Phyre2

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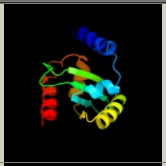
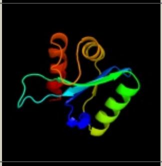
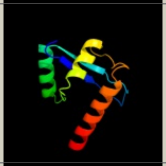
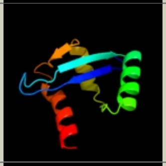
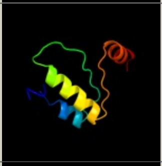
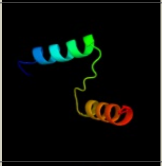
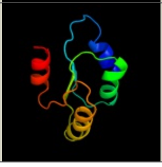
| Email | l.a.kelley@imperial.ac.uk |
| Description | P76299 |
| Date | Thu Jan 5 12:21:41 GMT 2012 |
| Unique Job ID | d3850a5c16b2d61f |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c2jlhA_ | Alignment |  | 100.0 | 34 | **PDB header:**protein transport<br>**Chain:** A: **PDB Molecule:**yop proteins translocation protein u;<br>**PDBTitle:** crystal structure of the cytoplasmic domain of yersinia2 pestis yscu n263a mutant |
| 2 | c3bzrA_ | Alignment |  | 100.0 | 28 | **PDB header:**membrane protein, protein transport<br>**Chain:** A: **PDB Molecule:**escu;<br>**PDBTitle:** crystal structure of escu c-terminal domain with n262d mutation, space2 group p 41 21 2 |
| 3 | d3bzra1 | Alignment |  | 100.0 | 28 | **Fold:**EscU C-terminal domain-like<br>**Superfamily:**EscU C-terminal domain-like<br>**Family:**EscU C-terminal domain-like |
| 4 | c3t7yB_ | Alignment |  | 100.0 | 31 | **PDB header:**protein transport<br>**Chain:** B: **PDB Molecule:**yop proteins translocation protein u;<br>**PDBTitle:** structure of an autocleavage-inactive mutant of the cytoplasmic domain2 of ct091, the yscu homologue of chlamydia trachomatis |
| 5 | c3c01H_ | Alignment |  | 99.9 | 20 | **PDB header:**membrane protein, protein transport<br>**Chain:** H: **PDB Molecule:**surface presentation of antigens protein spas;<br>**PDBTitle:** crystal structural of native spas c-terminal domain |
| 6 | c3c00B_ | Alignment |  | 99.9 | 30 | **PDB header:**membrane protein, protein transport<br>**Chain:** B: **PDB Molecule:**escu;<br>**PDBTitle:** crystal structural of the mutated g247t escu/spas c-terminal domain |
| 7 | c2vt1B_ | Alignment |  | 99.9 | 23 | **PDB header:**membrane protein<br>**Chain:** B: **PDB Molecule:**surface presentation of antigens protein spas;<br>**PDBTitle:** crystal structure of the cytoplasmic domain of spa40, the2 specificity switch for the shigella flexneri type iii3 secretion system |
| 8 | c2yvqA_ | Alignment |  | 87.1 | 17 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**carbamoyl-phosphate synthase;<br>**PDBTitle:** crystal structure of mgs domain of carbamoyl-phosphate2 synthetase from homo sapiens |
| 9 | d1a0rp_ | Alignment |  | 76.9 | 17 | **Fold:**Thioredoxin fold<br>**Superfamily:**Thioredoxin-like<br>**Family:**Phosducin |
| 10 | d1wo8a1 | Alignment |  | 75.8 | 20 | **Fold:**Methylglyoxal synthase-like<br>**Superfamily:**Methylglyoxal synthase-like<br>**Family:**Methylglyoxal synthase, MgsA |
| 11 | d2nu7b1 | Alignment |  | 73.4 | 17 | **Fold:**Flavodoxin-like<br>**Superfamily:**Succinyl-CoA synthetase domains<br>**Family:**Succinyl-CoA synthetase domains |

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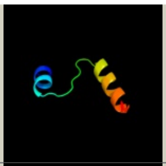
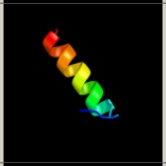
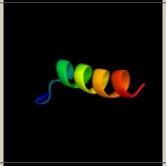
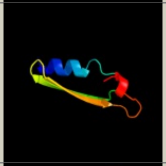
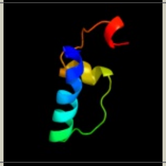
|---|---|---|---|---|---|---|
| 12 | d1a9xa2 | Alignment |  | 64.9 | 13 | **Fold:**Methylglyoxal synthase-like<br>**Superfamily:**Methylglyoxal synthase-like<br>**Family:**Carbamoyl phosphate synthetase, large subunit allosteric, C-terminal domain |
| 13 | d1uk5a_ | Alignment |  | 62.6 | 24 | **Fold:**Spectrin repeat-like<br>**Superfamily:**BAG domain<br>**Family:**BAG domain |
| 14 | d1ugoa_ | Alignment |  | 62.5 | 14 | **Fold:**Spectrin repeat-like<br>**Superfamily:**BAG domain<br>**Family:**BAG domain |
| 15 | c3peuB_ | Alignment |  | 62.0 | 21 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**nucleoporin gle1;<br>**PDBTitle:** s. cerevisiae dbp5 l327v c-terminal domain bound to gle1 h337r and ip6 |
| 16 | d1m7ka_ | Alignment |  | 57.9 | 10 | **Fold:**Spectrin repeat-like<br>**Superfamily:**BAG domain<br>**Family:**BAG domain |
| 17 | c1yj7A_ | Alignment |  | 57.0 | 17 | **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 |
| 18 | d1d8ja_ | Alignment |  | 56.0 | 10 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**"Winged helix" DNA-binding domain<br>**Family:**The central core domain of TFIIE beta |
| 19 | c3a8yD_ | Alignment |  | 53.9 | 24 | **PDB header:**hydrolase<br>**Chain:** D: **PDB Molecule:**bag family molecular chaperone regulator 5;<br>**PDBTitle:** crystal structure of the complex between the bag5 bd5 and2 hsp70 nbd |
| 20 | d1rv3a_ | Alignment |  | 53.6 | 34 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**GABA-aminotransferase-like |
| 21 | d1eucb1 | Alignment | not modelled | 50.1 | 17 | **Fold:**Flavodoxin-like<br>**Superfamily:**Succinyl-CoA synthetase domains<br>**Family:**Succinyl-CoA synthetase domains |
| 22 | d1mv8a2 | Alignment | not modelled | 49.8 | 10 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain |
| 23 | c1r6xA_ | Alignment | not modelled | 49.5 | 25 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**atp:sulfate adenylyltransferase;<br>**PDBTitle:** the crystal structure of a truncated form of yeast atp2 sulfurylase, lacking the c-terminal aps kinase-like domain,3 in complex with sulfate |
| 24 | d2a7va1 | Alignment | not modelled | 49.1 | 34 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**GABA-aminotransferase-like |
| 25 | c2a7vA_ | Alignment | not modelled | 49.1 | 34 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**serine hydroxymethyltransferase;<br>**PDBTitle:** human mitochondrial serine hydroxymethyltransferase 2 |
| 26 | d1ko7a1 | Alignment | not modelled | 48.5 | 12 | **Fold:**MurF and HprK N-domain-like<br>**Superfamily:**HprK N-terminal domain-like<br>**Family:**HPr kinase/phoshatase HprK N-terminal domain |
| 27 | d1g8fa2 | Alignment | not modelled | 47.8 | 24 | **Fold:**Adenine nucleotide alpha hydrolase-like<br>**Superfamily:**Nucleotidylyl transferase<br>**Family:**ATP sulfurylase catalytic domain |
| 28 | c2o14A_ | Alignment | not modelled | 47.2 | 16 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**hypothetical protein yxim;<br>**PDBTitle:** x-ray crystal structure of protein yxim_bacsu from bacillus2 subtilis. northeast structural genomics consortium target3 sr595 |

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| 29 | c2vycA_ | Alignment | not modelled | 46.8 | 22 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**biodegradative arginine decarboxylase;<br>**PDBTitle:** crystal structure of acid induced arginine decarboxylase2 from e. coli |
| 30 | d2csua3 | Alignment | not modelled | 44.8 | 27 | **Fold:**Flavodoxin-like<br>**Superfamily:**Succinyl-CoA synthetase domains<br>**Family:**Succinyl-CoA synthetase domains |
| 31 | d1t9ba1 | Alignment | not modelled | 43.5 | 13 | **Fold:**DHS-like NAD/FAD-binding domain<br>**Superfamily:**DHS-like NAD/FAD-binding domain<br>**Family:**Pyruvate oxidase and decarboxylase, middle domain |
| 32 | d1knxa1 | Alignment | not modelled | 43.4 | 15 | **Fold:**MurF and HprK N-domain-like<br>**Superfamily:**HprK N-terminal domain-like<br>**Family:**HPr kinase/phoshatase HprK N-terminal domain |
| 33 | c3nysA_ | Alignment | not modelled | 41.2 | 19 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**aminotransferase wbpe;<br>**PDBTitle:** x-ray structure of the k185a mutant of wbpe (wlbe) from pseudomonas2 aeruginosa in complex with plp at 1.45 angstrom resolution |
| 34 | d1bj4a_ | Alignment | not modelled | 37.6 | 29 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**GABA-aminotransferase-like |
| 35 | c1c4kA_ | Alignment | not modelled | 37.5 | 13 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**protein (ornithine decarboxylase);<br>**PDBTitle:** ornithine decarboxylase mutant (gly121tyr) |
| 36 | c2r18A_ | Alignment | not modelled | 37.2 | 26 | **PDB header:**viral protein<br>**Chain:** A: **PDB Molecule:**capsid assembly protein vp3;<br>**PDBTitle:** structural insights into the multifunctional protein vp3 of2 birnaviruses |
| 37 | d1oi7a1 | Alignment | not modelled | 36.7 | 15 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**CoA-binding domain |
| 38 | c3iynO_ | Alignment | not modelled | 35.9 | 24 | **PDB header:**virus<br>**Chain:** O: **PDB Molecule:**hexon-associated protein;<br>**PDBTitle:** 3.6-angstrom cryoem structure of human adenovirus type 5 |
| 39 | c2qjfB_ | Alignment | not modelled | 35.0 | 18 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**bifunctional 3'-phosphoadenosine 5'-<br>**PDBTitle:** crystal structure of atp-sulfurylase domain of human paps2 synthetase 1 |
| 40 | c3bcxA_ | Alignment | not modelled | 34.0 | 18 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**cdp-6-deoxy-l-threo-d-glycero-4-hexulose-3-<br>**PDBTitle:** e1 dehydrase |
| 41 | d2nu7a1 | Alignment | not modelled | 33.8 | 12 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**CoA-binding domain |
| 42 | d1gqoa_ | Alignment | not modelled | 33.1 | 34 | **Fold:**Flavodoxin-like<br>**Superfamily:**Type II 3-dehydroquinate dehydratase<br>**Family:**Type II 3-dehydroquinate dehydratase |
| 43 | d1f6ga_ | Alignment | not modelled | 32.9 | 13 | **Fold:**Voltage-gated potassium channels<br>**Superfamily:**Voltage-gated potassium channels<br>**Family:**Voltage-gated potassium channels |
| 44 | d1vmda_ | Alignment | not modelled | 32.7 | 14 | **Fold:**Methylglyoxal synthase-like<br>**Superfamily:**Methylglyoxal synthase-like<br>**Family:**Methylglyoxal synthase, MgsA |
| 45 | c3me5A_ | Alignment | not modelled | 31.9 | 26 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**cytosine-specific methyltransferase;<br>**PDBTitle:** crystal structure of putative dna cytosine methylase from shigella2 flexneri 2a str. 301 |
| 46 | d1qzxa2 | Alignment | not modelled | 31.3 | 35 | **Fold:**Signal peptide-binding domain<br>**Superfamily:**Signal peptide-binding domain<br>**Family:**Signal peptide-binding domain |
| 47 | c1yrwA_ | Alignment | not modelled | 30.6 | 18 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**protein arna;<br>**PDBTitle:** crystal structure of e.coli arna transformylase domain |
| 48 | c3e6gA_ | Alignment | not modelled | 30.2 | 18 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**cystathionine gamma-lyase-like protein;<br>**PDBTitle:** crystal structure of xometc, a cystathionine c-lyase-like2 protein from xanthomonas oryzae pv.oryzae |
| 49 | d2naca2 | Alignment | not modelled | 29.5 | 27 | **Fold:**Flavodoxin-like<br>**Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like<br>**Family:**Formate/glycerate dehydrogenases, substrate-binding domain |
| 50 | c3dm5A_ | Alignment | not modelled | 29.5 | 19 | **PDB header:**rna binding protein, transport protein<br>**Chain:** A: **PDB Molecule:**signal recognition 54 kda protein;<br>**PDBTitle:** structures of srp54 and srp19, the two proteins assembling2 the ribonucleic core of the signal recognition particle3 from the archaeon pyrococcus furiosus. |
| 51 | d1c4ka2 | Alignment | not modelled | 28.7 | 13 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**Ornithine decarboxylase major domain |
| 52 | d1ydwa1 | Alignment | not modelled | 28.6 | 16 | **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 |
| 53 | d1vl2a1 | Alignment | not modelled | 28.5 | 17 | **Fold:**Adenine nucleotide alpha hydrolase-like<br>**Superfamily:**Adenine nucleotide alpha hydrolases-like<br>**Family:**N-type ATP pyrophosphatases |
| 54 | c2po3B_ | Alignment | not modelled | 28.4 | 17 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**4-dehydrase;<br>**PDBTitle:** crystal structure analysis of desi in the presence of its2 tdp-sugar product |

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| 55 | c3n8kG_ | Alignment | not modelled | 28.1 | 39 | **PDB header:**lyase<br>**Chain:** G: **PDB Molecule:**3-dehydroquinate dehydratase;<br>**PDBTitle:** type ii dehydroquinase from mycobacterium tuberculosis complexed with2 citrazinic acid |
| 56 | d1ni5a1 | Alignment | not modelled | 28.0 | 6 | **Fold:**Adenine nucleotide alpha hydrolase-like<br>**Superfamily:**Adenine nucleotide alpha hydrolases-like<br>**Family:**PP-loop ATPase |
| 57 | c2jqeA_ | Alignment | not modelled | 27.6 | 25 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**signal recognition 54 kda protein;<br>**PDBTitle:** soution structure of af54 m-domain |
| 58 | c3qi6B_ | Alignment | not modelled | 27.5 | 17 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**cystathionine gamma-synthase metb (cgs);<br>**PDBTitle:** crystal structure of cystathionine gamma-synthase metb (cgs) from2 mycobacterium ulcerans agy99 |
| 59 | d1cs1a_ | Alignment | not modelled | 27.5 | 12 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**Cystathionine synthase-like |
| 60 | d1wy5a1 | Alignment | not modelled | 27.4 | 16 | **Fold:**Adenine nucleotide alpha hydrolase-like<br>**Superfamily:**Adenine nucleotide alpha hydrolases-like<br>**Family:**PP-loop ATPase |
| 61 | c3h7uA_ | Alignment | not modelled | 27.0 | 20 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**aldo-keto reductase;<br>**PDBTitle:** crystal structure of the plant stress-response enzyme akr4c9 |
| 62 | d1d2ta_ | Alignment | not modelled | 27.0 | 8 | **Fold:**Acid phosphatase/Vanadium-dependent haloperoxidase<br>**Superfamily:**Acid phosphatase/Vanadium-dependent haloperoxidase<br>**Family:**Type 2 phosphatidic acid phosphatase, PAP2 |
| 63 | c2uygF_ | Alignment | not modelled | 26.6 | 43 | **PDB header:**lyase<br>**Chain:** F: **PDB Molecule:**3-dehydroquinate dehydratase;<br>**PDBTitle:** crystallographic structure of the typeii 3-dehydroquinase2 from thermus thermophilus |
| 64 | d1j20a1 | Alignment | not modelled | 26.4 | 8 | **Fold:**Adenine nucleotide alpha hydrolase-like<br>**Superfamily:**Adenine nucleotide alpha hydrolases-like<br>**Family:**N-type ATP pyrophosphatases |
| 65 | c2csuB_ | Alignment | not modelled | 26.4 | 27 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**457aa long hypothetical protein;<br>**PDBTitle:** crystal structure of ph0766 from pyrococcus horikoshii ot3 |
| 66 | c3f4lF_ | Alignment | not modelled | 26.4 | 12 | **PDB header:**oxidoreductase<br>**Chain:** F: **PDB Molecule:**putative oxidoreductase yhhx;<br>**PDBTitle:** crystal structure of a probable oxidoreductase yhhx in2 triclinic form. northeast structural genomics target er647 |
| 67 | d1hq1a_ | Alignment | not modelled | 26.4 | 20 | **Fold:**Signal peptide-binding domain<br>**Superfamily:**Signal peptide-binding domain<br>**Family:**Signal peptide-binding domain |
| 68 | c3nt5B_ | Alignment | not modelled | 26.3 | 14 | **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 |
| 69 | c2c7tA_ | Alignment | not modelled | 26.3 | 35 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**glutamine-2-deoxy-scyllo-inosose<br>**PDBTitle:** crystal structure of the plp-bound form of btrr,2 a dual functional aminotransferase involved in butirosin3 biosynthesis. |
| 70 | c3dc1A_ | Alignment | not modelled | 26.2 | 24 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**kynurenine/alpha-aminoadipate aminotransferase<br>**PDBTitle:** crystal structure of kynurenine aminotransferase ii complex with2 alpha-ketoglutarate |
| 71 | c1wziA_ | Alignment | not modelled | 26.0 | 16 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**malate dehydrogenase;<br>**PDBTitle:** structural basis for alteration of cofactor specificity of2 malate dehydrogenase from thermus flavus |
| 72 | d2ffha2 | Alignment | not modelled | 25.9 | 25 | **Fold:**Signal peptide-binding domain<br>**Superfamily:**Signal peptide-binding domain<br>**Family:**Signal peptide-binding domain |
| 73 | d1ekqa_ | Alignment | not modelled | 25.9 | 19 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**Thiamin biosynthesis kinases |
| 74 | c3u80A_ | Alignment | not modelled | 25.7 | 53 | **PDB header:**unknown function<br>**Chain:** A: **PDB Molecule:**3-dehydroquinate dehydratase, type ii;<br>**PDBTitle:** 1.60 angstrom resolution crystal structure of a 3-dehydroquinate2 dehydratase-like protein from bifidobacterium longum |
| 75 | d1uqra_ | Alignment | not modelled | 25.7 | 43 | **Fold:**Flavodoxin-like<br>**Superfamily:**Type II 3-dehydroquinate dehydratase<br>**Family:**Type II 3-dehydroquinate dehydratase |
| 76 | c2hroA_ | Alignment | not modelled | 25.0 | 17 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**phosphoenolpyruvate-protein phosphotransferase;<br>**PDBTitle:** structure of the full-lenght enzyme i of the pts system from2 staphylococcus carnosus |
| 77 | c1a5zA_ | Alignment | not modelled | 25.0 | 25 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**l-lactate dehydrogenase;<br>**PDBTitle:** lactate dehydrogenase from thermotoga maritima (tmldh) |
| 78 | c3aemD_ | Alignment | not modelled | 25.0 | 9 | **PDB header:**lyase<br>**Chain:** D: **PDB Molecule:**methionine gamma-lyase;<br>**PDBTitle:** reaction intermediate structure of entamoeba histolytica methionine2 gamma-lyase 1 containing michaelis complex and methionine imine-3 pyridoxamine-5'-phosphate |
| 79 | c3dpiA_ | Alignment | not modelled | 24.5 | 16 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**nad+ synthetase;<br>**PDBTitle:** crystal structure of nad+ synthetase from burkholderia pseudomallei |

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| 80 | d1h05a_ | Alignment | not modelled | 24.5 | 39 | **Fold:**Flavodoxin-like<br>**Superfamily:**Type II 3-dehydroquinate dehydratase<br>**Family:**Type II 3-dehydroquinate dehydratase |
| 81 | c3ndnC_ | Alignment | not modelled | 24.3 | 6 | **PDB header:**lyase<br>**Chain:** C: **PDB Molecule:**o-succinylhomoserine sulfhydrylase;<br>**PDBTitle:** crystal structure of o-succinylhomoserine sulfhydrylase from2 mycobacterium tuberculosis covalently bound to pyridoxal-5-phosphate |
| 82 | d2ji7a1 | Alignment | not modelled | 23.8 | 23 | **Fold:**DHS-like NAD/FAD-binding domain<br>**Superfamily:**DHS-like NAD/FAD-binding domain<br>**Family:**Pyruvate oxidase and decarboxylase, middle domain |
| 83 | c2lbwA_ | Alignment | not modelled | 23.2 | 22 | **PDB header:**rna binding protein<br>**Chain:** A: **PDB Molecule:**h/aca ribonucleoprotein complex subunit 2;<br>**PDBTitle:** solution structure of the s. cerevisiae h/aca rnp protein nhp2p-s82w2 mutant |
| 84 | c2y8nC_ | Alignment | not modelled | 22.8 | 19 | **PDB header:**lyase<br>**Chain:** C: **PDB Molecule:**4-hydroxyphenylacetate decarboxylase large subunit;<br>**PDBTitle:** crystal structure of glycyl radical enzyme |
| 85 | c2cb1A_ | Alignment | not modelled | 22.7 | 12 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**o-acetyl homoserine sulfhydrylase;<br>**PDBTitle:** crystal structure of o-actetyl homoserine sulfhydrylase2 from thermus thermophilus hb8,oah2. |
| 86 | c1zh8B_ | Alignment | not modelled | 22.7 | 8 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**oxidoreductase;<br>**PDBTitle:** crystal structure of oxidoreductase (tm0312) from thermotoga maritima2 at 2.50 a resolution |
| 87 | c2bn5A_ | Alignment | not modelled | 22.7 | 11 | **PDB header:**nuclear protein<br>**Chain:** A: **PDB Molecule:**psi;<br>**PDBTitle:** p-element somatic inhibitor protein complex with u1-70k2 proline-rich peptide |
| 88 | d1ui5a2 | Alignment | not modelled | 22.6 | 21 | **Fold:**Tetracyclin repressor-like, C-terminal domain<br>**Superfamily:**Tetracyclin repressor-like, C-terminal domain<br>**Family:**Tetracyclin repressor-like, C-terminal domain |
| 89 | c3lwzC_ | Alignment | not modelled | 22.4 | 34 | **PDB header:**lyase<br>**Chain:** C: **PDB Molecule:**3-dehydroquinate dehydratase;<br>**PDBTitle:** 1.65 angstrom resolution crystal structure of type ii 3-2 dehydroquinate dehydratase (aroq) from yersinia pestis |
| 90 | d1gtza_ | Alignment | not modelled | 22.4 | 47 | **Fold:**Flavodoxin-like<br>**Superfamily:**Type II 3-dehydroquinate dehydratase<br>**Family:**Type II 3-dehydroquinate dehydratase |
| 91 | c2r0tA_ | Alignment | not modelled | 22.3 | 24 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**pyridoxamine 5-phosphate-dependent dehydrase;<br>**PDBTitle:** crystal sructure of gdp-4-keto-6-deoxymannose-3-dehydratase2 with a trapped plp-glutamate geminal diamine |
| 92 | d2c4va1 | Alignment | not modelled | 22.1 | 25 | **Fold:**Flavodoxin-like<br>**Superfamily:**Type II 3-dehydroquinate dehydratase<br>**Family:**Type II 3-dehydroquinate dehydratase |
| 93 | c3c1aB_ | Alignment | not modelled | 22.1 | 12 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**putative oxidoreductase;<br>**PDBTitle:** crystal structure of a putative oxidoreductase (zp_00056571.1) from2 magnetospirillum magnetotacticum ms-1 at 1.85 a resolution |
| 94 | c3qh9A_ | Alignment | not modelled | 21.7 | 13 | **PDB header:**structural protein<br>**Chain:** A: **PDB Molecule:**liprin-beta-2;<br>**PDBTitle:** human liprin-beta2 coiled-coil |
| 95 | c3c19A_ | Alignment | not modelled | 21.7 | 38 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein mk0293;<br>**PDBTitle:** crystal structure of protein mk0293 from methanopyrus kandleri av19 |
| 96 | d1rlga_ | Alignment | not modelled | 21.5 | 20 | **Fold:**Bacillus chorismate mutase-like<br>**Superfamily:**L30e-like<br>**Family:**L30e/L7ae ribosomal proteins |
| 97 | c2f3oB_ | Alignment | not modelled | 21.5 | 17 | **PDB header:**unknown function<br>**Chain:** B: **PDB Molecule:**pyruvate formate-lyase 2;<br>**PDBTitle:** crystal structure of a glycyl radical enzyme from archaeoglobus2 fulgidus |
| 98 | d1ibja_ | Alignment | not modelled | 21.5 | 18 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**Cystathionine synthase-like |
| 99 | c1ibjC_ | Alignment | not modelled | 21.5 | 18 | **PDB header:**lyase<br>**Chain:** C: **PDB Molecule:**cystathionine beta-lyase;<br>**PDBTitle:** crystal structure of cystathionine beta-lyase from arabidopsis2 thaliana |
| 100 | d1b9ha_ | Alignment | not modelled | 21.4 | 27 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**GABA-aminotransferase-like |
| 101 | d1p3da1 | Alignment | not modelled | 21.3 | 7 | **Fold:**MurCD N-terminal domain<br>**Superfamily:**MurCD N-terminal domain<br>**Family:**MurCD N-terminal domain |
| 102 | c3iayA_ | Alignment | not modelled | 21.1 | 20 | **PDB header:**transferase/dna<br>**Chain:** A: **PDB Molecule:**dna polymerase delta catalytic subunit;<br>**PDBTitle:** ternary complex of dna polymerase delta |
| 103 | d2a6ta2 | Alignment | not modelled | 21.1 | 19 | **Fold:**Nudix<br>**Superfamily:**Nudix<br>**Family:**mRNA decapping enzyme-like |
| 104 | c2pq1B_ | Alignment | not modelled | 20.9 | 18 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**ap4a hydrolase;<br>**PDBTitle:** crystal structure of ap4a hydrolase complexed with amp and2 atp (aq_158) from aquifex aeolicus vf5 |
| 105 | c3ezyB_ | Alignment | not modelled | 20.7 | 17 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**dehydrogenase;<br>**PDBTitle:** crystal structure of probable dehydrogenase tm_0414 |

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|---|---|---|---|---|---|---|
|  |  |  |  |  |  | from2 thermotoga maritima |
| 106 | c2k9iB_ | Alignment | not modelled | 20.6 | 38 | **PDB header:**dna binding protein<br>**Chain:** B: **PDB Molecule:**plasmid prn1, complete sequence;<br>**PDBTitle:** nmr structure of plasmid copy control protein orf56 from2 sulfolobus islandicus |
| 107 | c2ogeC_ | Alignment | not modelled | 20.3 | 17 | **PDB header:**transferase<br>**Chain:** C: **PDB Molecule:**transaminase;<br>**PDBTitle:** x-ray structure of s. venezuelae desv in its internal2 aldimine form |