# Phyre2

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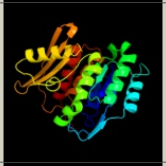
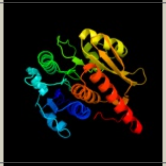
| Email | l.a.kelley@imperial.ac.uk |
| Description | P40191 |
| Date | Thu Jan 5 12:01:12 GMT 2012 |
| Unique Job ID | 9c035281fd14aac6 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | d1vi9a_ | Alignment |  | 100.0 | 27 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**PfkB-like kinase |
| 2 | d1lhpa_ | Alignment |  | 100.0 | 28 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**PfkB-like kinase |
| 3 | c2ddmA_ | Alignment |  | 100.0 | 100 | **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 |
| 4 | c3mbjA_ | Alignment |  | 100.0 | 25 | **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) |
| 5 | c3ibqA_ | Alignment |  | 100.0 | 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 |
| 6 | c3rm5B_ | Alignment |  | 100.0 | 19 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**hydroxymethylpyrimidine/phosphomethylpyrimidine kinase<br>**PDBTitle:** structure of trifunctional thi20 from yeast |
| 7 | c2i5bC_ | Alignment |  | 100.0 | 20 | **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 |
| 8 | d1ub0a_ | Alignment |  | 100.0 | 22 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**Thiamin biosynthesis kinases |
| 9 | d1jxha_ | Alignment |  | 100.0 | 18 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**Thiamin biosynthesis kinases |
| 10 | d1kyha_ | Alignment |  | 99.9 | 15 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**YjeF C-terminal domain-like |
| 11 | c2r3bA_ | Alignment |  | 99.9 | 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 |

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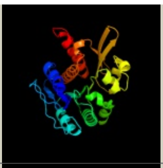
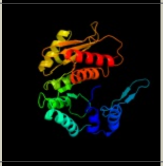
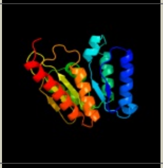
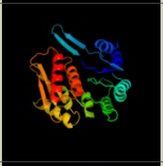
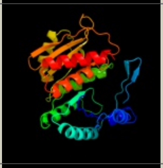
| 12 | d2ax3a1 | Alignment |  | 99.9 | 14 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**YjeF C-terminal domain-like |
| 13 | c2jg5B_ | Alignment |  | 99.9 | 16 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**fructose 1-phosphate kinase;<br>**PDBTitle:** crystal structure of a putative phosphofructokinase from2 staphylococcus aureus |
| 14 | d2abqa1 | Alignment |  | 99.9 | 21 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**Ribokinase-like |
| 15 | c3dzvB_ | Alignment |  | 99.9 | 20 | **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 |
| 16 | c3cqdB_ | Alignment |  | 99.8 | 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 |
| 17 | d2f02a1 | Alignment |  | 99.8 | 14 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**Ribokinase-like |
| 18 | c3bgkA_ | Alignment |  | 99.8 | 14 | **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 |
| 19 | c2jg1C_ | Alignment |  | 99.8 | 13 | **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 | d1v8aa_ | Alignment |  | 99.8 | 14 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**Thiamin biosynthesis kinases |
| 21 | d1rkda_ | Alignment | not modelled | 99.8 | 21 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**Ribokinase-like |
| 22 | c2ax3A_ | Alignment | not modelled | 99.8 | 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 |
| 23 | c3pl2D_ | Alignment | not modelled | 99.8 | 16 | **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 |
| 24 | c3kzhA_ | Alignment | not modelled | 99.8 | 19 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**probable sugar kinase;<br>**PDBTitle:** crystal structure of a putative sugar kinase from2 clostridium perfringens |
| 25 | c2xtbA_ | Alignment | not modelled | 99.8 | 17 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**adenosine kinase;<br>**PDBTitle:** crystal structure of trypanosoma brucei rhodesiense2 adenosine kinase complexed with activator |
| 26 | c3looC_ | Alignment | not modelled | 99.8 | 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 |
| 27 | c2qcvA_ | Alignment | not modelled | 99.8 | 13 | **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 |
| | | | | | | **PDB header:**transferase |

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| 28 | c3iq0B_ | Alignment | not modelled | 99.8 | 17 | **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 |
| 29 | d1bx4a_ | Alignment | not modelled | 99.7 | 12 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**Ribokinase-like |
| 30 | c2qhpA_ | Alignment | not modelled | 99.7 | 19 | **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 |
| 31 | c3ktnA_ | Alignment | not modelled | 99.7 | 16 | **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 |
| 32 | d2afba1 | Alignment | not modelled | 99.7 | 15 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**Ribokinase-like |
| 33 | d1v19a_ | Alignment | not modelled | 99.7 | 16 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**Ribokinase-like |
| 34 | c3b1qD_ | Alignment | not modelled | 99.7 | 17 | **PDB header:**transferase<br>**Chain:** D: **PDB Molecule:**ribokinase, putative;<br>**PDBTitle:** structure of burkholderia thailandensis nucleoside kinase (bthnk) in2 complex with inosine |
| 35 | c2pkkA_ | Alignment | not modelled | 99.7 | 17 | **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 |
| 36 | c3nm3D_ | Alignment | not modelled | 99.7 | 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 |
| 37 | d1ekqa_ | Alignment | not modelled | 99.7 | 14 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**Thiamin biosynthesis kinases |
| 38 | c3in1A_ | Alignment | not modelled | 99.7 | 20 | **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 |
| 39 | c3julA_ | Alignment | not modelled | 99.7 | 16 | **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 |
| 40 | c3lhxA_ | Alignment | not modelled | 99.7 | 16 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**ketodeoxygluconokinase;<br>**PDBTitle:** crystal structure of a ketodeoxygluconokinase (kdgk) from2 shigella flexneri |
| 41 | c2nwhA_ | Alignment | not modelled | 99.7 | 16 | **PDB header:**signaling protein,transferase<br>**Chain:** A: **PDB Molecule:**carbohydrate kinase;<br>**PDBTitle:** carbohydrate kinase from agrobacterium tumefaciens |
| 42 | c2c49A_ | Alignment | not modelled | 99.7 | 16 | **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 |
| 43 | c2absA_ | Alignment | not modelled | 99.7 | 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 | d2absa1 | Alignment | not modelled | 99.7 | 14 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**Ribokinase-like |
| 45 | d2ajra1 | Alignment | not modelled | 99.7 | 15 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**Ribokinase-like |
| 46 | d1tyya_ | Alignment | not modelled | 99.7 | 16 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**Ribokinase-like |
| 47 | d1vm7a_ | Alignment | not modelled | 99.6 | 20 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**Ribokinase-like |
| 48 | d2fv7a1 | Alignment | not modelled | 99.6 | 21 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**Ribokinase-like |
| 49 | d2dcna1 | Alignment | not modelled | 99.6 | 14 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**Ribokinase-like |
| 50 | c2varB_ | Alignment | not modelled | 99.6 | 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 |
| 51 | c3go6B_ | Alignment | not modelled | 99.6 | 20 | **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 |
| 52 | c1tz6B_ | Alignment | not modelled | 99.6 | 15 | **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 |
| 53 | c3k5wA_ | Alignment | not modelled | 99.6 | 19 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**carbohydrate kinase;<br>**PDBTitle:** crystal structure of a carbohydrate kinase (yjef family)from2 helicobacter pylori |
| | | | | | | **PDB header:**transferase |

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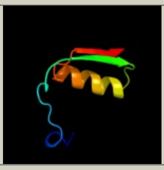
| 54 | c3kd6B_ | Alignment | not modelled | 99.6 | 15 | **Chain:** B: **PDB Molecule:**carbohydrate kinase, pfkb family;<br>**PDBTitle:** crystal structure of nucleoside kinase from chlorobium tepidum in2 complex with amp |
| 55 | c2rbcA_ | Alignment | not modelled | 99.6 | 17 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**sugar kinase;<br>**PDBTitle:** crystal structure of a putative ribokinase from agrobacterium2 tumefaciens |
| 56 | d1vk4a_ | Alignment | not modelled | 99.6 | 17 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**Ribokinase-like |
| 57 | c3i3yB_ | Alignment | not modelled | 99.6 | 17 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**carbohydrate kinase;<br>**PDBTitle:** crystal structure of ribokinase in complex with d-ribose from2 klebsiella pneumoniae |
| 58 | c3bf5A_ | Alignment | not modelled | 99.5 | 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 |
| 59 | c3b3lC_ | Alignment | not modelled | 99.5 | 19 | **PDB header:**transferase<br>**Chain:** C: **PDB Molecule:**ketohexokinase;<br>**PDBTitle:** crystal structures of alternatively-spliced isoforms of human2 ketohexokinase |
| 60 | c3hj6B_ | Alignment | not modelled | 99.5 | 16 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**fructokinase;<br>**PDBTitle:** structure of halothermothrix orenii fructokinase (frk) |
| 61 | c3gbuD_ | Alignment | not modelled | 99.5 | 14 | **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 |
| 62 | c3lkiA_ | Alignment | not modelled | 99.3 | 12 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**fructokinase;<br>**PDBTitle:** crystal structure of fructokinase with bound atp from2 xylella fastidiosa |
| 63 | d2g0ta1 | Alignment | not modelled | 89.4 | 15 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**Nitrogenase iron protein-like |
| 64 | d1gc5a_ | Alignment | not modelled | 86.2 | 17 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**ADP-specific Phosphofructokinase/Glucokinase |
| 65 | c2obnA_ | Alignment | not modelled | 80.0 | 16 | **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 |
| 66 | d1ua4a_ | Alignment | not modelled | 75.9 | 15 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**ADP-specific Phosphofructokinase/Glucokinase |
| 67 | d1l2la_ | Alignment | not modelled | 68.4 | 11 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**ADP-specific Phosphofructokinase/Glucokinase |
| 68 | c1y80A_ | Alignment | not modelled | 64.3 | 15 | **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 |
| 69 | d1u2xa_ | Alignment | not modelled | 59.2 | 15 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**ADP-specific Phosphofructokinase/Glucokinase |
| 70 | d1ps9a3 | Alignment |  | 55.3 | 16 | **Fold:**Nucleotide-binding domain<br>**Superfamily:**Nucleotide-binding domain<br>**Family:**N-terminal domain of adrenodoxin reductase-like |
| 71 | d1a9xa3 | Alignment | not modelled | 55.2 | 22 | **Fold:**PreATP-grasp domain<br>**Superfamily:**PreATP-grasp domain<br>**Family:**BC N-terminal domain-like |
| 72 | c3d8xB_ | Alignment | not modelled | 49.7 | 6 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**thioredoxin reductase 1;<br>**PDBTitle:** crystal structure of saccharomyces cerevisiae nadph dependent2 thioredoxin reductase 1 |
| 73 | c2bcpA_ | Alignment | not modelled | 49.6 | 18 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**nadh oxidase;<br>**PDBTitle:** structural analysis of streptococcus pyogenes nadh oxidase:2 c44s nox with azide |
| 74 | c3ezxA_ | Alignment | not modelled | 43.7 | 13 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**monomethylamine corrinoid protein 1;<br>**PDBTitle:** structure of methanosarcina barkeri monomethylamine2 corrinoid protein |
| 75 | c1zu4A_ | Alignment | not modelled | 37.6 | 10 | **PDB header:**protein transport<br>**Chain:** A: **PDB Molecule:**ftsy;<br>**PDBTitle:** crystal structure of ftsy from mycoplasma mycoides- space2 group p21212 |
| 76 | d1eucb1 | Alignment | not modelled | 37.5 | 16 | **Fold:**Flavodoxin-like<br>**Superfamily:**Succinyl-CoA synthetase domains<br>**Family:**Succinyl-CoA synthetase domains |
| 77 | c3drwA_ | Alignment | not modelled | 36.0 | 15 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**adp-specific phosphofructokinase;<br>**PDBTitle:** crystal structure of a phosphofructokinase from pyrococcus2 horikoshii ot3 with amp |
| 78 | d1su0b_ | Alignment | not modelled | 35.6 | 21 | **Fold:**SufE/NifU<br>**Superfamily:**SufE/NifU<br>**Family:**NifU/IscU domain |
| 79 | c2ejcA_ | Alignment | not modelled | 33.9 | 13 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**pantoate--beta-alanine ligase;<br>**PDBTitle:** crystal structure of pantoate--beta-alanine ligase (panc)2 |

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| | | | | | | from thermotoga maritima |
| 80 | d1vcha1 | Alignment | not modelled | 30.2 | 21 | **Fold:**PRTase-like<br>**Superfamily:**PRTase-like<br>**Family:**Phosphoribosyltransferases (PRTases) |
| 81 | c1ps9A_ | Alignment | not modelled | 29.1 | 16 | **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 |
| 82 | d1s8na_ | Alignment | not modelled | 29.1 | 10 | **Fold:**Flavodoxin-like<br>**Superfamily:**CheY-like<br>**Family:**CheY-related |
| 83 | d2b7oa1 | Alignment | not modelled | 27.3 | 14 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Aldolase<br>**Family:**Class-II DAHP synthetase |
| 84 | c3r89A_ | Alignment | not modelled | 26.0 | 19 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**orotidine 5'-phosphate decarboxylase;<br>**PDBTitle:** crystal structure of orotidine 5-phosphate decarboxylase from2 anaerococcus prevotii dsm 20548 |
| 85 | c3rhtB_ | Alignment | not modelled | 25.8 | 16 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**(gatase1)-like protein;<br>**PDBTitle:** crystal structure of type 1 glutamine amidotransferase (gatase1)-like2 protein from planctomyces limnophilus |
| 86 | d1ihoa_ | Alignment | not modelled | 25.8 | 14 | **Fold:**Adenine nucleotide alpha hydrolase-like<br>**Superfamily:**Nucleotidylyl transferase<br>**Family:**Pantothenate synthetase (Pantoate-beta-alanine ligase, PanC) |
| 87 | c3iuuA_ | Alignment | not modelled | 25.1 | 18 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**putative metallopeptidase;<br>**PDBTitle:** crystal structure of putative metallopeptidase (yp_676511.1) from2 mesorhizobium sp. bnc1 at 2.13 a resolution |
| 88 | d2nu7b1 | Alignment | not modelled | 25.0 | 14 | **Fold:**Flavodoxin-like<br>**Superfamily:**Succinyl-CoA synthetase domains<br>**Family:**Succinyl-CoA synthetase domains |
| 89 | c1vmaA_ | Alignment | not modelled | 24.9 | 11 | **PDB header:**protein transport<br>**Chain:** A: **PDB Molecule:**cell division protein ftsy;<br>**PDBTitle:** crystal structure of cell division protein ftsy (tm0570) from2 thermotoga maritima at 1.60 a resolution |
| 90 | c2x5fB_ | Alignment | not modelled | 24.7 | 28 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**aspartate_tyrosine_phenylalanine pyridoxal-5'<br>**PDBTitle:** crystal structure of the methicillin-resistant2 staphylococcus aureus sar2028, an3 aspartate_tyrosine_phenylalanine pyridoxal-5'-phosphate4 dependent aminotransferase |
| 91 | d1fuia2 | Alignment | not modelled | 24.2 | 20 | **Fold:**FucI/AraA N-terminal and middle domains<br>**Superfamily:**FucI/AraA N-terminal and middle domains<br>**Family:**L-fucose isomerase, N-terminal and second domains |
| 92 | d1z7da1 | Alignment | not modelled | 24.1 | 13 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**GABA-aminotransferase-like |
| 93 | c3euaD_ | Alignment | not modelled | 23.8 | 10 | **PDB header:**isomerase<br>**Chain:** D: **PDB Molecule:**putative fructose-aminoacid-6-phosphate deglycase;<br>**PDBTitle:** crystal structure of a putative phosphosugar isomerase (bsu32610) from2 bacillus subtilis at 1.90 a resolution |
| 94 | c3ag5A_ | Alignment | not modelled | 22.5 | 16 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**pantothenate synthetase;<br>**PDBTitle:** crystal structure of pantothenate synthetase from staphylococcus2 aureus |
| 95 | d2gtad1 | Alignment | not modelled | 22.3 | 19 | **Fold:**all-alpha NTP pyrophosphatases<br>**Superfamily:**all-alpha NTP pyrophosphatases<br>**Family:**MazG-like |
| 96 | c1djnB_ | Alignment | not modelled | 22.2 | 20 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**trimethylamine dehydrogenase;<br>**PDBTitle:** structural and biochemical characterization of recombinant wild type2 trimethylamine dehydrogenase from methylophilus methylotrophus (sp.3 w3a1) |
| 97 | c2yxbA_ | Alignment | not modelled | 21.4 | 12 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**coenzyme b12-dependent mutase;<br>**PDBTitle:** crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix |
| 98 | c3mxtA_ | Alignment | not modelled | 21.3 | 18 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**pantothenate synthetase;<br>**PDBTitle:** crystal structure of pantoate-beta-alanine ligase from campylobacter2 jejuni |
| 99 | c2gacD_ | Alignment | not modelled | 20.7 | 15 | **PDB header:**hydrolase<br>**Chain:** D: **PDB Molecule:**glycosylasparaginase;<br>**PDBTitle:** t152c mutant glycosylasparaginase from flavobacterium2 meningosepticum |