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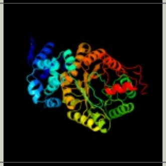
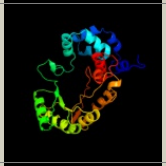
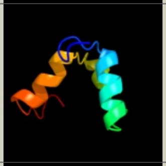
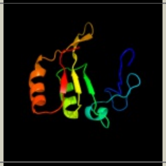
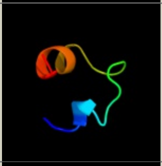
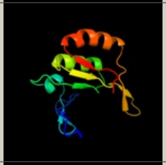
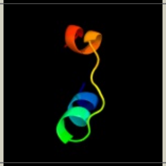
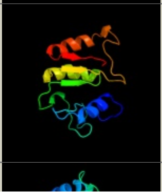
|---|---|
| Email | l.a.kelley@imperial.ac.uk |
| Description | P0AEJ6 |
| Date | Thu Jan 5 11:23:29 GMT 2012 |
| Unique Job ID | 44fc224cd67433e5 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c3abqA_ | Alignment |  | 100.0 | 100 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**ethanolamine ammonia-lyase heavy chain;<br>**PDBTitle:** crystal structure of ethanolamine ammonia-lyase from escherichia coli2 complexed with cn-cbl and 2-amino-1-propanol |
| 2 | c2qezC_ | Alignment |  | 100.0 | 60 | **PDB header:**lyase<br>**Chain:** C: **PDB Molecule:**ethanolamine ammonia-lyase heavy chain;<br>**PDBTitle:** crystal structure of ethanolamine ammonia-lyase heavy chain2 (yp_013784.1) from listeria monocytogenes 4b f2365 at 2.15 a3 resolution |
| 3 | d1eexa_ | Alignment |  | 94.6 | 16 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Cobalamin (vitamin B12)-dependent enzymes<br>**Family:**Diol dehydratase, alpha subunit |
| 4 | d1iwpa_ | Alignment |  | 93.9 | 18 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Cobalamin (vitamin B12)-dependent enzymes<br>**Family:**Diol dehydratase, alpha subunit |
| 5 | c3bwwA_ | Alignment |  | 53.4 | 16 | **PDB header:**metal binding protein<br>**Chain:** A: **PDB Molecule:**protein of unknown function duf692/cog3220;<br>**PDBTitle:** crystal structure of a duf692 family protein (hs_1138) from2 haemophilus somnus 129pt at 2.20 a resolution |
| 6 | c3bq7A_ | Alignment |  | 51.1 | 16 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**diacylglycerol kinase delta;<br>**PDBTitle:** sam domain of diacylglycerol kinase delta1 (e35g) |
| 7 | c2fpgA_ | Alignment |  | 43.0 | 22 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**succinyl-coa ligase [gdp-forming] alpha-chain,<br>**PDBTitle:** crystal structure of pig gtp-specific succinyl-coa2 synthetase in complex with gdp |
| 8 | c1v85A_ | Alignment |  | 39.8 | 10 | **PDB header:**apoptosis<br>**Chain:** A: **PDB Molecule:**similar to ring finger protein 36;<br>**PDBTitle:** sterile alpha motif (sam) domain of mouse bifunctional2 apoptosis regulator |
| 9 | c2nu8D_ | Alignment |  | 37.2 | 21 | **PDB header:**ligase<br>**Chain:** D: **PDB Molecule:**succinyl-coa ligase [adp-forming] subunit alpha;<br>**PDBTitle:** c123at mutant of e. coli succinyl-coa synthetase |
| 10 | c3qmlC_ | Alignment |  | 35.9 | 17 | **PDB header:**chaperone/protein transport<br>**Chain:** C: **PDB Molecule:**nucleotide exchange factor sil1;<br>**PDBTitle:** the structural analysis of sil1-bip complex reveals the mechanism for2 sil1 to function as a novel nucleotide exchange factor |
| 11 | d2csua1 | Alignment |  | 35.9 | 19 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**CoA-binding domain |
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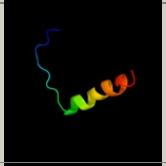
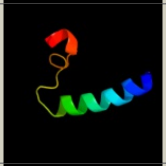
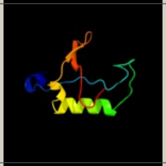
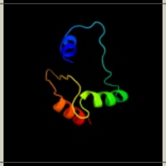
| 12 | c3fokH_ | Alignment |  | 32.5 | 11 | **PDB header:**structural genomics, unknown function<br>**Chain:** H: **PDB Molecule:**uncharacterized protein cgl0159;<br>**PDBTitle:** crystal structure of cgl0159 from corynebacterium2 glutamicum (brevibacterium flavum). northeast structural3 genomics target cgr115 |
| 13 | c3njbA_ | Alignment |  | 30.5 | 10 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**enoyl-coa hydratase;<br>**PDBTitle:** crystal structure of enoyl-coa hydratase from mycobacterium smegmatis,2 iodide soak |
| 14 | c3oqhB_ | Alignment |  | 28.6 | 19 | **PDB header:**ligase<br>**Chain:** B: **PDB Molecule:**putative uncharacterized protein yvmc;<br>**PDBTitle:** crystal structure of b. licheniformis cdps yvmc-blic |
| 15 | c2bh7A_ | Alignment |  | 28.1 | 15 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**n-acetylmuramoyl-l-alanine amidase;<br>**PDBTitle:** crystal structure of a semet derivative of amid at 2.22 angstroms |
| 16 | c2duwA_ | Alignment |  | 28.0 | 28 | **PDB header:**ligand binding protein<br>**Chain:** A: **PDB Molecule:**putative coa-binding protein;<br>**PDBTitle:** solution structure of putative coa-binding protein of2 klebsiella pneumoniae |
| 17 | d1j3ba1 | Alignment |  | 26.5 | 18 | **Fold:**PEP carboxykinase-like<br>**Superfamily:**PEP carboxykinase-like<br>**Family:**PEP carboxykinase C-terminal domain |
| 18 | c3pcsB_ | Alignment |  | 26.2 | 27 | **PDB header:**protein transport/transferase<br>**Chain:** B: **PDB Molecule:**espg;<br>**PDBTitle:** structure of espg-pak2 autoinhibitory ialpha3 helix complex |
| 19 | c3qd5B_ | Alignment |  | 23.7 | 24 | **PDB header:**isomerase<br>**Chain:** B: **PDB Molecule:**putative ribose-5-phosphate isomerase;<br>**PDBTitle:** crystal structure of a putative ribose-5-phosphate isomerase from2 coccidioides immitis solved by combined iodide ion sad and mr |
| 20 | d1iuka_ | Alignment |  | 21.7 | 24 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**CoA-binding domain |
| 21 | d1o1xa_ | Alignment | not modelled | 21.1 | 22 | **Fold:**Ribose/Galactose isomerase RpiB/AlsB<br>**Superfamily:**Ribose/Galactose isomerase RpiB/AlsB<br>**Family:**Ribose/Galactose isomerase RpiB/AlsB |
| 22 | c1ye9E_ | Alignment | not modelled | 20.5 | 25 | **PDB header:**oxidoreductase<br>**Chain:** E: **PDB Molecule:**catalase hpii;<br>**PDBTitle:** crystal structure of proteolytically truncated catalase2 hpii from e. coli |
| 23 | c3bs5A_ | Alignment | not modelled | 20.4 | 14 | **PDB header:**signaling protein/membrane protein<br>**Chain:** A: **PDB Molecule:**protein aveugle;<br>**PDBTitle:** crystal structure of hcnk2-sam/dhyp-sam complex |
| 24 | d1pk1c1 | Alignment | not modelled | 18.8 | 21 | **Fold:**SAM domain-like<br>**Superfamily:**SAM/Pointed domain<br>**Family:**SAM (sterile alpha motif) domain |
| 25 | c2iufA_ | Alignment | not modelled | 18.2 | 25 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**catalase;<br>**PDBTitle:** the structures of penicillium vitale catalase: resting2 state, oxidised state (compound i) and complex with3 aminotriazole |
| 26 | d1a4ea_ | Alignment | not modelled | 18.2 | 17 | **Fold:**Heme-dependent catalase-like<br>**Superfamily:**Heme-dependent catalase-like<br>**Family:**Heme-dependent catalases |
| 27 | c1zcjA_ | Alignment | not modelled | 17.8 | 23 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**peroxisomal bifunctional enzyme;<br>**PDBTitle:** crystal structure of 3-hydroxyacyl-coa dehydrogenase |
| 28 | d1y81a1 | Alignment | not modelled | 17.6 | 37 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**CoA-binding domain |
| 29 | c3oqvA_ | Alignment | not modelled | 17.4 | 27 | **PDB header:**protein binding<br>**Chain:** A: **PDB Molecule:**albc;<br>**PDBTitle:** albc, a cyclodipeptide synthase from streptomyces noursei |

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| 30 | d1si8a_ | Alignment | not modelled | 17.0 | 25 | **Fold:**Heme-dependent catalase-like<br>**Superfamily:**Heme-dependent catalase-like<br>**Family:**Heme-dependent catalases |
| 31 | d1sqia2 | Alignment | not modelled | 17.0 | 19 | **Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Family:**Extradiol dioxygenases |
| 32 | d1e93a_ | Alignment | not modelled | 16.9 | 25 | **Fold:**Heme-dependent catalase-like<br>**Superfamily:**Heme-dependent catalase-like<br>**Family:**Heme-dependent catalases |
| 33 | d1dkua1 | Alignment | not modelled | 16.5 | 18 | **Fold:**PRTase-like<br>**Superfamily:**PRTase-like<br>**Family:**Phosphoribosylpyrophosphate synthetase-like |
| 34 | d1gwea_ | Alignment | not modelled | 16.5 | 38 | **Fold:**Heme-dependent catalase-like<br>**Superfamily:**Heme-dependent catalase-like<br>**Family:**Heme-dependent catalases |
| 35 | d4blca_ | Alignment | not modelled | 16.4 | 33 | **Fold:**Heme-dependent catalase-like<br>**Superfamily:**Heme-dependent catalase-like<br>**Family:**Heme-dependent catalases |
| 36 | d1p80a2 | Alignment | not modelled | 16.4 | 25 | **Fold:**Heme-dependent catalase-like<br>**Superfamily:**Heme-dependent catalase-like<br>**Family:**Heme-dependent catalases |
| 37 | c3ej6D_ | Alignment | not modelled | 16.4 | 25 | **PDB header:**oxidoreductase<br>**Chain:** D: **PDB Molecule:**catalase-3;<br>**PDBTitle:** neurospora crassa catalase-3 crystal structure |
| 38 | d1qwla_ | Alignment | not modelled | 16.2 | 29 | **Fold:**Heme-dependent catalase-like<br>**Superfamily:**Heme-dependent catalase-like<br>**Family:**Heme-dependent catalases |
| 39 | d1otha2 | Alignment | not modelled | 16.1 | 10 | **Fold:**ATC-like<br>**Superfamily:**Aspartate/ornithine carbamoyltransferase<br>**Family:**Aspartate/ornithine carbamoyltransferase |
| 40 | c3lq1A_ | Alignment | not modelled | 16.0 | 21 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-<br>**PDBTitle:** crystal structure of 2-succinyl-6-hydroxy-2,4-cyclohexadiene2 1-carboxylic acid synthase/2-oxoglutarate decarboxylase3 from listeria monocytogenes str. 4b f2365 |
| 41 | c2pc9B_ | Alignment | not modelled | 15.6 | 21 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**phosphoenolpyruvate carboxykinase [atp];<br>**PDBTitle:** crystal structure of atp-dependent phosphoenolpyruvate carboxykinase2 from thermus thermophilus hb8 |
| 42 | c1sy7B_ | Alignment | not modelled | 15.5 | 29 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**catalase 1;<br>**PDBTitle:** crystal structure of the catalase-1 from neurospora crassa, native2 structure at 1.75a resolution. |
| 43 | d1mj3a_ | Alignment | not modelled | 15.2 | 20 | **Fold:**ClpP/crotonase<br>**Superfamily:**ClpP/crotonase<br>**Family:**Crotonase-like |
| 44 | d1m7sa_ | Alignment | not modelled | 15.1 | 25 | **Fold:**Heme-dependent catalase-like<br>**Superfamily:**Heme-dependent catalase-like<br>**Family:**Heme-dependent catalases |
| 45 | c2j2mD_ | Alignment | not modelled | 14.7 | 29 | **PDB header:**oxidoreductase<br>**Chain:** D: **PDB Molecule:**catalase;<br>**PDBTitle:** crystal structure analysis of catalase from exiguobacterium2 oxidotolerans |
| 46 | c2kp7A_ | Alignment | not modelled | 14.4 | 50 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**crossover junction endonuclease mus81;<br>**PDBTitle:** solution nmr structure of the mus81 n-terminal hhh.2 northeast structural genomics consortium target mmt1a |
| 47 | d1ofua2 | Alignment | not modelled | 14.2 | 32 | **Fold:**Bacillus chorismate mutase-like<br>**Superfamily:**Tubulin C-terminal domain-like<br>**Family:**Tubulin, C-terminal domain |
| 48 | c2dhmA_ | Alignment | not modelled | 14.2 | 10 | **PDB header:**protein binding<br>**Chain:** A: **PDB Molecule:**protein bola;<br>**PDBTitle:** solution structure of the bola protein from escherichia coli |
| 49 | c1p81A_ | Alignment | not modelled | 13.7 | 25 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**catalase hpii;<br>**PDBTitle:** crystal structure of the d181e variant of catalase hpii2 from e. coli |
| 50 | c3tr3A_ | Alignment | not modelled | 13.6 | 15 | **PDB header:**unknown function<br>**Chain:** A: **PDB Molecule:**bola;<br>**PDBTitle:** structure of a bola protein homologue from coxiella burnetii |
| 51 | c2xq1M_ | Alignment | not modelled | 13.6 | 29 | **PDB header:**oxidoreductase<br>**Chain:** M: **PDB Molecule:**peroxisomal catalase;<br>**PDBTitle:** crystal structure of peroxisomal catalase from the yeast hansenula2 polymorpha |
| 52 | d1dgfa_ | Alignment | not modelled | 13.6 | 33 | **Fold:**Heme-dependent catalase-like<br>**Superfamily:**Heme-dependent catalase-like<br>**Family:**Heme-dependent catalases |
| 53 | c1xs3A_ | Alignment | not modelled | 13.6 | 15 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**hypothetical protein xc975;<br>**PDBTitle:** solution structure analysis of the xc975 protein |
| 54 | c3mogA_ | Alignment | not modelled | 13.4 | 19 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**probable 3-hydroxybutyryl-coa dehydrogenase;<br>**PDBTitle:** crystal structure of 3-hydroxybutyryl-coa dehydrogenase from2 escherichia coli k12 substr. mg1655 |
| 55 | d2ae9a1 | Alignment | not modelled | 13.1 | 32 | **Fold:**DNA polymerase III theta subunit-like<br>**Superfamily:**DNA polymerase III theta subunit-like |

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|  |  |  |  |  |  | **Family:**DNA polymerase III theta subunit-like |
| 56 | c2gleA_ | Alignment | not modelled | 12.9 | 11 | **PDB header:**protein binding<br>**Chain:** A: **PDB Molecule:**neurabin-1;<br>**PDBTitle:** solution structure of neurabin sam domain |
| 57 | d1kw4a_ | Alignment | not modelled | 12.7 | 13 | **Fold:**SAM domain-like<br>**Superfamily:**SAM/Pointed domain<br>**Family:**SAM (sterile alpha motif) domain |
| 58 | c1f4jC_ | Alignment | not modelled | 12.5 | 33 | **PDB header:**oxidoreductase<br>**Chain:** C: **PDB Molecule:**catalase;<br>**PDBTitle:** structure of tetragonal crystals of human erythrocyte2 catalase |
| 59 | d1nxha_ | Alignment | not modelled | 12.1 | 15 | **Fold:**Hypothetical protein MTH393<br>**Superfamily:**Hypothetical protein MTH393<br>**Family:**Hypothetical protein MTH393 |
| 60 | c3imoC_ | Alignment | not modelled | 12.1 | 42 | **PDB header:**unknown function<br>**Chain:** C: **PDB Molecule:**integron cassette protein;<br>**PDBTitle:** structure from the mobile metagenome of vibrio cholerae.2 integron cassette protein vch_cass14 |
| 61 | d2f6qa1 | Alignment | not modelled | 11.9 | 17 | **Fold:**ClpP/crotonase<br>**Superfamily:**ClpP/crotonase<br>**Family:**Crotonase-like |
| 62 | c1pk1A_ | Alignment | not modelled | 11.7 | 11 | **PDB header:**transcription repression<br>**Chain:** A: **PDB Molecule:**polyhomeotic-proximal chromatin protein;<br>**PDBTitle:** hetero sam domain structure of ph and scm. |
| 63 | c3onoA_ | Alignment | not modelled | 11.5 | 19 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**ribose/galactose isomerase;<br>**PDBTitle:** crystal structure of ribose-5-phosphate isomerase lacab_rpib from2 vibrio parahaemolyticus |
| 64 | d1yzya1 | Alignment | not modelled | 11.5 | 16 | **Fold:**YgbK-like<br>**Superfamily:**YgbK-like<br>**Family:**YgbK-like |
| 65 | d2f2aa1 | Alignment | not modelled | 11.0 | 20 | **Fold:**Amidase signature (AS) enzymes<br>**Superfamily:**Amidase signature (AS) enzymes<br>**Family:**Amidase signature (AS) enzymes |
| 66 | c2pzlB_ | Alignment | not modelled | 10.9 | 15 | **PDB header:**sugar binding protein<br>**Chain:** B: **PDB Molecule:**putative nucleotide sugar epimerase/ dehydratase;<br>**PDBTitle:** crystal structure of the bordetella bronchiseptica enzyme2 wbmg in complex with nad and udp |
| 67 | d1ny8a_ | Alignment | not modelled | 10.6 | 15 | **Fold:**Alpha-lytic protease prodomain-like<br>**Superfamily:**BolA-like<br>**Family:**BolA-like |
| 68 | c3fksY_ | Alignment | not modelled | 10.6 | 16 | **PDB header:**hydrolase<br>**Chain:** Y: **PDB Molecule:**atp synthase subunit gamma, mitochondrial;<br>**PDBTitle:** yeast f1 atpase in the absence of bound nucleotides |
| 69 | d1wwva1 | Alignment | not modelled | 10.1 | 7 | **Fold:**SAM domain-like<br>**Superfamily:**SAM/Pointed domain<br>**Family:**SAM (sterile alpha motif) domain |
| 70 | c3c5yD_ | Alignment | not modelled | 10.0 | 30 | **PDB header:**isomerase<br>**Chain:** D: **PDB Molecule:**ribose/galactose isomerase;<br>**PDBTitle:** crystal structure of a putative ribose 5-phosphate isomerase2 (saro_3514) from novosphingobium aromaticivorans dsm at 1.81 a3 resolution |
| 71 | d2idob1 | Alignment | not modelled | 9.5 | 29 | **Fold:**DNA polymerase III theta subunit-like<br>**Superfamily:**DNA polymerase III theta subunit-like<br>**Family:**DNA polymerase III theta subunit-like |
| 72 | c3bs7A_ | Alignment | not modelled | 9.5 | 14 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**protein aveugle;<br>**PDBTitle:** crystal structure of the sterile alpha motif (sam) domain2 of hyphen/aveugle |
| 73 | c2la7A_ | Alignment | not modelled | 9.5 | 29 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** nmr structure of the protein yp_557733.1 from burkholderia xenovorans |
| 74 | c2ppwA_ | Alignment | not modelled | 9.3 | 17 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**conserved domain protein;<br>**PDBTitle:** the crystal structure of uncharacterized ribose 5-phosphate isomerase2 rpib from streptococcus pneumoniae |
| 75 | d1chka_ | Alignment | not modelled | 9.2 | 17 | **Fold:**Lysozyme-like<br>**Superfamily:**Lysozyme-like<br>**Family:**Chitosanase |
| 76 | c3dqqB_ | Alignment | not modelled | 9.0 | 20 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**putative trna synthase;<br>**PDBTitle:** the crystal structure of the putative trna synthase from salmonella2 typhimurium lt2 |
| 77 | d1ucua_ | Alignment | not modelled | 8.9 | 16 | **Fold:**Phase 1 flagellin<br>**Superfamily:**Phase 1 flagellin<br>**Family:**Phase 1 flagellin |
| 78 | d2bgxa2 | Alignment | not modelled | 8.9 | 15 | **Fold:**N-acetylmuramoyl-L-alanine amidase-like<br>**Superfamily:**N-acetylmuramoyl-L-alanine amidase-like<br>**Family:**N-acetylmuramoyl-L-alanine amidase-like |
| 79 | c2dc0A_ | Alignment | not modelled | 8.7 | 10 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**probable amidase;<br>**PDBTitle:** crystal structure of amidase |
| 80 | c2d3tB_ | Alignment | not modelled | 8.6 | 28 | **PDB header:**lyase, oxidoreductase/transferase<br>**Chain:** B: **PDB Molecule:**fatty oxidation complex alpha subunit;<br>**PDBTitle:** fatty acid beta-oxidation multienzyme complex from2 pseudomonas fragi, form v |
| 81 | c2h2mA_ | Alignment | not modelled | 8.4 | 16 | **PDB header:**metal transport<br>**Chain:** A: **PDB Molecule:**comm domain-containing protein 1;<br>**PDBTitle:** solution structure of the n-terminal domain of commd12 (murr1) |

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| 82 | c2wtbA_ | Alignment | not modelled | 8.3 | 25 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**fatty acid multifunctional protein (atmfp2);<br>**PDBTitle:** arabidopsis thaliana multifuctional protein, mfp2 |
| 83 | c1v60A_ | Alignment | not modelled | 8.2 | 10 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**riken cdna 1810037g04;<br>**PDBTitle:** solution structure of bola1 protein from mus musculus |
| 84 | c3lfmA_ | Alignment | not modelled | 8.1 | 28 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**protein fto;<br>**PDBTitle:** crystal structure of the fat mass and obesity associated (fto) protein2 reveals basis for its substrate specificity |
| 85 | c3ayhB_ | Alignment | not modelled | 8.0 | 12 | **PDB header:**transcription<br>**Chain:** B: **PDB Molecule:**dna-directed rna polymerase iii subunit rpc8;<br>**PDBTitle:** crystal structure of the c17/25 subcomplex from s. pombe rna2 polymerase iii |
| 86 | d1se7a_ | Alignment | not modelled | 7.7 | 29 | **Fold:**DNA polymerase III theta subunit-like<br>**Superfamily:**DNA polymerase III theta subunit-like<br>**Family:**DNA polymerase III theta subunit-like |
| 87 | c2wa0A_ | Alignment | not modelled | 7.6 | 33 | **PDB header:**immune system<br>**Chain:** A: **PDB Molecule:**melanoma-associated antigen 4;<br>**PDBTitle:** crystal structure of the human magea4 |
| 88 | d1t47a2 | Alignment | not modelled | 7.5 | 23 | **Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Family:**Extradiol dioxygenases |
| 89 | d1vmja_ | Alignment | not modelled | 7.5 | 24 | **Fold:**YjbQ-like<br>**Superfamily:**YjbQ-like<br>**Family:**YjbQ-like |
| 90 | d2vvpa1 | Alignment | not modelled | 7.5 | 16 | **Fold:**Ribose/Galactose isomerase RpiB/AlsB<br>**Superfamily:**Ribose/Galactose isomerase RpiB/AlsB<br>**Family:**Ribose/Galactose isomerase RpiB/AlsB |
| 91 | c2fvuA_ | Alignment | not modelled | 7.5 | 50 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**regulatory protein sir3;<br>**PDBTitle:** structure of the yeast sir3 bah domain |
| 92 | d1bqva_ | Alignment | not modelled | 7.4 | 18 | **Fold:**SAM domain-like<br>**Superfamily:**SAM/Pointed domain<br>**Family:**Pointed domain |
| 93 | c3n5lA_ | Alignment | not modelled | 7.3 | 7 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**binding protein component of abc phosphonate transporter;<br>**PDBTitle:** crystal structure of a binding protein component of abc phosphonate2 transporter (pa3383) from pseudomonas aeruginosa at 1.97 a resolution |
| 94 | c3gebC_ | Alignment | not modelled | 7.1 | 27 | **PDB header:**hydrolase<br>**Chain:** C: **PDB Molecule:**eyes absent homolog 2;<br>**PDBTitle:** crystal structure of edeya2 |
| 95 | c2yv1A_ | Alignment | not modelled | 7.1 | 19 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**succinyl-coa ligase [adp-forming] subunit alpha;<br>**PDBTitle:** crystal structure of succinyl-coa synthetase alpha chain from2 methanocaldococcus jannaschii dsm 2661 |
| 96 | c2kveA_ | Alignment | not modelled | 6.8 | 19 | **PDB header:**hormone<br>**Chain:** A: **PDB Molecule:**mesencephalic astrocyte-derived neurotrophic factor;<br>**PDBTitle:** c-terminal domain of mesencephalic astrocyte-derived neurotrophic2 factor (manf) |
| 97 | d1sp9a_ | Alignment | not modelled | 6.8 | 23 | **Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Family:**Extradiol dioxygenases |
| 98 | d1b33b_ | Alignment | not modelled | 6.7 | 25 | **Fold:**Globin-like<br>**Superfamily:**Globin-like<br>**Family:**Phycocyanin-like phycobilisome proteins |
| 99 | d1u1ha1 | Alignment | not modelled | 6.7 | 24 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**UROD/MetE-like<br>**Family:**Cobalamin-independent methionine synthase |