTitle:** crystal structure of human edc3p |
| 79 | d1pfka_ | Alignment | not modelled | 18.6 | 24 | **Fold:**Phosphofructokinase<br>**Superfamily:**Phosphofructokinase<br>**Family:**Phosphofructokinase |

| | | | | | | |
|---|---|---|---|---|---|---|
| 80 | c2nu9E_ | Alignment | not modelled | 17.6 | 16 | **PDB header:**ligase<br>**Chain:** E: **PDB Molecule:**succinyl-coa synthetase beta chain;<br>**PDBTitle:** c123at mutant of e. coli succinyl-coa synthetase2 orthorhombic crystal form |
| 81 | d2gtaa1 | Alignment | not modelled | 16.9 | 7 | **Fold:**all-alpha NTP pyrophosphatases<br>**Superfamily:**all-alpha NTP pyrophosphatases<br>**Family:**MazG-like |
| 82 | d2gtad1 | Alignment | not modelled | 15.2 | 7 | **Fold:**all-alpha NTP pyrophosphatases<br>**Superfamily:**all-alpha NTP pyrophosphatases<br>**Family:**MazG-like |
| 83 | d3adka_ | Alignment | not modelled | 14.4 | 16 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**Nucleotide and nucleoside kinases |
| 84 | d1gc5a_ | Alignment | not modelled | 13.5 | 24 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**ADP-specific Phosphofructokinase/Glucokinase |
| 85 | c3lp8A_ | Alignment | not modelled | 12.8 | 15 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**phosphoribosylamine-glycine ligase;<br>**PDBTitle:** crystal structure of phosphoribosylamine-glycine ligase from2 ehrlichia chaffeensis |
| 86 | d1xjsa_ | Alignment | not modelled | 12.2 | 15 | **Fold:**SufE/NifU<br>**Superfamily:**SufE/NifU<br>**Family:**NifU/IscU domain |
| 87 | c3crcB_ | Alignment | not modelled | 12.0 | 20 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**protein mazg;<br>**PDBTitle:** crystal structure of escherichia coli mazg, the regulator2 of nutritional stress response |
| 88 | c3kljA_ | Alignment | not modelled | 11.9 | 23 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**nad(fad)-dependent dehydrogenase, nirb-family (n-terminal<br>**PDBTitle:** crystal structure of nadh:rubredoxin oxidoreductase from clostridium2 acetobutylicum |
| 89 | c3e18A_ | Alignment | not modelled | 11.8 | 12 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**oxidoreductase;<br>**PDBTitle:** crystal structure of nad-binding protein from listeria innocua |
| 90 | c1qr6A_ | Alignment | not modelled | 11.2 | 10 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**malic enzyme 2;<br>**PDBTitle:** human mitochondrial nad(p)-dependent malic enzyme |
| 91 | c1apzB_ | Alignment | not modelled | 11.1 | 14 | **PDB header:**complex (hydrolase/peptide)<br>**Chain:** B: **PDB Molecule:**aspartylglucosaminidase;<br>**PDBTitle:** human aspartylglucosaminidase complex with reaction product |
| 92 | c3atrA_ | Alignment | not modelled | 11.0 | 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 |
| 93 | d1auga_ | Alignment | not modelled | 11.0 | 16 | **Fold:**Phosphorylase/hydrolase-like<br>**Superfamily:**Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase)<br>**Family:**Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase) |
| 94 | c3tqtB_ | Alignment | not modelled | 10.5 | 13 | **PDB header:**ligase<br>**Chain:** B: **PDB Molecule:**d-alanine--d-alanine ligase;<br>**PDBTitle:** structure of the d-alanine-d-alanine ligase from coxiella burnetii |
| 95 | d1krwa_ | Alignment | not modelled | 10.0 | 22 | **Fold:**Flavodoxin-like<br>**Superfamily:**CheY-like<br>**Family:**CheY-related |
| 96 | c3e5nA_ | Alignment | not modelled | 10.0 | 14 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**d-alanine-d-alanine ligase a;<br>**PDBTitle:** crystal strucutre of d-alanine-d-alanine ligase from2 xanthomonas oryzae pv. oryzae kacc10331 |
| 97 | c2xdoC_ | Alignment | not modelled | 10.0 | 22 | **PDB header:**oxidoreductase<br>**Chain:** C: **PDB Molecule:**tetx2 protein;<br>**PDBTitle:** structure of the tetracycline degrading monooxygenase tetx2 from2 bacteroides thetaiotaomicron |
| 98 | c1txlA_ | Alignment | not modelled | 9.8 | 46 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**metal-binding protein yoda;<br>**PDBTitle:** crystal structure of metal-binding protein yoda from e.2 coli, pfam duf149 |
| 99 | d1txla_ | Alignment | not modelled | 9.8 | 46 | **Fold:**Lipocalins<br>**Superfamily:**Lipocalins<br>**Family:**Hypothetical protein YodA |