# Phyre$^2$

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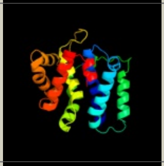
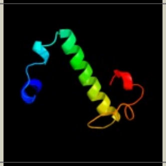
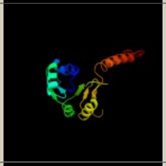
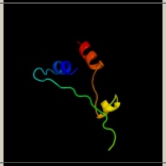
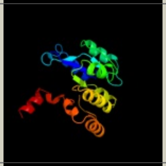
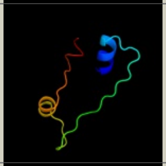
| Description | P39160 |
| Date | Thu Jan 5 11:58:16 GMT 2012 |
| Unique Job ID | e586d0cd936b0f91 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c1m2wA_ | Alignment |  | 100.0 | 38 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**mannitol dehydrogenase;<br>**PDBTitle:** pseudomonas fluorescens mannitol 2-dehydrogenase ternary complex with2 nad and d-mannitol |
| 2 | c3h2zA_ | Alignment |  | 100.0 | 24 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**mannitol-1-phosphate 5-dehydrogenase;<br>**PDBTitle:** the crystal structure of mannitol-1-phosphate dehydrogenase from2 shigella flexneri |
| 3 | d1lj8a4 | Alignment |  | 100.0 | 41 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain |
| 4 | d1lj8a3 | Alignment |  | 100.0 | 32 | **Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like<br>**Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like<br>**Family:**Mannitol 2-dehydrogenase |
| 5 | c2ph5A_ | Alignment |  | 50.5 | 14 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**homospermidine synthase;<br>**PDBTitle:** crystal structure of the homospermidine synthase hss from legionella2 pneumophila in complex with nad, northeast structural genomics target3 lgr54 |
| 6 | c3fggA_ | Alignment |  | 45.0 | 20 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein bce2196;<br>**PDBTitle:** crystal structure of putative ecf-type sigma factor negative effector2 from bacillus cereus |
| 7 | c2axqA_ | Alignment |  | 41.2 | 10 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**saccharopine dehydrogenase;<br>**PDBTitle:** apo histidine-tagged saccharopine dehydrogenase (l-glu2 forming) from saccharomyces cerevisiae |
| 8 | d1k4ia_ | Alignment |  | 35.0 | 16 | **Fold:**YrdC/RibB<br>**Superfamily:**YrdC/RibB<br>**Family:**3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB |
| 9 | c3euwB_ | Alignment |  | 27.8 | 16 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**myo-inositol dehydrogenase;<br>**PDBTitle:** crystal structure of a myo-inositol dehydrogenase from corynebacterium2 glutamicum atcc 13032 |
| 10 | d1snna_ | Alignment |  | 27.5 | 15 | **Fold:**YrdC/RibB<br>**Superfamily:**YrdC/RibB<br>**Family:**3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB |
| 11 | c3egoB_ | Alignment |  | 25.4 | 13 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**probable 2-dehydropantoate 2-reductase;<br>**PDBTitle:** crystal structure of probable 2-dehydropantoate 2-reductase2 pane from bacillus subtilis |

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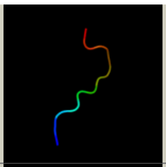
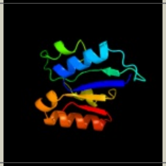
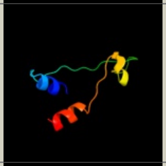
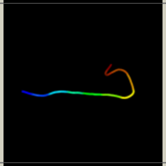
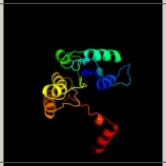
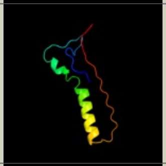
|---|---|---|---|---|---|---|
| 12 | d2o8ra3 | Alignment |  | 24.5 | 33 | **Fold:**Phospholipase D/nuclease<br>**Superfamily:**Phospholipase D/nuclease<br>**Family:**Polyphosphate kinase C-terminal domain |
| 13 | c3mtjA_ | Alignment |  | 23.5 | 11 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**homoserine dehydrogenase;<br>**PDBTitle:** the crystal structure of a homoserine dehydrogenase from thiobacillus2 denitrificans to 2.15a |
| 14 | c1ceuA_ | Alignment |  | 22.6 | 44 | **PDB header:**viral protein<br>**Chain:** A: **PDB Molecule:**protein (hiv-1 regulatory protein n-terminal<br>**PDBTitle:** nmr structure of the (1-51) n-terminal domain of the hiv-12 regulatory protein |
| 15 | c3mioA_ | Alignment |  | 22.1 | 24 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**3,4-dihydroxy-2-butanone 4-phosphate synthase;<br>**PDBTitle:** crystal structure of 3,4-dihydroxy-2-butanone 4-phosphate synthase2 domain from mycobacterium tuberculosis at ph 6.00 |
| 16 | c2o8rA_ | Alignment |  | 21.5 | 36 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**polyphosphate kinase;<br>**PDBTitle:** crystal structure of polyphosphate kinase from2 porphyromonas gingivalis |
| 17 | d1r0ka2 | Alignment |  | 20.2 | 10 | **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 |
| 18 | c3nt5B_ | Alignment |  | 19.8 | 19 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**inositol 2-dehydrogenase/d-chiro-inositol 3-dehydrogenase;<br>**PDBTitle:** crystal structure of myo-inositol dehydrogenase from bacillus subtilis2 with bound cofactor and product inosose |
| 19 | c3h8gC_ | Alignment |  | 19.7 | 12 | **PDB header:**hydrolase<br>**Chain:** C: **PDB Molecule:**cytosol aminopeptidase;<br>**PDBTitle:** bestatin complex structure of leucine aminopeptidase from pseudomonas2 putida |
| 20 | c1e5lA_ | Alignment |  | 18.2 | 11 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**saccharopine reductase;<br>**PDBTitle:** apo saccharopine reductase from magnaporthe grisea |
| 21 | d2oc5a1 | Alignment | not modelled | 18.0 | 31 | **Fold:**Ferritin-like<br>**Superfamily:**Ferritin-like<br>**Family:**PMT1231-like |
| 22 | d1v8fa_ | Alignment | not modelled | 17.1 | 31 | **Fold:**Adenine nucleotide alpha hydrolase-like<br>**Superfamily:**Nucleotidylyl transferase<br>**Family:**Pantothenate synthetase (Pantoate-beta-alanine ligase, PanC) |
| 23 | c3ceaA_ | Alignment | not modelled | 17.0 | 18 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**myo-inositol 2-dehydrogenase;<br>**PDBTitle:** crystal structure of myo-inositol 2-dehydrogenase (np_786804.1) from2 lactobacillus plantarum at 2.40 a resolution |
| 24 | c1z9bA_ | Alignment | not modelled | 15.6 | 17 | **PDB header:**translation<br>**Chain:** A: **PDB Molecule:**translation initiation factor if-2;<br>**PDBTitle:** solution structure of the c1-subdomain of bacillus2 stearothermophilus translation initiation factor if2 |
| 25 | c1lanA_ | Alignment | not modelled | 15.4 | 13 | **PDB header:**hydrolase (alpha-aminoacylpeptide)<br>**Chain:** A: **PDB Molecule:**leucine aminopeptidase;<br>**PDBTitle:** leucine aminopeptidase complex with l-leucinal |
| 26 | d1gyta2 | Alignment | not modelled | 15.1 | 13 | **Fold:**Phosphorylase/hydrolase-like<br>**Superfamily:**Zn-dependent exopeptidases<br>**Family:**Leucine aminopeptidase, C-terminal domain |
| 27 | d1uj8a1 | Alignment | not modelled | 15.1 | 18 | **Fold:**Another 3-helical bundle<br>**Superfamily:**IscX-like<br>**Family:**IscX-like |
| 28 | c3docD_ | Alignment | not modelled | 14.8 | 19 | **PDB header:**oxidoreductase<br>**Chain:** D: **PDB Molecule:**glyceraldehyde 3-phosphate dehydrogenase;<br>**PDBTitle:** crystal structure of trka glyceraldehyde-3-phosphate2 dehydrogenase from brucella melitensis |

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|---|---|---|---|---|---|---|
| 29 | c2c9lZ_ | Alignment | not modelled | 14.5 | 33 | **PDB header:**viral protein<br>**Chain:** Z: **PDB Molecule:**bzlf1 trans-activator protein;<br>**PDBTitle:** structure of the epstein-barr virus zebra protein |
| 30 | c3guzB_ | Alignment | not modelled | 14.5 | 17 | **PDB header:**ligase<br>**Chain:** B: **PDB Molecule:**pantothenate synthetase;<br>**PDBTitle:** structural and substrate-binding studies of pantothenate2 synthenate (ps)provide insights into homotropic inhibition3 by pantoate in ps's |
| 31 | c1dvpA_ | Alignment | not modelled | 14.0 | 13 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**hepatocyte growth factor-regulated tyrosine<br>**PDBTitle:** crystal structure of the vhs and fyve tandem domains of hrs,2 a protein involved in membrane trafficking and signal3 transduction |
| 32 | c3ketA_ | Alignment | not modelled | 13.9 | 25 | **PDB header:**transcription/dna<br>**Chain:** A: **PDB Molecule:**redox-sensing transcriptional repressor rex;<br>**PDBTitle:** crystal structure of a rex-family transcriptional regulatory protein2 from streptococcus agalactiae bound to a palindromic operator |
| 33 | c1gytG_ | Alignment | not modelled | 13.4 | 13 | **PDB header:**hydrolase<br>**Chain:** G: **PDB Molecule:**cytosol aminopeptidase;<br>**PDBTitle:** e. coli aminopeptidase a (pepa) |
| 34 | c3kzwD_ | Alignment | not modelled | 13.1 | 15 | **PDB header:**hydrolase<br>**Chain:** D: **PDB Molecule:**cytosol aminopeptidase;<br>**PDBTitle:** crystal structure of cytosol aminopeptidase from staphylococcus aureus2 col |
| 35 | d2py6a1 | Alignment | not modelled | 13.0 | 25 | **Fold:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Family:**FkbM-like |
| 36 | c3omdB_ | Alignment | not modelled | 12.1 | 14 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** crystal structure of unknown function protein from leptospirillum2 rubarum |
| 37 | d2v0fa1 | Alignment | not modelled | 11.9 | 46 | **Fold:**GYF/BRK domain-like<br>**Superfamily:**BRK domain-like<br>**Family:**BRK domain-like |
| 38 | d1k8kg_ | Alignment | not modelled | 11.8 | 15 | **Fold:**alpha-alpha superhelix<br>**Superfamily:**Arp2/3 complex 16 kDa subunit ARPC5<br>**Family:**Arp2/3 complex 16 kDa subunit ARPC5 |
| 39 | d1qusa_ | Alignment | not modelled | 11.6 | 14 | **Fold:**Lysozyme-like<br>**Superfamily:**Lysozyme-like<br>**Family:**Bacterial muramidase, catalytic domain |
| 40 | c3n8hA_ | Alignment | not modelled | 11.4 | 27 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**pantothenate synthetase;<br>**PDBTitle:** crystal structure of pantoate-beta-alanine ligase from francisella2 tularensis |
| 41 | d2cu2a2 | Alignment | not modelled | 11.2 | 12 | **Fold:**Nucleotide-diphospho-sugar transferases<br>**Superfamily:**Nucleotide-diphospho-sugar transferases<br>**Family:**mannose-1-phosphate guanylyl transferase |
| 42 | d1lama1 | Alignment | not modelled | 11.2 | 14 | **Fold:**Phosphorylase/hydrolase-like<br>**Superfamily:**Zn-dependent exopeptidases<br>**Family:**Leucine aminopeptidase, C-terminal domain |
| 43 | c3q2kB_ | Alignment | not modelled | 10.9 | 13 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**oxidoreductase;<br>**PDBTitle:** crystal structure of the wlba dehydrogenase from bordetella pertussis2 in complex with nadh and udp-glcnaca |
| 44 | d1dvpa1 | Alignment | not modelled | 10.7 | 14 | **Fold:**alpha-alpha superhelix<br>**Superfamily:**ENTH/VHS domain<br>**Family:**VHS domain |
| 45 | d2dt5a2 | Alignment | not modelled | 10.7 | 19 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**Transcriptional repressor Rex, C-terminal domain |
| 46 | d1xdpa3 | Alignment | not modelled | 10.6 | 50 | **Fold:**Phospholipase D/nuclease<br>**Superfamily:**Phospholipase D/nuclease<br>**Family:**Polyphosphate kinase C-terminal domain |
| 47 | d1gzsb_ | Alignment | not modelled | 10.3 | 18 | **Fold:**SopE-like GEF domain<br>**Superfamily:**SopE-like GEF domain<br>**Family:**SopE-like GEF domain |
| 48 | d1q7ra_ | Alignment | not modelled | 10.2 | 24 | **Fold:**Flavodoxin-like<br>**Superfamily:**Class I glutamine amidotransferase-like<br>**Family:**Class I glutamine amidotransferases (GAT) |
| 49 | c1fi0A_ | Alignment | not modelled | 9.8 | 44 | **PDB header:**viral protein<br>**Chain:** A: **PDB Molecule:**vpr protein;<br>**PDBTitle:** solution structure of hiv-1 vpr (13-33) peptide in micells |
| 50 | c3bjrA_ | Alignment | not modelled | 9.8 | 8 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**putative carboxylesterase;<br>**PDBTitle:** crystal structure of a putative carboxylesterase (lp_1002) from2 lactobacillus plantarum wcfs1 at 2.09 a resolution |
| 51 | d1au7a2 | Alignment | not modelled | 9.7 | 19 | **Fold:**lambda repressor-like DNA-binding domains<br>**Superfamily:**lambda repressor-like DNA-binding domains<br>**Family:**POU-specific domain |
| 52 | c2ejcA_ | Alignment | not modelled | 9.4 | 19 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**pantoate--beta-alanine ligase;<br>**PDBTitle:** crystal structure of pantoate--beta-alanine ligase (panc)2 from thermotoga maritima |
| 53 | c3innB_ | Alignment | not modelled | 9.3 | 19 | **PDB header:**ligase<br>**Chain:** B: **PDB Molecule:**pantothenate synthetase;<br>**PDBTitle:** crystal structure of pantoate-beta-alanine-ligase in complex2 with atp at low occupancy at 2.1 a resolution |
| 54 | d1o7fa1 | Alignment | not modelled | 9.3 | 22 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**"Winged helix" DNA-binding domain |

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| | | | | | | **Family:**DEP domain |
| 55 | c2cu2A_ | Alignment | not modelled | 9.1 | 11 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**putative mannose-1-phosphate guanylyl transferase;<br>**PDBTitle:** crystal structure of mannose-1-phosphate geranyltransferase from2 thermus thermophilus hb8 |
| 56 | c2hc9A_ | Alignment | not modelled | 9.1 | 13 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**leucine aminopeptidase 1;<br>**PDBTitle:** structure of caenorhabditis elegans leucine aminopeptidase-zinc2 complex (lap1) |
| 57 | c1x5bA_ | Alignment | not modelled | 8.9 | 12 | **PDB header:**protein binding<br>**Chain:** A: **PDB Molecule:**signal transducing adaptor molecule 2;<br>**PDBTitle:** the solution structure of the vhs domain of human signal2 transducing adaptor molecule 2 |
| 58 | c3moiA_ | Alignment | not modelled | 8.7 | 21 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**probable dehydrogenase;<br>**PDBTitle:** the crystal structure of the putative dehydrogenase from bordetella2 bronchiseptica rb50 |
| 59 | d2hiqa1 | Alignment | not modelled | 8.5 | 16 | **Fold:**Ferredoxin-like<br>**Superfamily:**Dimeric alpha+beta barrel<br>**Family:**Hypothetical protein YdhR |
| 60 | c2qytA_ | Alignment | not modelled | 8.5 | 19 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**2-dehydropantoate 2-reductase;<br>**PDBTitle:** crystal structure of 2-dehydropantoate 2-reductase from porphyromonas2 gingivalis w83 |
| 61 | c3t38B_ | Alignment | not modelled | 8.4 | 7 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**arsenate reductase;<br>**PDBTitle:** corynebacterium glutamicum thioredoxin-dependent arsenate reductase2 cg_arsc1' |
| 62 | c3dapB_ | Alignment | not modelled | 8.2 | 17 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**diaminopimelic acid dehydrogenase;<br>**PDBTitle:** c. glutamicum dap dehydrogenase in complex with nadp+ and2 the inhibitor 5s-isoxazoline |
| 63 | d1gtra2 | Alignment | not modelled | 8.0 | 11 | **Fold:**Adenine nucleotide alpha hydrolase-like<br>**Superfamily:**Nucleotidylyl transferase<br>**Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain |
| 64 | d1f06a1 | Alignment | not modelled | 7.9 | 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 |
| 65 | c1lw7A_ | Alignment | not modelled | 7.6 | 13 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**transcriptional regulator nadr;<br>**PDBTitle:** nadr protein from haemophilus influenzae |
| 66 | c3ag5A_ | Alignment | not modelled | 7.6 | 31 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**pantothenate synthetase;<br>**PDBTitle:** crystal structure of pantothenate synthetase from staphylococcus2 aureus |
| 67 | c2hz7A_ | Alignment | not modelled | 7.5 | 15 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**glutaminyl-trna synthetase;<br>**PDBTitle:** crystal structure of the glutaminyl-trna synthetase from2 deinococcus radiodurans |
| 68 | c2k2iB_ | Alignment | not modelled | 7.4 | 55 | **PDB header:**cell cycle<br>**Chain:** B: **PDB Molecule:**sfi1 peptide;<br>**PDBTitle:** nmr solution structure of the c-terminal domain (t94-y172)2 of the human centrin 2 in complex with a repeat sequence of3 human sfi1 (r641-t660) |
| 69 | d1hcia1 | Alignment | not modelled | 7.3 | 21 | **Fold:**Spectrin repeat-like<br>**Superfamily:**Spectrin repeat<br>**Family:**Spectrin repeat |
| 70 | d1zh8a1 | Alignment | not modelled | 7.3 | 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 |
| 71 | c1iq5B_ | Alignment | not modelled | 7.3 | 67 | **PDB header:**metal binding protein/protein binding<br>**Chain:** B: **PDB Molecule:**ca2+/calmodulin dependent kinase kinase;<br>**PDBTitle:** calmodulin/nematode ca2+/calmodulin dependent kinase kinase2 fragment |
| 72 | d1f0xa1 | Alignment | not modelled | 7.2 | 50 | **Fold:**Ferredoxin-like<br>**Superfamily:**FAD-linked oxidases, C-terminal domain<br>**Family:**D-lactate dehydrogenase |
| 73 | c3b20R_ | Alignment | not modelled | 7.1 | 15 | **PDB header:**oxidoreductase<br>**Chain:** R: **PDB Molecule:**glyceraldehyde 3-phosphate dehydrogenase (nadp+);<br>**PDBTitle:** crystal structure analysis of dehydrogenase complexed with nad |
| 74 | c1u2jC_ | Alignment | not modelled | 6.9 | 29 | **PDB header:**oxidoreductase<br>**Chain:** C: **PDB Molecule:**peroxidase/catalase hpi;<br>**PDBTitle:** crystal structure of the c-terminal domain from the2 catalase-peroxidase katg of escherichia coli (p21 21 21) |
| 75 | c3jruB_ | Alignment | not modelled | 6.7 | 13 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**probable cytosol aminopeptidase;<br>**PDBTitle:** crystal structure of leucyl aminopeptidase (pepa) from xoo0834,2 xanthomonas oryzae pv. oryzae kacc10331 |
| 76 | d1u2ka_ | Alignment | not modelled | 6.7 | 29 | **Fold:**Heme-dependent peroxidases<br>**Superfamily:**Heme-dependent peroxidases<br>**Family:**Catalase-peroxidase KatG |
| 77 | c3r24A_ | Alignment | not modelled | 6.6 | 37 | **PDB header:**transferase, viral protein<br>**Chain:** A: **PDB Molecule:**2'-o-methyl transferase;<br>**PDBTitle:** crystal structure of nsp10/nsp16 complex of sars coronavirus" if2 possible |
| 78 | c3dwlG_ | Alignment | not modelled | 6.6 | 10 | **PDB header:**structural protein<br>**Chain:** G: **PDB Molecule:**actin-related protein 2/3 complex subunit 5;<br>**PDBTitle:** crystal structure of fission yeast arp2/3 complex lacking the arp22 subunit |
| | | | | | | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**putative apha-like transcription factor; |

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|---|---|---|---|---|---|---|
| 79 | c2rkhA_ | Alignment | not modelled | 6.6 | 24 | **PDBTitle:** crystal structure of a putative apha-like transcription factor2 (zp_00208345.1) from magnetospirillum magnetotacticum ms-1 at 2.00 a3 resolution |
| 80 | c3euhB_ | Alignment | not modelled | 6.6 | 15 | **PDB header:**cell cycle<br>**Chain:** B: **PDB Molecule:**chromosome partition protein mukf;<br>**PDBTitle:** crystal structure of the muke-mukf complex |
| 81 | c3tsuA_ | Alignment | not modelled | 6.5 | 29 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**transcriptional regulatory protein;<br>**PDBTitle:** crystal structure of e. coli hypf with amp-pnp and carbamoyl phosphate |
| 82 | d1m9fd_ | Alignment | not modelled | 6.5 | 25 | **Fold:**Retrovirus capsid protein, N-terminal core domain<br>**Superfamily:**Retrovirus capsid protein, N-terminal core domain<br>**Family:**Retrovirus capsid protein, N-terminal core domain |
| 83 | c3hn2A_ | Alignment | not modelled | 6.5 | 13 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**2-dehydropantoate 2-reductase;<br>**PDBTitle:** crystal structure of 2-dehydropantoate 2-reductase from geobacter2 metallireducens gs-15 |
| 84 | c3ghyA_ | Alignment | not modelled | 6.4 | 13 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**ketopantoate reductase protein;<br>**PDBTitle:** crystal structure of a putative ketopantoate reductase from ralstonia2 solanacearum molk2 |
| 85 | d1ebfa1 | Alignment | not modelled | 6.4 | 9 | **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 |
| 86 | d2a84a1 | Alignment | not modelled | 6.3 | 27 | **Fold:**Adenine nucleotide alpha hydrolase-like<br>**Superfamily:**Nucleotidylyl transferase<br>**Family:**Pantothenate synthetase (Pantoate-beta-alanine ligase, PanC) |
| 87 | c3ij3A_ | Alignment | not modelled | 6.3 | 18 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**cytosol aminopeptidase;<br>**PDBTitle:** 1.8 angstrom resolution crystal structure of cytosol aminopeptidase2 from coxiella burnetii |
| 88 | c1s6cB_ | Alignment | not modelled | 6.2 | 38 | **PDB header:**transport protein<br>**Chain:** B: **PDB Molecule:**potassium voltage-gated channel subfamily d member 2;<br>**PDBTitle:** crystal structure of the complex between kchip1 and kv4.2 n1-30 |
| 89 | c2gzdC_ | Alignment | not modelled | 6.2 | 33 | **PDB header:**protein transport<br>**Chain:** C: **PDB Molecule:**rab11 family-interacting protein 2;<br>**PDBTitle:** crystal structure of rab11 in complex with rab11-fip2 |
| 90 | d1ekxa2 | Alignment | not modelled | 6.2 | 16 | **Fold:**ATC-like<br>**Superfamily:**Aspartate/ornithine carbamoyltransferase<br>**Family:**Aspartate/ornithine carbamoyltransferase |
| 91 | d2pxrc1 | Alignment | not modelled | 6.2 | 25 | **Fold:**Retrovirus capsid protein, N-terminal core domain<br>**Superfamily:**Retrovirus capsid protein, N-terminal core domain<br>**Family:**Retrovirus capsid protein, N-terminal core domain |
| 92 | d1mbsa_ | Alignment | not modelled | 6.1 | 11 | **Fold:**Globin-like<br>**Superfamily:**Globin-like<br>**Family:**Globins |
| 93 | d1mrza2 | Alignment | not modelled | 6.0 | 28 | **Fold:**Adenine nucleotide alpha hydrolase-like<br>**Superfamily:**Nucleotidylyl transferase<br>**Family:**Adenylyltransferase |
| 94 | c2h8oA_ | Alignment | not modelled | 6.0 | 19 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**geranyltranstransferase;<br>**PDBTitle:** the 1.6a crystal structure of the geranyltransferase from2 agrobacterium tumefaciens |
| 95 | c2q4eB_ | Alignment | not modelled | 6.0 | 11 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**probable oxidoreductase at4g09670;<br>**PDBTitle:** ensemble refinement of the protein crystal structure of gene product2 from arabidopsis thaliana at4g09670 |
| 96 | c1r0lD_ | Alignment | not modelled | 6.0 | 18 | **PDB header:**oxidoreductase<br>**Chain:** D: **PDB Molecule:**1-deoxy-d-xylulose 5-phosphate reductoisomerase;<br>**PDBTitle:** 1-deoxy-d-xylulose 5-phosphate reductoisomerase from2 zymomonas mobilis in complex with nadph |
| 97 | c2x5sB_ | Alignment | not modelled | 6.0 | 8 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**mannose-1-phosphate guanylyltransferase;<br>**PDBTitle:** crystal structure of t. maritima gdp-mannose2 pyrophosphorylase in apo state. |
| 98 | d1ccda_ | Alignment | not modelled | 6.0 | 25 | **Fold:**Uteroglobin-like<br>**Superfamily:**Uteroglobin-like<br>**Family:**Uteroglobin-like |
| 99 | d1r6ea_ | Alignment | not modelled | 5.9 | 21 | **Fold:**SopE-like GEF domain<br>**Superfamily:**SopE-like GEF domain<br>**Family:**SopE-like GEF domain |