Phyre$^2$

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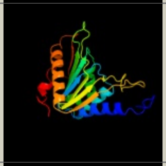
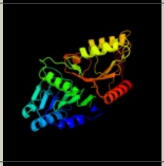
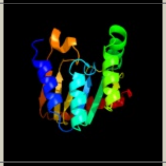
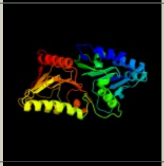
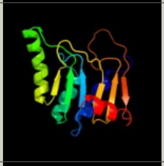
| Email | l.a.kelley@imperial.ac.uk |
| Description | P75919 |
| Date | Thu Jan 5 12:16:03 GMT 2012 |
| Unique Job ID | c8eb5f8ce3b5b1b6 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c1v0sA_ | Alignment |  | 100.0 | 15 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**phospholipase d;<br>**PDBTitle:** uninhibited form of phospholipase d from streptomyces sp.2 strain pmf |
| 2 | c3hsiC_ | Alignment |  | 100.0 | 18 | **PDB header:**transferase<br>**Chain:** C: **PDB Molecule:**phosphatidylserine synthase;<br>**PDBTitle:** crystal structure of phosphatidylserine synthase haemophilus2 influenzae rd kw20 |
| 3 | d1v0wa1 | Alignment |  | 100.0 | 15 | **Fold:**Phospholipase D/nuclease<br>**Superfamily:**Phospholipase D/nuclease<br>**Family:**Phospholipase D |
| 4 | c1xdoB_ | Alignment |  | 100.0 | 18 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**polyphosphate kinase;<br>**PDBTitle:** crystal structure of escherichia coli polyphosphate kinase |
| 5 | d1v0wa2 | Alignment |  | 99.9 | 18 | **Fold:**Phospholipase D/nuclease<br>**Superfamily:**Phospholipase D/nuclease<br>**Family:**Phospholipase D |
| 6 | d1xdpa3 | Alignment |  | 99.9 | 20 | **Fold:**Phospholipase D/nuclease<br>**Superfamily:**Phospholipase D/nuclease<br>**Family:**Polyphosphate kinase C-terminal domain |
| 7 | d1byra_ | Alignment |  | 99.9 | 19 | **Fold:**Phospholipase D/nuclease<br>**Superfamily:**Phospholipase D/nuclease<br>**Family:**Nuclease |
| 8 | c2o8rA_ | Alignment |  | 99.8 | 18 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**polyphosphate kinase;<br>**PDBTitle:** crystal structure of polyphosphate kinase from2 porphyromonas gingivalis |
| 9 | d2o8ra3 | Alignment |  | 98.9 | 16 | **Fold:**Phospholipase D/nuclease<br>**Superfamily:**Phospholipase D/nuclease<br>**Family:**Polyphosphate kinase C-terminal domain |
| 10 | d1xdpa4 | Alignment |  | 98.6 | 14 | **Fold:**Phospholipase D/nuclease<br>**Superfamily:**Phospholipase D/nuclease<br>**Family:**Polyphosphate kinase C-terminal domain |
| 11 | d2o8ra4 | Alignment |  | 98.3 | 17 | **Fold:**Phospholipase D/nuclease<br>**Superfamily:**Phospholipase D/nuclease<br>**Family:**Polyphosphate kinase C-terminal domain |

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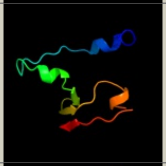
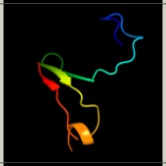
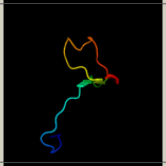
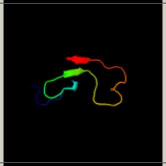
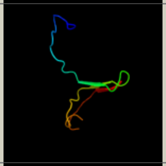
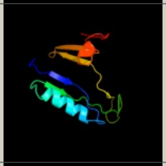
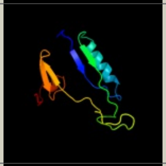
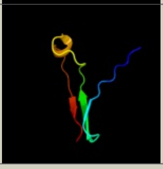
| 12 | c2c1lA_ | Alignment |  | 97.2 | 22 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**restriction endonuclease;<br>**PDBTitle:** structure of the bfii restriction endonuclease |
| 13 | d1jy1a2 | Alignment |  | 96.5 | 23 | **Fold:**Phospholipase D/nuclease<br>**Superfamily:**Phospholipase D/nuclease<br>**Family:**Tyrosyl-DNA phosphodiesterase TDP1 |
| 14 | c1nopB_ | Alignment |  | 96.2 | 28 | **PDB header:**hydrolase/dna<br>**Chain:** B: **PDB Molecule:**tyrosyl-dna phosphodiesterase 1;<br>**PDBTitle:** crystal structure of human tyrosyl-dna phosphodiesterase2 (tdp1) in complex with vanadate, dna and a human3 topoisomerase i-derived peptide |
| 15 | d1q32a2 | Alignment |  | 95.9 | 20 | **Fold:**Phospholipase D/nuclease<br>**Superfamily:**Phospholipase D/nuclease<br>**Family:**Tyrosyl-DNA phosphodiesterase TDP1 |
| 16 | c1q32C_ | Alignment |  | 95.7 | 20 | **PDB header:**replication,transcription,hydrolase<br>**Chain:** C: **PDB Molecule:**tyrosyl-dna phosphodiesterase;<br>**PDBTitle:** crystal structure analysis of the yeast tyrosyl-dna2 phosphodiesterase |
| 17 | c3sq3C_ | Alignment |  | 95.0 | 20 | **PDB header:**hydrolase<br>**Chain:** C: **PDB Molecule:**tyrosyl-dna phosphodiesterase 1;<br>**PDBTitle:** crystal structure analysis of the yeast tyrosyl-dna phosphodiesterase2 h182a mutant |
| 18 | d1qzqa1 | Alignment |  | 86.2 | 13 | **Fold:**Phospholipase D/nuclease<br>**Superfamily:**Phospholipase D/nuclease<br>**Family:**Tyrosyl-DNA phosphodiesterase TDP1 |
| 19 | d1jy1a1 | Alignment |  | 85.3 | 13 | **Fold:**Phospholipase D/nuclease<br>**Superfamily:**Phospholipase D/nuclease<br>**Family:**Tyrosyl-DNA phosphodiesterase TDP1 |
| 20 | d1q32a1 | Alignment |  | 68.2 | 26 | **Fold:**Phospholipase D/nuclease<br>**Superfamily:**Phospholipase D/nuclease<br>**Family:**Tyrosyl-DNA phosphodiesterase TDP1 |
| 21 | d1tfra2 | Alignment | not modelled | 44.8 | 9 | **Fold:**PIN domain-like<br>**Superfamily:**PIN domain-like<br>**Family:**5' to 3' exonuclease catalytic domain |
| 22 | c2a5hC_ | Alignment | not modelled | 39.2 | 17 | **PDB header:**isomerase<br>**Chain:** C: **PDB Molecule:**l-lysine 2,3-aminomutase;<br>**PDBTitle:** 2.1 angstrom x-ray crystal structure of lysine-2,3-aminomutase from2 clostridium subterminale sb4, with michaelis analog (l-alpha-lysine3 external aldimine form of pyridoxal-5'-phosphate). |
| 23 | d2f5tx2 | Alignment | not modelled | 29.3 | 20 | **Fold:**Phospholipase D/nuclease<br>**Superfamily:**Phospholipase D/nuclease<br>**Family:**TrmB middle domain-like |
| 24 | d2pkqo1 | Alignment | not modelled | 28.1 | 11 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain |
| 25 | d1gz0a2 | Alignment | not modelled | 26.6 | 22 | **Fold:**Bacillus chorismate mutase-like<br>**Superfamily:**L30e-like<br>**Family:**RNA 2'-O ribose methyltransferase substrate binding domain |
| 26 | c3dy0B_ | Alignment | not modelled | 26.2 | 33 | **PDB header:**blood clotting, hydrolase inhibitor<br>**Chain:** B: **PDB Molecule:**c-terminus plasma serine protease inhibitor;<br>**PDBTitle:** crystal structure of cleaved pci bound to heparin |
| 27 | d1d7ya2 | Alignment | not modelled | 25.8 | 13 | **Fold:**FAD/NAD(P)-binding domain<br>**Superfamily:**FAD/NAD(P)-binding domain<br>**Family:**FAD/NAD-linked reductases, N-terminal and central domains |
| 28 | d1gado1 | Alignment | not modelled | 25.4 | 16 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N- |

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| | | | | | | terminal domain |
| 29 | c1lq8H_ | Alignment | not modelled | 24.7 | 33 | **PDB header:**blood clotting<br>**Chain:** H: **PDB Molecule:**plasma serine protease inhibitor;<br>**PDBTitle:** crystal structure of cleaved protein c inhibitor |
| 30 | c3kgkA_ | Alignment | not modelled | 24.5 | 13 | **PDB header:**chaperone<br>**Chain:** A: **PDB Molecule:**arsenical resistance operon trans-acting repressor arsd;<br>**PDBTitle:** crystal structure of arsd |
| 31 | c2l82A_ | Alignment | not modelled | 22.2 | 21 | **PDB header:**de novo protein<br>**Chain:** A: **PDB Molecule:**designed protein or32;<br>**PDBTitle:** solution nmr structure of de novo designed protein, p-loop ntpase2 fold, northeast structural genomics consortium target or32 |
| 32 | c3ecsD_ | Alignment | not modelled | 21.8 | 15 | **PDB header:**translation<br>**Chain:** D: **PDB Molecule:**translation initiation factor eif-2b subunit<br>**PDBTitle:** crystal structure of human eif2b alpha |
| 33 | d2bdea1 | Alignment | not modelled | 21.0 | 41 | **Fold:**HAD-like<br>**Superfamily:**HAD-like<br>**Family:**5' nucleotidase-like |
| 34 | d1gz0f2 | Alignment | not modelled | 18.9 | 22 | **Fold:**Bacillus chorismate mutase-like<br>**Superfamily:**L30e-like<br>**Family:**RNA 2'-O ribose methyltransferase substrate binding domain |
| 35 | c2f5tX_ | Alignment | not modelled | 18.9 | 20 | **PDB header:**transcription<br>**Chain:** X: **PDB Molecule:**archaeal transcriptional regulator trmb;<br>**PDBTitle:** crystal structure of the sugar binding domain of the archaeal2 transcriptional regulator trmb |
| 36 | d1u8fo1 | Alignment | not modelled | 18.3 | 14 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain |
| 37 | d2c4va1 | Alignment | not modelled | 18.3 | 15 | **Fold:**Flavodoxin-like<br>**Superfamily:**Type II 3-dehydroquinate dehydratase<br>**Family:**Type II 3-dehydroquinate dehydratase |
| 38 | d1x94a_ | Alignment | not modelled | 18.1 | 15 | **Fold:**SIS domain<br>**Superfamily:**SIS domain<br>**Family:**mono-SIS domain |
| 39 | d1vc2a1 | Alignment | not modelled | 16.9 | 13 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain |
| 40 | c2krcA_ | Alignment | not modelled | 16.8 | 26 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**dna-directed rna polymerase subunit delta;<br>**PDBTitle:** solution structure of the n-terminal domain of bacillus2 subtilis delta subunit of rna polymerase |
| 41 | d1g5ha1 | Alignment | not modelled | 16.3 | 8 | **Fold:**Anticodon-binding domain-like<br>**Superfamily:**Class II aaRS ABD-related<br>**Family:**Anticodon-binding domain of Class II aaRS |
| 42 | d1j0xo1 | Alignment | not modelled | 15.3 | 13 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain |
| 43 | d2g82a1 | Alignment | not modelled | 14.8 | 14 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain |
| 44 | d2cula1 | Alignment | not modelled | 14.7 | 21 | **Fold:**FAD/NAD(P)-binding domain<br>**Superfamily:**FAD/NAD(P)-binding domain<br>**Family:**GidA-like |
| 45 | c2jcmA_ | Alignment | not modelled | 14.3 | 36 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**cytosolic purine 5'-nucleotidase;<br>**PDBTitle:** crystal structure of human cytosolic 5'-nucleotidase ii in2 complex with beryllium trifluoride |
| 46 | c3gbcA_ | Alignment | not modelled | 13.0 | 14 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**pyrazinamidase/nicotinamidas pnca;<br>**PDBTitle:** determination of the crystal structure of the pyrazinamidase from2 m.tuberculosis : a structure-function analysis for prediction3 resistance to pyrazinamide |
| 47 | c3fxaA_ | Alignment | not modelled | 12.9 | 20 | **PDB header:**sugar binding protein<br>**Chain:** A: **PDB Molecule:**sis domain protein;<br>**PDBTitle:** crystal structure of a putative sugar-phosphate isomerase2 (lmof2365_0531) from listeria monocytogenes str. 4b f2365 at 1.60 a3 resolution |
| 48 | d1tk9a_ | Alignment | not modelled | 12.8 | 10 | **Fold:**SIS domain<br>**Superfamily:**SIS domain<br>**Family:**mono-SIS domain |
| 49 | c3a11D_ | Alignment | not modelled | 12.7 | 13 | **PDB header:**isomerase<br>**Chain:** D: **PDB Molecule:**translation initiation factor eif-2b, delta<br>**PDBTitle:** crystal structure of ribose-1,5-bisphosphate isomerase from2 thermococcus kodakaraensis kod1 |
| 50 | d1v2da_ | Alignment | not modelled | 12.7 | 14 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**AAT-like |
| 51 | c2xhzC_ | Alignment | not modelled | 12.3 | 15 | **PDB header:**isomerase<br>**Chain:** C: **PDB Molecule:**arabinose 5-phosphate isomerase;<br>**PDBTitle:** probing the active site of the sugar isomerase domain from e. coli2 arabinose-5-phosphate isomerase via x-ray crystallography |
| 52 | d1jeoa_ | Alignment | not modelled | 12.2 | 10 | **Fold:**SIS domain<br>**Superfamily:**SIS domain<br>**Family:**mono-SIS domain |
| 53 | c2r60A_ | Alignment | not modelled | 12.0 | 20 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**glycosyl transferase, group 1;<br>**PDBTitle:** structure of apo sucrose phosphate synthase (sps) of2 halothermothrix orenii |

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| 54 | c5acnA_ | Alignment | not modelled | 11.8 | 13 | **PDB header:**lyase(carbon-oxygen)<br>**Chain:** A: **PDB Molecule:**aconitase;<br>**PDBTitle:** structure of activated aconitase. formation of the (4fe-4s)2 cluster in the crystal |
| 55 | c2uygF_ | Alignment | not modelled | 10.7 | 18 | **PDB header:**lyase<br>**Chain:** F: **PDB Molecule:**3-dehydroquinate dehydratase;<br>**PDBTitle:** crystallographic structure of the typeii 3-dehydroquinase2 from thermus thermophilus |
| 56 | d1vb5a_ | Alignment | not modelled | 10.7 | 15 | **Fold:**NagB/RpiA/CoA transferase-like<br>**Superfamily:**NagB/RpiA/CoA transferase-like<br>**Family:**IF2B-like |
| 57 | c3trjC_ | Alignment | not modelled | 10.5 | 10 | **PDB header:**isomerase<br>**Chain:** C: **PDB Molecule:**phosphoheptose isomerase;<br>**PDBTitle:** structure of a phosphoheptose isomerase from francisella tularensis |
| 58 | d1qd1a1 | Alignment | not modelled | 10.5 | 13 | **Fold:**Ferredoxin-like<br>**Superfamily:**Formiminotransferase domain of formiminotransferase-cyclodeaminase.<br>**Family:**Formiminotransferase domain of formiminotransferase-cyclodeaminase. |
| 59 | d1q1ra2 | Alignment | not modelled | 10.4 | 8 | **Fold:**FAD/NAD(P)-binding domain<br>**Superfamily:**FAD/NAD(P)-binding domain<br>**Family:**FAD/NAD-linked reductases, N-terminal and central domains |
| 60 | d1j98a_ | Alignment | not modelled | 10.4 | 24 | **Fold:**LuxS/MPP-like metallohydrolase<br>**Superfamily:**LuxS/MPP-like metallohydrolase<br>**Family:**Autoinducer-2 production protein LuxS |
| 61 | c3hq4R_ | Alignment | not modelled | 10.3 | 17 | **PDB header:**oxidoreductase<br>**Chain:** R: **PDB Molecule:**glyceraldehyde-3-phosphate dehydrogenase 1;<br>**PDBTitle:** crystal structure of c151s mutant of glyceraldehyde-3-phosphate2 dehydrogenase 1 (gapdh1) complexed with nad from staphylococcus3 aureus mrsa252 at 2.2 angstrom resolution |
| 62 | d2qi2a3 | Alignment | not modelled | 10.2 | 7 | **Fold:**Bacillus chorismate mutase-like<br>**Superfamily:**L30e-like<br>**Family:**ERF1/Dom34 C-terminal domain-like |
| 63 | c2yvaB_ | Alignment | not modelled | 10.1 | 18 | **PDB header:**dna binding protein<br>**Chain:** B: **PDB Molecule:**dnaa initiator-associating protein diaa;<br>**PDBTitle:** crystal structure of escherichia coli diaa |
| 64 | c3shoA_ | Alignment | not modelled | 10.0 | 22 | **PDB header:**transcription regulator<br>**Chain:** A: **PDB Molecule:**transcriptional regulator, rpir family;<br>**PDBTitle:** crystal structure of rpir transcription factor from sphaerobacter2 thermophilus (sugar isomerase domain) |
| 65 | c1zhvA_ | Alignment | not modelled | 9.9 | 9 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**hypothetical protein atu0741;<br>**PDBTitle:** x-ray crystal structure protein atu0741 from agobacterium tumefaciens.2 northeast structural genomics consortium target atr8. |
| 66 | d1o98a1 | Alignment | not modelled | 9.5 | 20 | **Fold:**2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain<br>**Superfamily:**2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain<br>**Family:**2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain |
| 67 | c2x3yA_ | Alignment | not modelled | 9.3 | 15 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**phosphoheptose isomerase;<br>**PDBTitle:** crystal structure of gmha from burkholderia pseudomallei |
| 68 | d3gpdg1 | Alignment | not modelled | 9.2 | 17 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain |
| 69 | c2pr7A_ | Alignment | not modelled | 8.7 | 23 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**haloacid dehalogenase/epoxide hydrolase family;<br>**PDBTitle:** crystal structure of uncharacterized protein (np_599989.1) from2 corynebacterium glutamicum atcc 13032 kitasato at 1.44 a resolution |
| 70 | c3e9kA_ | Alignment | not modelled | 8.6 | 2 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**kynureninase;<br>**PDBTitle:** crystal structure of homo sapiens kynureninase-3-hydroxyhippuric acid2 inhibitor complex |
| 71 | d1obfo1 | Alignment | not modelled | 8.5 | 12 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain |
| 72 | c3hjaB_ | Alignment | not modelled | 8.2 | 15 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**glyceraldehyde-3-phosphate dehydrogenase;<br>**PDBTitle:** crystal structure of glyceraldehyde-3-phosphate2 dehydrogenase from borrelia burgdorferi |
| 73 | d1pdoa_ | Alignment | not modelled | 8.2 | 12 | **Fold:**PTS system fructose IIA component-like<br>**Superfamily:**PTS system fructose IIA component-like<br>**Family:**EIIA-man component-like |
| 74 | c2b34C_ | Alignment | not modelled | 8.1 | 9 | **PDB header:**hydrolase<br>**Chain:** C: **PDB Molecule:**mar1 ribonuclease;<br>**PDBTitle:** structure of mar1 ribonuclease from caenorhabditis elegans |
| 75 | d1x92a_ | Alignment | not modelled | 7.9 | 8 | **Fold:**SIS domain<br>**Superfamily:**SIS domain<br>**Family:**mono-SIS domain |
| 76 | d1bxka_ | Alignment | not modelled | 7.8 | 13 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**Tyrosine-dependent oxidoreductases |
| 77 | c2d1kC_ | Alignment | not modelled | 7.7 | 36 | **PDB header:**structural protein<br>**Chain:** C: **PDB Molecule:**metastasis suppressor protein 1;<br>**PDBTitle:** ternary complex of the wh2 domain of mim with actin-dnase i |

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| 78 | c3l23A_ | Alignment | not modelled | 7.5 | 6 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**sugar phosphate isomerase/epimerase;<br>**PDBTitle:** crystal structure of sugar phosphate isomerase/epimerase2 (yp_001303399.1) from parabacteroides distasonis atcc 8503 at 1.70 a3 resolution |
| 79 | d1rm4a1 | Alignment | not modelled | 7.4 | 13 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain |
| 80 | d1w6ka2 | Alignment | not modelled | 7.3 | 20 | **Fold:**alpha/alpha toroid<br>**Superfamily:**Terpenoid cyclases/Protein prenyltransferases<br>**Family:**Terpene synthases |
| 81 | c2y92A_ | Alignment | not modelled | 7.2 | 17 | **PDB header:**immune system<br>**Chain:** A: **PDB Molecule:**toll/interleukin-1 receptor domain-containing adapter<br>**PDBTitle:** crystal structure of mal adaptor protein |
| 82 | d3cmco1 | Alignment | not modelled | 7.1 | 18 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain |
| 83 | d1vima_ | Alignment | not modelled | 7.1 | 15 | **Fold:**SIS domain<br>**Superfamily:**SIS domain<br>**Family:**mono-SIS domain |
| 84 | d1kewa_ | Alignment | not modelled | 7.0 | 13 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**Tyrosine-dependent oxidoreductases |
| 85 | d1wo8a1 | Alignment | not modelled | 7.0 | 18 | **Fold:**Methylglyoxal synthase-like<br>**Superfamily:**Methylglyoxal synthase-like<br>**Family:**Methylglyoxal synthase, MgsA |
| 86 | d1acoa2 | Alignment | not modelled | 7.0 | 13 | **Fold:**Aconitase iron-sulfur domain<br>**Superfamily:**Aconitase iron-sulfur domain<br>**Family:**Aconitase iron-sulfur domain |
| 87 | d2bisa1 | Alignment | not modelled | 6.8 | 18 | **Fold:**UDP-Glycosyltransferase/glycogen phosphorylase<br>**Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase<br>**Family:**Glycosyl transferases group 1 |
| 88 | d2d59a1 | Alignment | not modelled | 6.7 | 11 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**CoA-binding domain |
| 89 | c3ff4A_ | Alignment | not modelled | 6.6 | 14 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** crystal structure of uncharacterized protein chu_1412 |
| 90 | c3ii7A_ | Alignment | not modelled | 6.5 | 25 | **PDB header:**protein binding<br>**Chain:** A: **PDB Molecule:**kelch-like protein 7;<br>**PDBTitle:** crystal structure of the kelch domain of human klhl7 |
| 91 | d1nr3a_ | Alignment | not modelled | 6.5 | 21 | **Fold:**DNA-binding protein Tfx<br>**Superfamily:**DNA-binding protein Tfx<br>**Family:**DNA-binding protein Tfx |
| 92 | c3h75A_ | Alignment | not modelled | 6.5 | 12 | **PDB header:**sugar binding protein<br>**Chain:** A: **PDB Molecule:**periplasmic sugar-binding domain protein;<br>**PDBTitle:** crystal structure of a periplasmic sugar-binding protein from the2 pseudomonas fluorescens |
| 93 | d1rzua_ | Alignment | not modelled | 6.4 | 20 | **Fold:**UDP-Glycosyltransferase/glycogen phosphorylase<br>**Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase<br>**Family:**Glycosyl transferases group 1 |
| 94 | c3l2iB_ | Alignment | not modelled | 6.4 | 12 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**3-dehydroquinate dehydratase;<br>**PDBTitle:** 1.85 angstrom crystal structure of the 3-dehydroquinate dehydratase2 (arod) from salmonella typhimurium lt2. |
| 95 | d3beda1 | Alignment | not modelled | 6.3 | 15 | **Fold:**PTS system fructose IIA component-like<br>**Superfamily:**PTS system fructose IIA component-like<br>**Family:**EIIA-man component-like |
| 96 | d1nhpa2 | Alignment | not modelled | 6.3 | 8 | **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 | d1m3sa_ | Alignment | not modelled | 6.2 | 18 | **Fold:**SIS domain<br>**Superfamily:**SIS domain<br>**Family:**mono-SIS domain |
| 98 | d1h70a_ | Alignment | not modelled | 6.1 | 14 | **Fold:**Pentein, beta/alpha-propeller<br>**Superfamily:**Pentein<br>**Family:**Dimethylarginine dimethylaminohydrolase DDAH |
| 99 | d1ygha_ | Alignment | not modelled | 6.0 | 9 | **Fold:**Acyl-CoA N-acyltransferases (Nat)<br>**Superfamily:**Acyl-CoA N-acyltransferases (Nat)<br>**Family:**N-acetyl transferase, NAT |