# Phyre2

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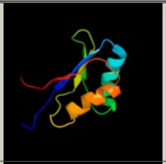
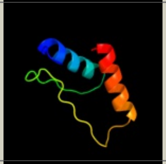
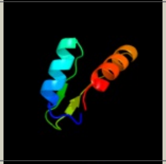
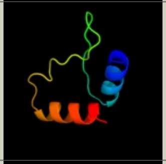
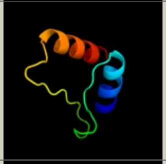
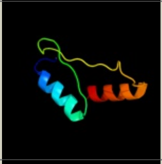
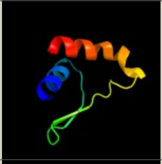
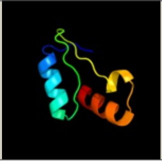
| Email | l.a.kelley@imperial.ac.uk |
| Description | P29131 |
| Date | Thu Jan 5 11:45:35 GMT 2012 |
| Unique Job ID | 73a762ade1748b15 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | d1utaa_ | Alignment |  | 99.9 | 100 | **Fold:**Ferredoxin-like<br>**Superfamily:**Sporulation related repeat<br>**Family:**Sporulation related repeat |
| 2 | c1x60A_ | Alignment |  | 99.8 | 29 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**sporulation-specific n-acetylmuramoyl-l-alanine<br>**PDBTitle:** solution structure of the peptidoglycan binding domain of2 b. subtilis cell wall lytic enzyme cwlc |
| 3 | c3caiA_ | Alignment |  | 88.0 | 22 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**possible aminotransferase;<br>**PDBTitle:** crystal structure of mycobacterium tuberculosis rv3778c2 protein |
| 4 | d1bs0a_ | Alignment |  | 87.6 | 17 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**GABA-aminotransferase-like |
| 5 | d1elua_ | Alignment |  | 85.5 | 13 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**Cystathionine synthase-like |
| 6 | c3f9tB_ | Alignment |  | 81.6 | 19 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**l-tyrosine decarboxylase mfna;<br>**PDBTitle:** crystal structure of l-tyrosine decarboxylase mfna (ec 4.1.1.25)2 (np_247014.1) from methanococcus jannaschii at 2.11 a resolution |
| 7 | d1t3ia_ | Alignment |  | 65.9 | 23 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**Cystathionine synthase-like |
| 8 | c2k49A_ | Alignment |  | 59.9 | 10 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**upf0339 protein so_3888;<br>**PDBTitle:** solution nmr structure of upf0339 protein so3888 from shewanella2 oneidensis. northeast structural genomics consortium target sor190 |
| 9 | d1iuga_ | Alignment |  | 59.2 | 10 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**Cystathionine synthase-like |
| 10 | c3hdoB_ | Alignment |  | 59.1 | 24 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**histidinol-phosphate aminotransferase;<br>**PDBTitle:** crystal structure of a histidinol-phosphate aminotransferase from2 geobacter metallireducens |
| 11 | c3cq6E_ | Alignment |  | 58.3 | 18 | **PDB header:**transferase<br>**Chain:** E: **PDB Molecule:**histidinol-phosphate aminotransferase;<br>**PDBTitle:** histidinol-phosphate aminotransferase from corynebacterium2 glutamicum holo-form (plp covalently bound ) |

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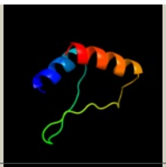
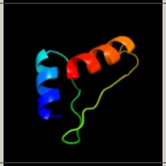
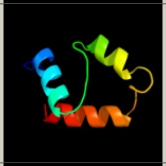
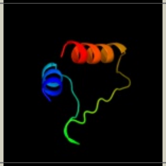
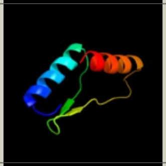
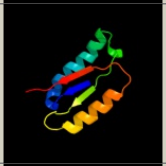
|---|---|---|---|---|---|---|
| 12 | d1m32a_ | Alignment |  | 58.0 | 13 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**Cystathionine synthase-like |
| 13 | c2fyfB_ | Alignment |  | 56.4 | 18 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**phosphoserine aminotransferase;<br>**PDBTitle:** structure of a putative phosphoserine aminotransferase from2 mycobacterium tuberculosis |
| 14 | c2yrrA_ | Alignment |  | 52.9 | 23 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**aminotransferase, class v;<br>**PDBTitle:** hypothetical alanine aminotransferase (tth0173) from thermus2 thermophilus hb8 |
| 15 | d1qz9a_ | Alignment |  | 52.8 | 13 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**Cystathionine synthase-like |
| 16 | d1v72a1 | Alignment |  | 52.6 | 22 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**AAT-like |
| 17 | c3hqtB_ | Alignment |  | 49.8 | 19 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**cai-1 autoinducer synthase;<br>**PDBTitle:** plp-dependent acyl-coa transferase cqsa |
| 18 | d1wyua1 | Alignment |  | 47.6 | 20 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**Glycine dehydrogenase subunits (GDC-P) |
| 19 | c3rggD_ | Alignment |  | 46.5 | 19 | **PDB header:**lyase<br>**Chain:** D: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase, pure protein;<br>**PDBTitle:** crystal structure of treponema denticola pure bound to air |
| 20 | d2f8ja1 | Alignment |  | 46.5 | 22 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**AAT-like |
| 21 | c2k8eA_ | Alignment | not modelled | 46.3 | 11 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**upf0339 protein yegp;<br>**PDBTitle:** solution nmr structure of protein of unknown function yegp from e.2 coli. ontario center for structural proteomics target ec0640_1_1233 northeast structural genomics consortium target et102. |
| 22 | d1eg5a_ | Alignment | not modelled | 44.5 | 17 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**Cystathionine synthase-like |
| 23 | c3p3dA_ | Alignment | not modelled | 44.2 | 21 | **PDB header:**nuclear protein<br>**Chain:** A: **PDB Molecule:**nucleoporin 53;<br>**PDBTitle:** crystal structure of the nup53 rrm domain from pichia guilliermondii |
| 24 | d1gcca_ | Alignment | not modelled | 43.5 | 26 | **Fold:**DNA-binding domain<br>**Superfamily:**DNA-binding domain<br>**Family:**GCC-box binding domain |
| 25 | c2adbA_ | Alignment | not modelled | 43.0 | 9 | **PDB header:**rna binding protein/rna<br>**Chain:** A: **PDB Molecule:**polypyrimidine tract-binding protein 1;<br>**PDBTitle:** solution structure of polypyrimidine tract binding protein2 rbd2 complexed with cucucu rna |
| 26 | d1dq3a4 | Alignment | not modelled | 41.6 | 14 | **Fold:**Homing endonuclease-like<br>**Superfamily:**Homing endonucleases<br>**Family:**Intein endonuclease |
| 27 | c2y9jt_ | Alignment | not modelled | 41.0 | 14 | **PDB header:**protein transport<br>**Chain:** T: **PDB Molecule:**protein prgh;<br>**PDBTitle:** three-dimensional model of salmonella's needle complex at2 subnanometer resolution |
| 28 | d1u11a_ | Alignment | not modelled | 40.0 | 16 | **Fold:**Flavodoxin-like<br>**Superfamily:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) |

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|  |  |  |  |  |  | **Family:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) |
| 29 | c2w8wA_ | Alignment | not modelled | 39.7 | 19 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**serine palmitoyltransferase;<br>**PDBTitle:** n100y spt with plp-ser |
| 30 | d2c0ra1 | Alignment | not modelled | 38.5 | 16 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**GABA-aminotransferase-like |
| 31 | c2x7iA_ | Alignment | not modelled | 37.9 | 17 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**mevalonate kinase;<br>**PDBTitle:** crystal structure of mevalonate kinase from methicillin-2 resistant staphylococcus aureus mrsa252 |
| 32 | c3a2bA_ | Alignment | not modelled | 37.6 | 13 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**serine palmitoyltransferase;<br>**PDBTitle:** crystal structure of serine palmitoyltransferase from sphingobacterium2 multivorum with substrate l-serine |
| 33 | d1ztpa1 | Alignment | not modelled | 36.4 | 8 | **Fold:**eIF4e-like<br>**Superfamily:**eIF4e-like<br>**Family:**BLES03-like |
| 34 | d1nz8a_ | Alignment | not modelled | 35.9 | 17 | **Fold:**Ferredoxin-like<br>**Superfamily:**N-utilization substance G protein NusG, N-terminal domain<br>**Family:**N-utilization substance G protein NusG, N-terminal domain |
| 35 | d1wg1a_ | Alignment | not modelled | 35.7 | 8 | **Fold:**Ferredoxin-like<br>**Superfamily:**RNA-binding domain, RBD<br>**Family:**Canonical RBD |
| 36 | c2fw9A_ | Alignment | not modelled | 35.2 | 16 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**n5-carboxyaminoimidazole ribonucleotide mutase;<br>**PDBTitle:** structure of pure (n5-carboxyaminoimidazole ribonucleotide mutase)2 h59f from the acidophilic bacterium acetobacter aceti, at ph 8 |
| 37 | d2hk6a1 | Alignment | not modelled | 33.5 | 15 | **Fold:**Chelatase-like<br>**Superfamily:**Chelatase<br>**Family:**Ferrochelatase |
| 38 | d1jf9a_ | Alignment | not modelled | 33.3 | 17 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**Cystathionine synthase-like |
| 39 | c3f0hA_ | Alignment | not modelled | 33.2 | 13 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**aminotransferase;<br>**PDBTitle:** crystal structure of aminotransferase (rer070207000802) from2 eubacterium rectale at 1.70 a resolution |
| 40 | c3pn8A_ | Alignment | not modelled | 32.3 | 18 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**putative phospho-beta-glucosidase;<br>**PDBTitle:** the crystal structure of 6-phospho-beta-glucosidase from streptococcus2 mutans ua159 |
| 41 | c3lp6D_ | Alignment | not modelled | 32.1 | 21 | **PDB header:**lyase<br>**Chain:** D: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase catalytic subunit;<br>**PDBTitle:** crystal structure of rv3275c-e60a from mycobacterium tuberculosis at2 1.7a resolution |
| 42 | d1qcza_ | Alignment | not modelled | 31.8 | 16 | **Fold:**Flavodoxin-like<br>**Superfamily:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)<br>**Family:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) |
| 43 | c3e9kA_ | Alignment | not modelled | 31.1 | 17 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**kynureninase;<br>**PDBTitle:** crystal structure of homo sapiens kynureninase-3-hydroxyhippuric acid2 inhibitor complex |
| 44 | c3trhI_ | Alignment | not modelled | 30.8 | 16 | **PDB header:**lyase<br>**Chain:** I: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase<br>**PDBTitle:** structure of a phosphoribosylaminoimidazole carboxylase catalytic2 subunit (pure) from coxiella burnetii |
| 45 | c2dr1A_ | Alignment | not modelled | 29.2 | 11 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**386aa long hypothetical serine aminotransferase;<br>**PDBTitle:** crystal structure of the ph1308 protein from pyrococcus horikoshii ot3 |
| 46 | d1m6sa_ | Alignment | not modelled | 28.6 | 16 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**AAT-like |
| 47 | c1yj7A_ | Alignment | not modelled | 28.6 | 12 | **PDB header:**protein transport<br>**Chain:** A: **PDB Molecule:**escj;<br>**PDBTitle:** crystal structure of enteropathogenic e.coli (epec) type iii secretion2 system protein escj |
| 48 | d1nh8a2 | Alignment | not modelled | 28.1 | 12 | **Fold:**Ferredoxin-like<br>**Superfamily:**GlnB-like<br>**Family:**ATP phosphoribosyltransferase (ATP-PRTase, HisG), regulatory C-terminal domain |
| 49 | c3rfaA_ | Alignment | not modelled | 27.8 | 17 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**ribosomal rna large subunit methyltransferase n;<br>**PDBTitle:** x-ray structure of rlmn from escherichia coli in complex with s-2 adenosylmethionine |
| 50 | c2k06A_ | Alignment | not modelled | 27.5 | 13 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**transcription antitermination protein nusg;<br>**PDBTitle:** solution structure of the aminoterminal domain of e. coli2 nusg |
| 51 | c3cbfA_ | Alignment | not modelled | 26.8 | 15 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**alpha-aminodipate aminotransferase;<br>**PDBTitle:** crystal structure of lysn, alpha-aminoadipate2 aminotransferase, from thermus thermophilus hb27 |
| 52 | c2j75A_ | Alignment | not modelled | 26.7 | 18 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**beta-glucosidase a;<br>**PDBTitle:** beta-glucosidase from thermotoga maritima in complex |

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| | | | | | | with2 noeuromycin |
| 53 | c3hyjD_ | Alignment | not modelled | 26.5 | 22 | **PDB header:**transcription regulator<br>**Chain:** D: **PDB Molecule:**protein duf199/whia;<br>**PDBTitle:** crystal structure of the n-terminal laglidadg domain of duf199/whia |
| 54 | c3orsD_ | Alignment | not modelled | 26.3 | 17 | **PDB header:**isomerase,biosynthetic protein<br>**Chain:** D: **PDB Molecule:**n5-carboxyaminoimidazole ribonucleotide mutase;<br>**PDBTitle:** crystal structure of n5-carboxyaminoimidazole ribonucleotide mutase2 from staphylococcus aureus |
| 55 | d1xmpa_ | Alignment | not modelled | 26.2 | 18 | **Fold:**Flavodoxin-like<br>**Superfamily:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)<br>**Family:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) |
| 56 | c3nthA_ | Alignment | not modelled | 25.0 | 16 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**maternal protein tudor;<br>**PDBTitle:** crystal structure of tudor and aubergine [r13(me2s)] complex |
| 57 | c3mafB_ | Alignment | not modelled | 24.1 | 17 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**sphingosine-1-phosphate lyase;<br>**PDBTitle:** crystal structure of stspl (asymmetric form) |
| 58 | d1js3a_ | Alignment | not modelled | 23.7 | 6 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**Pyridoxal-dependent decarboxylase |
| 59 | c2hzpA_ | Alignment | not modelled | 23.7 | 17 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**kynureninase;<br>**PDBTitle:** crystal structure of homo sapiens kynureninase |
| 60 | c2p2uA_ | Alignment | not modelled | 23.6 | 41 | **PDB header:**dna binding protein<br>**Chain:** A: **PDB Molecule:**host-nuclease inhibitor protein gam, putative;<br>**PDBTitle:** crystal structure of putative host-nuclease inhibitor2 protein gam from desulfovibrio vulgaris |
| 61 | c2h31A_ | Alignment | not modelled | 23.3 | 18 | **PDB header:**ligase, lyase<br>**Chain:** A: **PDB Molecule:**multifunctional protein ade2;<br>**PDBTitle:** crystal structure of human paics, a bifunctional carboxylase and2 synthetase in purine biosynthesis |
| 62 | c3nohA_ | Alignment | not modelled | 23.1 | 50 | **PDB header:**peptide binding protein<br>**Chain:** A: **PDB Molecule:**putative peptide binding protein;<br>**PDBTitle:** crystal structure of a putative peptide binding protein (rumgna_00914)2 from ruminococcus gnavus atcc 29149 at 1.60 a resolution |
| 63 | d1u0bb1 | Alignment | not modelled | 22.5 | 16 | **Fold:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases<br>**Superfamily:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases<br>**Family:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases |
| 64 | c3bfjK_ | Alignment | not modelled | 21.3 | 15 | **PDB header:**oxidoreductase<br>**Chain:** K: **PDB Molecule:**1,3-propanediol oxidoreductase;<br>**PDBTitle:** crystal structure analysis of 1,3-propanediol oxidoreductase |
| 65 | c2q5cA_ | Alignment | not modelled | 21.1 | 18 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**ntrc family transcriptional regulator;<br>**PDBTitle:** crystal structure of ntrc family transcriptional regulator from2 clostridium acetobutylicum |
| 66 | d2cpia1 | Alignment | not modelled | 21.0 | 11 | **Fold:**Ferredoxin-like<br>**Superfamily:**RNA-binding domain, RBD<br>**Family:**Canonical RBD |
| 67 | d1oj4a2 | Alignment | not modelled | 20.4 | 11 | **Fold:**Ferredoxin-like<br>**Superfamily:**GHMP Kinase, C-terminal domain<br>**Family:**4-(cytidine 5'-diphospho)-2C-methyl-D-erythritol kinase IspE |
| 68 | d1lbqa_ | Alignment | not modelled | 20.1 | 13 | **Fold:**Chelatase-like<br>**Superfamily:**Chelatase<br>**Family:**Ferrochelatase |
| 69 | c2huuA_ | Alignment | not modelled | 20.1 | 13 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**alanine glyoxylate aminotransferase;<br>**PDBTitle:** crystal structure of aedes aegypti alanine glyoxylate2 aminotransferase in complex with alanine |
| 70 | c3ffrA_ | Alignment | not modelled | 20.0 | 13 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**phosphoserine aminotransferase serc;<br>**PDBTitle:** crystal structure of a phosphoserine aminotransferase serc (chu_0995)2 from cytophaga hutchinsonii atcc 33406 at 1.75 a resolution |
| 71 | d1rk8a_ | Alignment | not modelled | 19.7 | 11 | **Fold:**Ferredoxin-like<br>**Superfamily:**RNA-binding domain, RBD<br>**Family:**Canonical RBD |
| 72 | d1fg7a_ | Alignment | not modelled | 19.5 | 17 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**AAT-like |
| 73 | c3ox4D_ | Alignment | not modelled | 19.3 | 19 | **PDB header:**oxidoreductase<br>**Chain:** D: **PDB Molecule:**alcohol dehydrogenase 2;<br>**PDBTitle:** structures of iron-dependent alcohol dehydrogenase 2 from zymomonas2 mobilis zm4 complexed with nad cofactor |
| 74 | c2eqkA_ | Alignment | not modelled | 19.0 | 43 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**tudor domain-containing protein 4;<br>**PDBTitle:** solution structure of the tudor domain of tudor domain-2 containing protein 4 |
| 75 | d1wsta1 | Alignment | not modelled | 18.9 | 10 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**AAT-like |
| 76 | d2erra1 | Alignment | not modelled | 18.4 | 8 | **Fold:**Ferredoxin-like<br>**Superfamily:**RNA-binding domain, RBD<br>**Family:**Canonical RBD |
| 77 | c3o6cA_ | Alignment | not modelled | 18.1 | 12 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**pyridoxine 5'-phosphate synthase; |

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| 77 | c3o6cA_ | Alignment | not modelled | 18.1 | 12 | **PDBTitle:** pyridoxal phosphate biosynthetic protein pdxj from campylobacter2 jejuni |
| 78 | c3hyiA_ | Alignment | not modelled | 18.0 | 18 | **PDB header:**transcription regulator<br>**Chain:** A: **PDB Molecule:**protein duf199/whia;<br>**PDBTitle:** crystal structure of full-length duf199/whia from thermatoga maritima |
| 79 | d1s0aa_ | Alignment | not modelled | 17.9 | 6 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**GABA-aminotransferase-like |
| 80 | c2z1sA_ | Alignment | not modelled | 17.8 | 18 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**beta-glucosidase b;<br>**PDBTitle:** beta-glucosidase b from paenibacillus polymyxa complexed2 with cellotetraose |
| 81 | c2ordA_ | Alignment | not modelled | 17.6 | 15 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**acetylornithine aminotransferase;<br>**PDBTitle:** crystal structure of acetylornithine aminotransferase (ec 2.6.1.11)2 (acoat) (tm1785) from thermotoga maritima at 1.40 a resolution |
| 82 | d1kvka2 | Alignment | not modelled | 17.1 | 19 | **Fold:**Ferredoxin-like<br>**Superfamily:**GHMP Kinase, C-terminal domain<br>**Family:**Mevalonate kinase |
| 83 | c2hvzA_ | Alignment | not modelled | 16.8 | 7 | **PDB header:**rna binding protein<br>**Chain:** A: **PDB Molecule:**splicing factor, arginine/serine-rich 7;<br>**PDBTitle:** solution structure of the rrm domain of sr rich factor 9g8 |
| 84 | c2i38A_ | Alignment | not modelled | 16.6 | 12 | **PDB header:**rna binding protein/chimera<br>**Chain:** A: **PDB Molecule:**fusion protein consists of immunoglobin g-<br>**PDBTitle:** solution structure of the rrm of srp20 |
| 85 | c2zoxA_ | Alignment | not modelled | 16.1 | 18 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**cytosolic beta-glucosidase;<br>**PDBTitle:** crystal structure of the covalent intermediate of human cytosolic2 beta-glucosidase |
| 86 | c2iruA_ | Alignment | not modelled | 16.0 | 24 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**putative dna ligase-like protein rv0938/mt0965;<br>**PDBTitle:** crystal structure of the polymerase domain from mycobacterium2 tuberculosis ligase d |
| 87 | c2dclB_ | Alignment | not modelled | 15.9 | 19 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**hypothetical upf0166 protein ph1503;<br>**PDBTitle:** structure of ph1503 protein from pyrococcus horikoshii ot3 |
| 88 | d1fsha_ | Alignment | not modelled | 15.9 | 16 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**"Winged helix" DNA-binding domain<br>**Family:**DEP domain |
| 89 | c3md3A_ | Alignment | not modelled | 15.9 | 4 | **PDB header:**rna binding protein<br>**Chain:** A: **PDB Molecule:**nuclear and cytoplasmic polyadenylated rna-binding protein<br>**PDBTitle:** crystal structure of the first two rrm domains of yeast poly(u)2 binding protein (pub1) |
| 90 | d2p5ia1 | Alignment | not modelled | 15.7 | 27 | **Fold:**Class II aaRS and biotin synthetases<br>**Superfamily:**Class II aaRS and biotin synthetases<br>**Family:**LplA-like |
| 91 | c3ml6D_ | Alignment | not modelled | 15.5 | 15 | **PDB header:**protein transport<br>**Chain:** D: **PDB Molecule:**chimeric complex between protein dishevlled2 homolog dvl-2<br>**PDBTitle:** a complex between dishevlled2 and clathrin adaptor ap-2 |
| 92 | d1pbga_ | Alignment | not modelled | 15.2 | 14 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**(Trans)glycosidases<br>**Family:**Family 1 of glycosyl hydrolase |
| 93 | d1o51a_ | Alignment | not modelled | 14.6 | 16 | **Fold:**Ferredoxin-like<br>**Superfamily:**GlnB-like<br>**Family:**DUF190/COG1993 |
| 94 | c1v02F_ | Alignment | not modelled | 14.2 | 20 | **PDB header:**hydrolase<br>**Chain:** F: **PDB Molecule:**dhurrinase;<br>**PDBTitle:** crystal structure of the sorghum bicolor dhurrinase 1 |
| 95 | d1v02a_ | Alignment | not modelled | 14.2 | 20 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**(Trans)glycosidases<br>**Family:**Family 1 of glycosyl hydrolase |
| 96 | d2a21a1 | Alignment | not modelled | 14.2 | 15 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Aldolase<br>**Family:**Class I DAHP synthetase |
| 97 | d2k7ia1 | Alignment | not modelled | 14.1 | 11 | **Fold:**YegP-like<br>**Superfamily:**YegP-like<br>**Family:**YegP-like |
| 98 | c2k7iB_ | Alignment | not modelled | 14.1 | 11 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**upf0339 protein atu0232;<br>**PDBTitle:** solution nmr structure of protein atu0232 from agrobacterium2 tumefaciens. northeast structural genomics consortium (nesg) target3 att3. ontario center for structural proteomics target atc0223. |
| 99 | d1rv3a_ | Alignment | not modelled | 14.1 | 10 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**GABA-aminotransferase-like |