Phyre2

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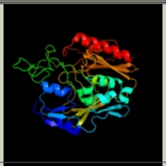
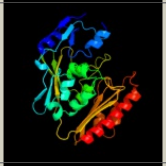
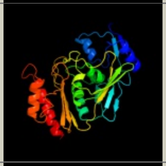
| Email | l.a.kelley@imperial.ac.uk |
| Description | P77324 |
| Date | Thu Jan 5 12:27:44 GMT 2012 |
| Unique Job ID | 5b5232c74c8925a7 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c1rm6E_ | Alignment |  | 100.0 | 29 | **PDB header:**oxidoreductase<br>**Chain:** E: **PDB Molecule:**4-hydroxybenzoyl-coa reductase beta subunit;<br>**PDBTitle:** structure of 4-hydroxybenzoyl-coa reductase from thauera2 aromatica |
| 2 | c3hrdC_ | Alignment |  | 100.0 | 26 | **PDB header:**oxidoreductase<br>**Chain:** C: **PDB Molecule:**nicotinate dehydrogenase fad-subunit;<br>**PDBTitle:** crystal structure of nicotinate dehydrogenase |
| 3 | c1n62C_ | Alignment |  | 100.0 | 28 | **PDB header:**oxidoreductase<br>**Chain:** C: **PDB Molecule:**carbon monoxide dehydrogenase medium chain;<br>**PDBTitle:** crystal structure of the mo,cu-co dehydrogenase (codh), n-2 butylisocyanide-bound state |
| 4 | c1t3qF_ | Alignment |  | 100.0 | 29 | **PDB header:**oxidoreductase<br>**Chain:** F: **PDB Molecule:**quinoline 2-oxidoreductase medium subunit;<br>**PDBTitle:** crystal structure of quinoline 2-oxidoreductase from pseudomonas2 putida 86 |
| 5 | c1ffuF_ | Alignment |  | 100.0 | 28 | **PDB header:**hydrolase<br>**Chain:** F: **PDB Molecule:**cutm, flavoprotein of carbon monoxide<br>**PDBTitle:** carbon monoxide dehydrogenase from hydrogenophaga2 pseudoflava which lacks the mo-pyranopterin moiety of the3 molybdenum cofactor |
| 6 | c2w3rG_ | Alignment |  | 100.0 | 25 | **PDB header:**oxidoreductase<br>**Chain:** G: **PDB Molecule:**xanthine dehydrogenase;<br>**PDBTitle:** crystal structure of xanthine dehydrogenase (desulfo form)2 from rhodobacter capsulatus in complex with hypoxanthine |
| 7 | c3etrM_ | Alignment |  | 100.0 | 17 | **PDB header:**oxidoreductase<br>**Chain:** M: **PDB Molecule:**xanthine dehydrogenase/oxidase;<br>**PDBTitle:** crystal structure of xanthine oxidase in complex with2 lumazine |
| 8 | c3b9jJ_ | Alignment |  | 100.0 | 17 | **PDB header:**oxidoreductase<br>**Chain:** J: **PDB Molecule:**xanthine oxidase;<br>**PDBTitle:** structure of xanthine oxidase with 2-hydroxy-6-methylpurine |
| 9 | c1wygA_ | Alignment |  | 100.0 | 18 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**xanthine dehydrogenase/oxidase;<br>**PDBTitle:** crystal structure of a rat xanthine dehydrogenase triple mutant2 (c535a, c992r and c1324s) |
| 10 | d1rm6b2 | Alignment |  | 100.0 | 31 | **Fold:**FAD-binding/transporter-associated domain-like<br>**Superfamily:**FAD-binding/transporter-associated domain-like<br>**Family:**CO dehydrogenase flavoprotein N-terminal domain-like |
| 11 | d1t3qc2 | Alignment |  | 100.0 | 32 | **Fold:**FAD-binding/transporter-associated domain-like<br>**Superfamily:**FAD-binding/transporter-associated domain-like<br>**Family:**CO dehydrogenase flavoprotein N-terminal domain-like |

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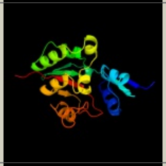
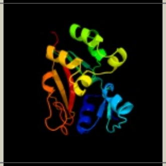
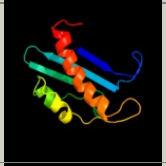
| 12 | d1n62c2 | Alignment |  | 100.0 | 32 | **Fold:**FAD-binding/transporter-associated domain-like<br>**Superfamily:**FAD-binding/transporter-associated domain-like<br>**Family:**CO dehydrogenase flavoprotein N-terminal domain-like |
| 13 | d1ffvc2 | Alignment |  | 100.0 | 29 | **Fold:**FAD-binding/transporter-associated domain-like<br>**Superfamily:**FAD-binding/transporter-associated domain-like<br>**Family:**CO dehydrogenase flavoprotein N-terminal domain-like |
| 14 | d1v97a6 | Alignment |  | 100.0 | 17 | **Fold:**FAD-binding/transporter-associated domain-like<br>**Superfamily:**FAD-binding/transporter-associated domain-like<br>**Family:**CO dehydrogenase flavoprotein N-terminal domain-like |
| 15 | d3b9jb2 | Alignment |  | 100.0 | 17 | **Fold:**FAD-binding/transporter-associated domain-like<br>**Superfamily:**FAD-binding/transporter-associated domain-like<br>**Family:**CO dehydrogenase flavoprotein N-terminal domain-like |
| 16 | d1jroa4 | Alignment |  | 100.0 | 27 | **Fold:**FAD-binding/transporter-associated domain-like<br>**Superfamily:**FAD-binding/transporter-associated domain-like<br>**Family:**CO dehydrogenase flavoprotein N-terminal domain-like |
| 17 | d1jroa3 | Alignment |  | 99.7 | 20 | **Fold:**CO dehydrogenase flavoprotein C-domain-like<br>**Superfamily:**CO dehydrogenase flavoprotein C-terminal domain-like<br>**Family:**CO dehydrogenase flavoprotein C-terminal domain-like |
| 18 | d1n62c1 | Alignment |  | 99.7 | 21 | **Fold:**CO dehydrogenase flavoprotein C-domain-like<br>**Superfamily:**CO dehydrogenase flavoprotein C-terminal domain-like<br>**Family:**CO dehydrogenase flavoprotein C-terminal domain-like |
| 19 | d1t3qc1 | Alignment |  | 99.7 | 26 | **Fold:**CO dehydrogenase flavoprotein C-domain-like<br>**Superfamily:**CO dehydrogenase flavoprotein C-terminal domain-like<br>**Family:**CO dehydrogenase flavoprotein C-terminal domain-like |
| 20 | d1ffvc1 | Alignment |  | 99.6 | 27 | **Fold:**CO dehydrogenase flavoprotein C-domain-like<br>**Superfamily:**CO dehydrogenase flavoprotein C-terminal domain-like<br>**Family:**CO dehydrogenase flavoprotein C-terminal domain-like |
| 21 | d1v97a4 | Alignment | not modelled | 99.6 | 14 | **Fold:**CO dehydrogenase flavoprotein C-domain-like<br>**Superfamily:**CO dehydrogenase flavoprotein C-terminal domain-like<br>**Family:**CO dehydrogenase flavoprotein C-terminal domain-like |
| 22 | d1rm6b1 | Alignment | not modelled | 99.6 | 27 | **Fold:**CO dehydrogenase flavoprotein C-domain-like<br>**Superfamily:**CO dehydrogenase flavoprotein C-terminal domain-like<br>**Family:**CO dehydrogenase flavoprotein C-terminal domain-like |
| 23 | c1mbbA_ | Alignment | not modelled | 97.9 | 22 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**uridine diphospho-n-acetylenolpyruvylglucosamine<br>**PDBTitle:** oxidoreductase |
| 24 | c3i99A_ | Alignment | not modelled | 97.8 | 17 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**udp-n-acetylenolpyruvoylglucosamine reductase;<br>**PDBTitle:** the crystal structure of the udp-n-acetylenolpyruvoylglucosamine2 reductase from the vibrio cholerae o1 biovar tor |
| 25 | d1hska1 | Alignment | not modelled | 97.7 | 14 | **Fold:**FAD-binding/transporter-associated domain-like<br>**Superfamily:**FAD-binding/transporter-associated domain-like<br>**Family:**Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase (MurB), N-terminal domain |
| 26 | c1hskA_ | Alignment | not modelled | 97.4 | 12 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**udp-n-acetylenolpyruvoylglucosamine reductase;<br>**PDBTitle:** crystal structure of s. aureus murb |
| 27 | c2vfvA_ | Alignment | not modelled | 97.4 | 23 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**xylitol oxidase;<br>**PDBTitle:** alditol oxidase from streptomyces coelicolor a3(2): complex2 with sulphite |
| 28 | c2wdwB | Alignment | not modelled | 97.3 | 13 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**putative hexose oxidase; |

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| | | Alignment | | | | **PDBTitle:** the native crystal structure of the primary hexose oxidase (2 dbv29) in antibiotic a40926 biosynthesis |
| 29 | d1uxya1 | Alignment | not modelled | 97.2 | 22 | **Fold:**FAD-binding/transporter-associated domain-like<br>**Superfamily:**FAD-binding/transporter-associated domain-like<br>**Family:**Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase (MurB), N-terminal domain |
| 30 | c2gquA_ | Alignment | not modelled | 97.1 | 25 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**udp-n-acetylenolpyruvylglucosamine reductase;<br>**PDBTitle:** crystal structure of udp-n-acetylenolpyruvylglucosamine2 reductase (murb) from thermus caldophilus |
| 31 | c3bw7A_ | Alignment | not modelled | 97.0 | 18 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**cytokinin dehydrogenase 1;<br>**PDBTitle:** maize cytokinin oxidase/dehydrogenase complexed with the allenic2 cytokinin analog ha-1 |
| 32 | c2ipiD_ | Alignment | not modelled | 96.9 | 14 | **PDB header:**oxidoreductase<br>**Chain:** D: **PDB Molecule:**aclacinomycin oxidoreductase (aknox);<br>**PDBTitle:** crystal structure of aclacinomycin oxidoreductase |
| 33 | c2y3rC_ | Alignment | not modelled | 96.9 | 14 | **PDB header:**oxidoreductase<br>**Chain:** C: **PDB Molecule:**taml;<br>**PDBTitle:** structure of the tirandamycin-bound fad-dependent2 tirandamycin oxidase taml in p21 space group |
| 34 | d1f0xa2 | Alignment | not modelled | 96.9 | 20 | **Fold:**FAD-binding/transporter-associated domain-like<br>**Superfamily:**FAD-binding/transporter-associated domain-like<br>**Family:**FAD-linked oxidases, N-terminal domain |
| 35 | c2uuvC_ | Alignment | not modelled | 96.8 | 14 | **PDB header:**transferase<br>**Chain:** C: **PDB Molecule:**alkyldihydroxyacetonephosphate synthase;<br>**PDBTitle:** alkyldihydroxyacetonephosphate synthase in p1 |
| 36 | c3popD_ | Alignment | not modelled | 96.8 | 18 | **PDB header:**oxidoreductase<br>**Chain:** D: **PDB Molecule:**gilr oxidase;<br>**PDBTitle:** the crystal structure of gilr, an oxidoreductase that catalyzes the2 terminal step of gilvocarcin biosynthesis |
| 37 | c3d2hA_ | Alignment | not modelled | 96.7 | 14 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**berberine bridge-forming enzyme;<br>**PDBTitle:** structure of berberine bridge enzyme from eschscholzia californica,2 monoclinic crystal form |
| 38 | c1f0xA_ | Alignment | not modelled | 96.5 | 17 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**d-lactate dehydrogenase;<br>**PDBTitle:** crystal structure of d-lactate dehydrogenase, a peripheral2 membrane respiratory enzyme. |
| 39 | c1zr6A_ | Alignment | not modelled | 96.5 | 12 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**glucooligosaccharide oxidase;<br>**PDBTitle:** the crystal structure of an acremonium strictum glucooligosaccharide2 oxidase reveals a novel flavinylation |
| 40 | c2bvfA_ | Alignment | not modelled | 96.5 | 21 | **PDB header:**oxidase<br>**Chain:** A: **PDB Molecule:**6-hydroxy-d-nicotine oxidase;<br>**PDBTitle:** crystal structure of 6-hydoxy-d-nicotine oxidase from2 arthrobacter nicotinovorans. crystal form 3 (p1) |
| 41 | c3fwaA_ | Alignment | not modelled | 96.5 | 13 | **PDB header:**flavoprotein<br>**Chain:** A: **PDB Molecule:**reticuline oxidase;<br>**PDBTitle:** structure of berberine bridge enzyme, c166a variant in complex with2 (s)-reticuline |
| 42 | c1wveB_ | Alignment | not modelled | 96.2 | 9 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**4-cresol dehydrogenase [hydroxylating]<br>**PDBTitle:** p-cresol methylhydroxylase: alteration of the structure of2 the flavoprotein subunit upon its binding to the3 cytochrome subunit |
| 43 | c2exrA_ | Alignment | not modelled | 95.8 | 17 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**cytokinin dehydrogenase 7;<br>**PDBTitle:** x-ray structure of cytokinin oxidase/dehydrogenase (ckx)2 from arabidopsis thaliana at5g21482 |
| 44 | d1wvfa2 | Alignment | not modelled | 95.7 | 8 | **Fold:**FAD-binding/transporter-associated domain-like<br>**Superfamily:**FAD-binding/transporter-associated domain-like<br>**Family:**FAD-linked oxidases, N-terminal domain |
| 45 | c3js8A_ | Alignment | not modelled | 95.7 | 13 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**cholesterol oxidase;<br>**PDBTitle:** solvent-stable cholesterol oxidase |
| 46 | c1i19B_ | Alignment | not modelled | 95.3 | 14 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**cholesterol oxidase;<br>**PDBTitle:** crystal structure of cholesterol oxidase from b.sterolicum |
| 47 | d2i0ka2 | Alignment | not modelled | 95.2 | 15 | **Fold:**FAD-binding/transporter-associated domain-like<br>**Superfamily:**FAD-binding/transporter-associated domain-like<br>**Family:**FAD-linked oxidases, N-terminal domain |
| 48 | c3pm9A_ | Alignment | not modelled | 94.8 | 13 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**putative oxidoreductase;<br>**PDBTitle:** crystal structure of a putative dehydrogenase (rpa1076) from2 rhodopseudomonas palustris cga009 at 2.57 a resolution |
| 49 | d1e8ga2 | Alignment | not modelled | 94.2 | 13 | **Fold:**FAD-binding/transporter-associated domain-like<br>**Superfamily:**FAD-binding/transporter-associated domain-like<br>**Family:**FAD-linked oxidases, N-terminal domain |
| 50 | c1ahuB_ | Alignment | not modelled | 93.9 | 11 | **PDB header:**flavoenzyme<br>**Chain:** B: **PDB Molecule:**vanillyl-alcohol oxidase;<br>**PDBTitle:** structure of the octameric flavoenzyme vanillyl-alcohol2 oxidase in complex with p-cresol |
| 51 | d1w1oa2 | Alignment | not modelled | 87.8 | 17 | **Fold:**FAD-binding/transporter-associated domain-like<br>**Superfamily:**FAD-binding/transporter-associated domain-like<br>**Family:**FAD-linked oxidases, N-terminal domain |
| 52 | c2yvsA_ | Alignment | not modelled | 60.3 | 17 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**glycolate oxidase subunit glce;<br>**PDBTitle:** crystal structure of glycolate oxidase subunit glce from thermus2 thermophilus hb8 |
| 53 | d1fmta1 | Alignment | not modelled | 30.1 | 19 | **Fold:**FMT C-terminal domain-like<br>**Superfamily:**FMT C-terminal domain-like<br>**Family:**Post formyltransferase domain |

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| 54 | d1ujpa_ | Alignment | not modelled | 27.9 | 10 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Ribulose-phoshate binding barrel<br>**Family:**Tryptophan biosynthesis enzymes |
| 55 | d1oj7a_ | Alignment | not modelled | 26.5 | 12 | **Fold:**Dehydroquinate synthase-like<br>**Superfamily:**Dehydroquinate synthase-like<br>**Family:**Iron-containing alcohol dehydrogenase |
| 56 | c3ix9B_ | Alignment | not modelled | 21.4 | 10 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**dihydrofolate reductase;<br>**PDBTitle:** crystal structure of streptococcus pneumoniae dihydrofolate2 reductase - sp9 mutant |
| 57 | c2blcA_ | Alignment | not modelled | 19.5 | 17 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**dihydrofolate reductase-thymidylate synthase;<br>**PDBTitle:** sp21 double mutant p. vivax dihydrofolate reductase in2 complex with des-chloropyrimethamine |
| 58 | d1j3ka_ | Alignment | not modelled | 19.1 | 17 | **Fold:**Dihydrofolate reductase-like<br>**Superfamily:**Dihydrofolate reductase-like<br>**Family:**Dihydrofolate reductases |
| 59 | d1vpaa_ | Alignment | not modelled | 17.8 | 19 | **Fold:**Nucleotide-diphospho-sugar transferases<br>**Superfamily:**Nucleotide-diphospho-sugar transferases<br>**Family:**Cytidylytransferase |
| 60 | c1zdrB_ | Alignment | not modelled | 16.9 | 21 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**dihydrofolate reductase;<br>**PDBTitle:** dhfr from bacillus stearothermophilus |
| 61 | c3dg8B_ | Alignment | not modelled | 16.6 | 17 | **PDB header:**oxidoreductase, transferase<br>**Chain:** B: **PDB Molecule:**bifunctional dihydrofolate reductase-thymidylate<br>**PDBTitle:** quadruple mutant (n51i+c59r+s108n+i164l) plasmodium2 falciparum dihydrofolate reductase-thymidylate synthase3 (pfdhfr-ts) complexed with rjf670, nadph, and dump |
| 62 | c1cf2Q_ | Alignment | not modelled | 15.5 | 13 | **PDB header:**oxidoreductase<br>**Chain:** Q: **PDB Molecule:**protein (glyceraldehyde-3-phosphate<br>**PDBTitle:** three-dimensional structure of d-glyceraldehyde-3-phosphate2 dehydrogenase from the hyperthermophilic archaeon3 methanothermus fervidus |
| 63 | c1b7gO_ | Alignment | not modelled | 14.2 | 10 | **PDB header:**oxidoreductase<br>**Chain:** O: **PDB Molecule:**protein (glyceraldehyde 3-phosphate dehydrogenase);<br>**PDBTitle:** glyceraldehyde 3-phosphate dehydrogenase |
| 64 | c2qyaA_ | Alignment | not modelled | 14.2 | 11 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized conserved protein;<br>**PDBTitle:** crystal structure of an uncharacterized conserved protein2 from methanopyrus kandleri |
| 65 | d1vlja_ | Alignment | not modelled | 14.0 | 18 | **Fold:**Dehydroquinate synthase-like<br>**Superfamily:**Dehydroquinate synthase-like<br>**Family:**Iron-containing alcohol dehydrogenase |
| 66 | d1aoea_ | Alignment | not modelled | 13.3 | 18 | **Fold:**Dihydrofolate reductase-like<br>**Superfamily:**Dihydrofolate reductase-like<br>**Family:**Dihydrofolate reductases |
| 67 | d2ji7a1 | Alignment | not modelled | 13.1 | 17 | **Fold:**DHS-like NAD/FAD-binding domain<br>**Superfamily:**DHS-like NAD/FAD-binding domain<br>**Family:**Pyruvate oxidase and decarboxylase, middle domain |
| 68 | c2dyoB_ | Alignment | not modelled | 12.5 | 33 | **PDB header:**protein turnover/protein turnover<br>**Chain:** B: **PDB Molecule:**autophagy protein 16;<br>**PDBTitle:** the crystal structure of saccharomyces cerevisiae atg5-2 atg16(1-57) complex |
| 69 | c3imkA_ | Alignment | not modelled | 11.8 | 21 | **PDB header:**metal binding protein<br>**Chain:** A: **PDB Molecule:**putative molybdenum carrier protein;<br>**PDBTitle:** crystal structure of putative molybdenum carrier protein (yp_461806.1)2 from syntrophus aciditrophicus sb at 1.45 a resolution |
| 70 | d1ozha1 | Alignment | not modelled | 10.8 | 13 | **Fold:**DHS-like NAD/FAD-binding domain<br>**Superfamily:**DHS-like NAD/FAD-binding domain<br>**Family:**Pyruvate oxidase and decarboxylase, middle domain |
| 71 | c2xecD_ | Alignment | not modelled | 10.4 | 17 | **PDB header:**isomerase<br>**Chain:** D: **PDB Molecule:**putative maleate isomerase;<br>**PDBTitle:** nocardia farcinica maleate cis-trans isomerase bound to2 tris |
| 72 | d1g97a2 | Alignment | not modelled | 10.1 | 24 | **Fold:**Nucleotide-diphospho-sugar transferases<br>**Superfamily:**Nucleotide-diphospho-sugar transferases<br>**Family:**UDP-glucose pyrophosphorylase |
| 73 | c1m6yA_ | Alignment | not modelled | 9.9 | 3 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**s-adenosyl-methyltransferase mraw;<br>**PDBTitle:** crystal structure analysis of tm0872, a putative sam-2 dependent methyltransferase, complexed with sah |
| 74 | c3tqqA_ | Alignment | not modelled | 9.5 | 25 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**methionyl-trna formyltransferase;<br>**PDBTitle:** structure of the methionyl-trna formyltransferase (fmt) from coxiella2 burnetii |
| 75 | c3q0iA_ | Alignment | not modelled | 9.5 | 18 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**methionyl-trna formyltransferase;<br>**PDBTitle:** methionyl-trna formyltransferase from vibrio cholerae |
| 76 | d1i1ga2 | Alignment | not modelled | 9.5 | 14 | **Fold:**Ferredoxin-like<br>**Superfamily:**Dimeric alpha+beta barrel<br>**Family:**Lrp/AsnC-like transcriptional regulator C-terminal domain |
| 77 | d1uz5a3 | Alignment | not modelled | 9.3 | 19 | **Fold:**Molybdenum cofactor biosynthesis proteins<br>**Superfamily:**Molybdenum cofactor biosynthesis proteins<br>**Family:**MoeA central domain-like |
| 78 | d1wp5a_ | Alignment | not modelled | 9.3 | 16 | **Fold:**6-bladed beta-propeller<br>**Superfamily:**GyrA/ParC C-terminal domain-like<br>**Family:**GyrA/ParC C-terminal domain-like |
| | | | | | | **PDB header:**biosynthetic protein<br>**Chain:** A: **PDB Molecule:**molybdopterin-guanine dinucleotide |

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| 79 | c3ngwA_ | Alignment | not modelled | 9.2 | 16 | biosynthesis protein a<br>**PDBTitle:** crystal structure of molybdopterin-guanine dinucleotide biosynthesis2 protein a from archaeoglobus fulgidus, northeast structural genomics3 consortium target gr189 |
| 80 | d1q6za1 | Alignment | not modelled | 9.1 | 4 | **Fold:**DHS-like NAD/FAD-binding domain<br>**Superfamily:**DHS-like NAD/FAD-binding domain<br>**Family:**Pyruvate oxidase and decarboxylase, middle domain |
| 81 | d2djia1 | Alignment | not modelled | 9.1 | 13 | **Fold:**DHS-like NAD/FAD-binding domain<br>**Superfamily:**DHS-like NAD/FAD-binding domain<br>**Family:**Pyruvate oxidase and decarboxylase, middle domain |
| 82 | d3dfra_ | Alignment | not modelled | 8.9 | 21 | **Fold:**Dihydrofolate reductase-like<br>**Superfamily:**Dihydrofolate reductase-like<br>**Family:**Dihydrofolate reductases |
| 83 | d1li4a2 | Alignment | not modelled | 8.8 | 18 | **Fold:**Flavodoxin-like<br>**Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like<br>**Family:**S-adenosylhomocystein hydrolase |
| 84 | d2ez9a1 | Alignment | not modelled | 8.8 | 9 | **Fold:**DHS-like NAD/FAD-binding domain<br>**Superfamily:**DHS-like NAD/FAD-binding domain<br>**Family:**Pyruvate oxidase and decarboxylase, middle domain |
| 85 | d2dpwa1 | Alignment | not modelled | 8.8 | 19 | **Fold:**Nucleotide-diphospho-sugar transferases<br>**Superfamily:**Nucleotide-diphospho-sugar transferases<br>**Family:**TTHA0179-like |
| 86 | d2blna1 | Alignment | not modelled | 8.7 | 13 | **Fold:**FMT C-terminal domain-like<br>**Superfamily:**FMT C-terminal domain-like<br>**Family:**Post formyltransferase domain |
| 87 | d1ybha1 | Alignment | not modelled | 8.1 | 9 | **Fold:**DHS-like NAD/FAD-binding domain<br>**Superfamily:**DHS-like NAD/FAD-binding domain<br>**Family:**Pyruvate oxidase and decarboxylase, middle domain |
| 88 | d1w55a1 | Alignment | not modelled | 7.6 | 9 | **Fold:**Nucleotide-diphospho-sugar transferases<br>**Superfamily:**Nucleotide-diphospho-sugar transferases<br>**Family:**Cytidylyltransferase |
| 89 | c3gxxB_ | Alignment | not modelled | 7.2 | 13 | **PDB header:**transcription<br>**Chain:** B: **PDB Molecule:**transcription elongation factor spt6;<br>**PDBTitle:** structure of the sh2 domain of the candida glabrata2 transcription elongation factor spt6, crystal form b |
| 90 | c2xwlB_ | Alignment | not modelled | 7.2 | 22 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**2-c-methyl-d-erythritol 4-phosphate cytidylyltransferase;<br>**PDBTitle:** crystal structure of ispd from mycobacterium smegmatis in complex2 with ctp and mg |
| 91 | d2oi6a2 | Alignment | not modelled | 7.1 | 17 | **Fold:**Nucleotide-diphospho-sugar transferases<br>**Superfamily:**Nucleotide-diphospho-sugar transferases<br>**Family:**UDP-glucose pyrophosphorylase |
| 92 | d2dx7a1 | Alignment | not modelled | 7.1 | 21 | **Fold:**ATC-like<br>**Superfamily:**Aspartate/glutamate racemase<br>**Family:**Aspartate/glutamate racemase |
| 93 | c2we9A_ | Alignment | not modelled | 7.1 | 17 | **PDB header:**unknown function<br>**Chain:** A: **PDB Molecule:**moba-related protein;<br>**PDBTitle:** crystal structure of rv0371c from mycobacterium2 tuberculosis h37rv |
| 94 | c2yyyB_ | Alignment | not modelled | 7.0 | 10 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**glyceraldehyde-3-phosphate dehydrogenase;<br>**PDBTitle:** crystal structure of glyceraldehyde-3-phosphate2 dehydrogenase |
| 95 | d1tzfa_ | Alignment | not modelled | 7.0 | 21 | **Fold:**Nucleotide-diphospho-sugar transferases<br>**Superfamily:**Nucleotide-diphospho-sugar transferases<br>**Family:**Cytidylyltransferase |
| 96 | d1o94c_ | Alignment | not modelled | 7.0 | 8 | **Fold:**Adenine nucleotide alpha hydrolase-like<br>**Superfamily:**Adenine nucleotide alpha hydrolases-like<br>**Family:**ETFP subunits |
| 97 | c3tq8A_ | Alignment | not modelled | 6.7 | 18 | **PDB header:**oxidoreductase/oxidoreductase inhibitor<br>**Chain:** A: **PDB Molecule:**dihydrofolate reductase;<br>**PDBTitle:** structure of the dihydrofolate reductase (fola) from coxiella burnetii2 in complex with trimethoprim |
| 98 | d1jfla2 | Alignment | not modelled | 6.6 | 21 | **Fold:**ATC-like<br>**Superfamily:**Aspartate/glutamate racemase<br>**Family:**Aspartate/glutamate racemase |
| 99 | c2yukA_ | Alignment | not modelled | 6.6 | 10 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**myeloid/lymphoid or mixed-lineage leukemia<br>**PDBTitle:** solution structure of the hmg box of human myeloid/lymphoid2 or mixed-lineage leukemia protein 3 homolog |