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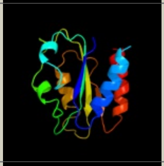
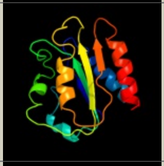
| Email | l.a.kelley@imperial.ac.uk |
| Description | P0A772 |
| Date | Thu Jan 5 11:04:59 GMT 2012 |
| Unique Job ID | fe2b0c749d87d3a6 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c3n39D_ | Alignment |  | 100.0 | 100 | **PDB header:**oxidoreductase<br>**Chain:** D: **PDB Molecule:**protein nrdi;<br>**PDBTitle:** ribonucleotide reductase dimanganese(ii)-nrdf from escherichia coli in2 complex with nrdi |
| 2 | d1rlja_ | Alignment |  | 100.0 | 33 | **Fold:**Flavodoxin-like<br>**Superfamily:**Flavoproteins<br>**Family:**Flavoprotein NrdI |
| 3 | c2x2oA_ | Alignment |  | 100.0 | 48 | **PDB header:**flavoprotein<br>**Chain:** A: **PDB Molecule:**nrdi protein;<br>**PDBTitle:** the flavoprotein nrdi from bacillus cereus with the2 initially oxidized fmn cofactor in an intermediate3 radiation reduced state |
| 4 | c1tllA_ | Alignment |  | 99.9 | 11 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**nitric-oxide synthase, brain;<br>**PDBTitle:** crystal structure of rat neuronal nitric-oxide synthase2 reductase module at 2.3 a resolution. |
| 5 | d1tlla2 | Alignment |  | 99.9 | 12 | **Fold:**Flavodoxin-like<br>**Superfamily:**Flavoproteins<br>**Family:**Cytochrome p450 reductase N-terminal domain-like |
| 6 | c3hr4C_ | Alignment |  | 99.9 | 10 | **PDB header:**oxidoreductase/metal binding protein<br>**Chain:** C: **PDB Molecule:**nitric oxide synthase, inducible;<br>**PDBTitle:** human inos reductase and calmodulin complex |
| 7 | c2bpoA_ | Alignment |  | 99.9 | 13 | **PDB header:**reductase<br>**Chain:** A: **PDB Molecule:**nadph-cytochrom p450 reductase;<br>**PDBTitle:** crystal structure of the yeast cpr triple mutant: d74g,2 y75f, k78a. |
| 8 | c1j9zB_ | Alignment |  | 99.9 | 16 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**nadph-cytochrome p450 reductase;<br>**PDBTitle:** cypor-w677g |
| 9 | d1b1ca_ | Alignment |  | 99.9 | 16 | **Fold:**Flavodoxin-like<br>**Superfamily:**Flavoproteins<br>**Family:**Cytochrome p450 reductase N-terminal domain-like |
| 10 | d1bvyf_ | Alignment |  | 99.9 | 17 | **Fold:**Flavodoxin-like<br>**Superfamily:**Flavoproteins<br>**Family:**Flavodoxin-related |
| 11 | c1bvyF_ | Alignment |  | 99.9 | 17 | **PDB header:**oxidoreductase<br>**Chain:** F: **PDB Molecule:**protein (cytochrome p450 bm-3);<br>**PDBTitle:** complex of the heme and fmn-binding domains of the2 cytochrome p450(bm-3) |

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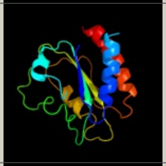
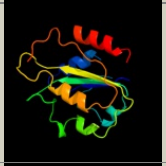
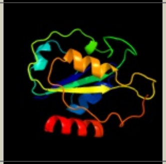
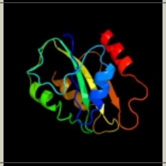
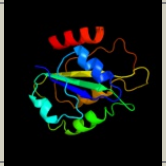
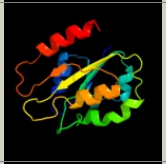
| 12 | d1ja1a2 | Alignment |  | 99.9 | 15 | **Fold:**Flavodoxin-like<br>**Superfamily:**Flavoproteins<br>**Family:**Cytochrome p450 reductase N-terminal domain-like |
| 13 | d1ykga1 | Alignment |  | 99.9 | 14 | **Fold:**Flavodoxin-like<br>**Superfamily:**Flavoproteins<br>**Family:**Cytochrome p450 reductase N-terminal domain-like |
| 14 | d1yoba1 | Alignment |  | 99.9 | 17 | **Fold:**Flavodoxin-like<br>**Superfamily:**Flavoproteins<br>**Family:**Flavodoxin-related |
| 15 | d2fcra_ | Alignment |  | 99.9 | 16 | **Fold:**Flavodoxin-like<br>**Superfamily:**Flavoproteins<br>**Family:**Flavodoxin-related |
| 16 | c2wc1A_ | Alignment |  | 99.9 | 14 | **PDB header:**electron transport<br>**Chain:** A: **PDB Molecule:**flavodoxin;<br>**PDBTitle:** three-dimensional structure of the nitrogen fixation2 flavodoxin (niff) from rhodobacter capsulatus at 2.2 a |
| 17 | c2hnbA_ | Alignment |  | 99.8 | 12 | **PDB header:**electron transport<br>**Chain:** A: **PDB Molecule:**protein mioc;<br>**PDBTitle:** solution structure of a bacterial holo-flavodoxin |
| 18 | d1oboa_ | Alignment |  | 99.8 | 15 | **Fold:**Flavodoxin-like<br>**Superfamily:**Flavoproteins<br>**Family:**Flavodoxin-related |
| 19 | d1czna_ | Alignment |  | 99.8 | 10 | **Fold:**Flavodoxin-like<br>**Superfamily:**Flavoproteins<br>**Family:**Flavodoxin-related |
| 20 | d1ag9a_ | Alignment |  | 99.8 | 20 | **Fold:**Flavodoxin-like<br>**Superfamily:**Flavoproteins<br>**Family:**Flavodoxin-related |
| 21 | d1f4pa_ | Alignment | not modelled | 99.8 | 13 | **Fold:**Flavodoxin-like<br>**Superfamily:**Flavoproteins<br>**Family:**Flavodoxin-related |
| 22 | c3f6sI_ | Alignment | not modelled | 99.8 | 14 | **PDB header:**electron transport<br>**Chain:** I: **PDB Molecule:**flavodoxin;<br>**PDBTitle:** desulfovibrio desulfuricans (atcc 29577) oxidized flavodoxin2 alternate conformers |
| 23 | d1fuea_ | Alignment | not modelled | 99.8 | 22 | **Fold:**Flavodoxin-like<br>**Superfamily:**Flavoproteins<br>**Family:**Flavodoxin-related |
| 24 | d2fz5a1 | Alignment | not modelled | 99.5 | 14 | **Fold:**Flavodoxin-like<br>**Superfamily:**Flavoproteins<br>**Family:**Flavodoxin-related |
| 25 | d5nula_ | Alignment | not modelled | 99.4 | 9 | **Fold:**Flavodoxin-like<br>**Superfamily:**Flavoproteins<br>**Family:**Flavodoxin-related |
| 26 | d1vmea1 | Alignment | not modelled | 99.4 | 17 | **Fold:**Flavodoxin-like<br>**Superfamily:**Flavoproteins<br>**Family:**Flavodoxin-related |
| 27 | c1vmeB_ | Alignment | not modelled | 99.4 | 15 | **PDB header:**electron transport<br>**Chain:** B: **PDB Molecule:**flavoprotein;<br>**PDBTitle:** crystal structure of flavoprotein (tm0755) from thermotoga maritima at2 1.80 a resolution |
| 28 | c3hlyA_ | Alignment | not modelled | 99.3 | 11 | **PDB header:**flavoprotein<br>**Chain:** A: **PDB Molecule:**flavodoxin-like domain;<br>**PDBTitle:** crystal structure of the flavodoxin-like domain from2 synechococcus sp q5mzp6_synp6 protein. northeast structural3 genomics consortium target snr135d. |

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| 29 | d1e5da1 | Alignment | not modelled | 99.3 | 15 | **Fold:**Flavodoxin-like<br>**Superfamily:**Flavoproteins<br>**Family:**Flavodoxin-related |
| 30 | c3klbA_ | Alignment | not modelled | 99.3 | 19 | **PDB header:**flavoprotein<br>**Chain:** A: **PDB Molecule:**putative flavoprotein;<br>**PDBTitle:** crystal structure of putative flavoprotein in complex with fmn2 (yp_213683.1) from bacteroides fragilis nctc 9343 at 1.75 a3 resolution |
| 31 | d1ycga1 | Alignment | not modelled | 99.3 | 10 | **Fold:**Flavodoxin-like<br>**Superfamily:**Flavoproteins<br>**Family:**Flavodoxin-related |
| 32 | c3fniA_ | Alignment | not modelled | 99.2 | 14 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**putative diflavin flavoprotein a 3;<br>**PDBTitle:** crystal structure of a diflavin flavoprotein a3 (all3895) from nostoc2 sp., northeast structural genomics consortium target nsr431a |
| 33 | c1ychD_ | Alignment | not modelled | 99.1 | 11 | **PDB header:**oxidoreductase<br>**Chain:** D: **PDB Molecule:**nitric oxide reductase;<br>**PDBTitle:** x-ray crystal structures of moorella thermoacetica fpra.2 novel diiron site structure and mechanistic insights into3 a scavenging nitric oxide reductase |
| 34 | d2arka1 | Alignment | not modelled | 99.1 | 17 | **Fold:**Flavodoxin-like<br>**Superfamily:**Flavoproteins<br>**Family:**WrbA-like |
| 35 | c3edoA_ | Alignment | not modelled | 99.0 | 15 | **PDB header:**flavoprotein<br>**Chain:** A: **PDB Molecule:**putative trp repressor binding protein;<br>**PDBTitle:** crystal structure of flavoprotein in complex with fmn2 (yp_193882.1) from lactobacillus acidophilus ncfm at 1.203 a resolution |
| 36 | c2ohiB_ | Alignment | not modelled | 99.0 | 15 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**type a flavoprotein fpra;<br>**PDBTitle:** crystal structure of coenzyme f420h2 oxidase (fpra), a diiron2 flavoprotein, reduced state |
| 37 | c2q9uB_ | Alignment | not modelled | 99.0 | 15 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**a-type flavoprotein;<br>**PDBTitle:** crystal structure of the flavodiiron protein from giardia2 intestinalis |
| 38 | c1e5dA_ | Alignment | not modelled | 98.9 | 15 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**rubredoxin\:oxygen oxidoreductase;<br>**PDBTitle:** rubredoxin oxygen:oxidoreductase (roo) from anaerobe2 desulfovibrio gigas |
| 39 | c3d7nA_ | Alignment | not modelled | 98.9 | 16 | **PDB header:**electron transport<br>**Chain:** A: **PDB Molecule:**flavodoxin, wrba-like protein;<br>**PDBTitle:** the crystal structure of the flavodoxin, wrba-like protein from2 agrobacterium tumefaciens |
| 40 | d2a5la1 | Alignment | not modelled | 98.8 | 14 | **Fold:**Flavodoxin-like<br>**Superfamily:**Flavoproteins<br>**Family:**WrbA-like |
| 41 | c3b6iB_ | Alignment | not modelled | 98.6 | 18 | **PDB header:**flavoprotein<br>**Chain:** B: **PDB Molecule:**flavoprotein wrba;<br>**PDBTitle:** wrba from escherichia coli, native structure |
| 42 | d1ydga_ | Alignment | not modelled | 98.6 | 16 | **Fold:**Flavodoxin-like<br>**Superfamily:**Flavoproteins<br>**Family:**WrbA-like |
| 43 | c2zkiH_ | Alignment | not modelled | 98.4 | 16 | **PDB header:**transcription<br>**Chain:** H: **PDB Molecule:**199aa long hypothetical trp repressor binding<br>**PDBTitle:** crystal structure of hypothetical trp repressor binding2 protein from sul folobus tokodaii (st0872) |
| 44 | d1rtta_ | Alignment | not modelled | 97.4 | 14 | **Fold:**Flavodoxin-like<br>**Superfamily:**Flavoproteins<br>**Family:**NADPH-dependent FMN reductase |
| 45 | d1rlia_ | Alignment | not modelled | 97.4 | 20 | **Fold:**Flavodoxin-like<br>**Superfamily:**Flavoproteins<br>**Family:**Hypothetical protein YwqN |
| 46 | d1t0ia_ | Alignment | not modelled | 97.3 | 16 | **Fold:**Flavodoxin-like<br>**Superfamily:**Flavoproteins<br>**Family:**NADPH-dependent FMN reductase |
| 47 | c3lcmB_ | Alignment | not modelled | 97.3 | 16 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**putative oxidoreductase;<br>**PDBTitle:** crystal structure of smu.1420 from streptococcus mutans ua159 |
| 48 | d1t5ba_ | Alignment | not modelled | 96.4 | 16 | **Fold:**Flavodoxin-like<br>**Superfamily:**Flavoproteins<br>**Family:**Quinone reductase |
| 49 | d1nni1_ | Alignment | not modelled | 96.3 | 15 | **Fold:**Flavodoxin-like<br>**Superfamily:**Flavoproteins<br>**Family:**NADPH-dependent FMN reductase |
| 50 | c3k1yE_ | Alignment | not modelled | 96.2 | 13 | **PDB header:**oxidoreductase<br>**Chain:** E: **PDB Molecule:**oxidoreductase;<br>**PDBTitle:** x-ray structure of oxidoreductase from corynebacterium2 diphtheriae. orthorombic crystal form, northeast structural3 genomics consortium target cdr100d |
| 51 | c2q62A_ | Alignment | not modelled | 96.0 | 13 | **PDB header:**flavoprotein<br>**Chain:** A: **PDB Molecule:**arsh;<br>**PDBTitle:** crystal structure of arsh from sinorhizobium meliloti |
| 52 | c2hpvA_ | Alignment | not modelled | 95.4 | 17 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**fmn-dependent nadh-azoreductase;<br>**PDBTitle:** crystal structure of fmn-dependent azoreductase from enterococcus2 faecalis |
| 53 | c2fzvC_ | Alignment | not modelled | 94.1 | 13 | **PDB header:**structural genomics, unknown function<br>**Chain:** C: **PDB Molecule:**putative arsenical resistance protein;<br>**PDBTitle:** crystal structure of an apo form of a flavin-binding protein from2 shigella flexneri |
|  |  |  |  |  |  | **PDB header:**oxidoreductase |

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| 54 | c2vzhA_ | Alignment | not modelled | 93.9 | 20 | **Chain:** A: **PDB Molecule:**nadh-dependent fmn reductase;<br>**PDBTitle:** structures of nadh:fmn oxidoreductase (emob)-fmn complex |
| 55 | c3f2vA_ | Alignment | not modelled | 93.5 | 10 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**general stress protein 14;<br>**PDBTitle:** crystal structure of the general stress protein 142 (tde0354) in complex with fmn from treponema denticola,3 northeast structural genomics consortium target tdr58. |
| 56 | d2fzva1 | Alignment | not modelled | 92.8 | 18 | **Fold:**Flavodoxin-like<br>**Superfamily:**Flavoproteins<br>**Family:**NADPH-dependent FMN reductase |
| 57 | d1sqsa_ | Alignment | not modelled | 92.4 | 13 | **Fold:**Flavodoxin-like<br>**Superfamily:**Flavoproteins<br>**Family:**Hypothetical protein SP1951 |
| 58 | c3fvwA_ | Alignment | not modelled | 91.3 | 16 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**putative nad(p)h-dependent fmn reductase;<br>**PDBTitle:** crystal structure of the q8dwd8_strmu protein from2 streptococcus mutans. northeast structural genomics3 consortium target smr99. |
| 59 | d2z98a1 | Alignment | not modelled | 90.9 | 14 | **Fold:**Flavodoxin-like<br>**Superfamily:**Flavoproteins<br>**Family:**Quinone reductase |
| 60 | c3rpeA_ | Alignment | not modelled | 88.4 | 16 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**modulator of drug activity b;<br>**PDBTitle:** 1.1 angstrom crystal structure of putative modulator of drug activity2 (mdab) from yersinia pestis co92. |
| 61 | c3p0rA_ | Alignment | not modelled | 86.1 | 13 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**azoreductase;<br>**PDBTitle:** crystal structure of azoreductase from bacillus anthracis str. sterne |
| 62 | c2amjD_ | Alignment | not modelled | 79.1 | 20 | **PDB header:**oxidoreductase<br>**Chain:** D: **PDB Molecule:**modulator of drug activity b;<br>**PDBTitle:** crystal structure of modulator of drug activity b from escherichia2 coli o157:h7 |
| 63 | d2c42a3 | Alignment | not modelled | 77.2 | 16 | **Fold:**TK C-terminal domain-like<br>**Superfamily:**TK C-terminal domain-like<br>**Family:**Pyruvate-ferredoxin oxidoreductase, PFOR, domain II |
| 64 | c2v9cA_ | Alignment | not modelled | 74.9 | 16 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**fmn-dependent nadh-azoreductase 1;<br>**PDBTitle:** x-ray crystallographic structure of a pseudomonas2 aeruginosa azoreductase in complex with methyl red. |
| 65 | d2qwxa1 | Alignment | not modelled | 70.9 | 11 | **Fold:**Flavodoxin-like<br>**Superfamily:**Flavoproteins<br>**Family:**Quinone reductase |
| 66 | d1z0sa1 | Alignment | not modelled | 67.7 | 16 | **Fold:**NAD kinase/diacylglycerol kinase-like<br>**Superfamily:**NAD kinase/diacylglycerol kinase-like<br>**Family:**NAD kinase-like |
| 67 | c1z0zC_ | Alignment | not modelled | 67.1 | 16 | **PDB header:**transferase<br>**Chain:** C: **PDB Molecule:**probable inorganic polyphosphate/atp-nad kinase;<br>**PDBTitle:** crystal structure of a nad kinase from archaeoglobus2 fulgidus in complex with nad |
| 68 | c3czcA_ | Alignment | not modelled | 60.8 | 4 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**rmpb;<br>**PDBTitle:** the crystal structure of a putative pts iib(ptxb) from2 streptococcus mutans |
| 69 | d1ik6a2 | Alignment | not modelled | 45.6 | 16 | **Fold:**TK C-terminal domain-like<br>**Superfamily:**TK C-terminal domain-like<br>**Family:**Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain |
| 70 | d1qrda_ | Alignment | not modelled | 44.6 | 18 | **Fold:**Flavodoxin-like<br>**Superfamily:**Flavoproteins<br>**Family:**Quinone reductase |
| 71 | d2a9va1 | Alignment | not modelled | 42.6 | 12 | **Fold:**Flavodoxin-like<br>**Superfamily:**Class I glutamine amidotransferase-like<br>**Family:**Class I glutamine amidotransferases (GAT) |
| 72 | c2ct6A_ | Alignment | not modelled | 35.5 | 33 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**sh3 domain-binding glutamic acid-rich-like<br>**PDBTitle:** solution structure of the sh3 domain-binding glutamic acid-2 rich-like protein 2 |
| 73 | d1dxqa_ | Alignment | not modelled | 34.7 | 21 | **Fold:**Flavodoxin-like<br>**Superfamily:**Flavoproteins<br>**Family:**Quinone reductase |
| 74 | d1f46a_ | Alignment | not modelled | 29.6 | 15 | **Fold:**TBP-like<br>**Superfamily:**Cell-division protein ZipA, C-terminal domain<br>**Family:**Cell-division protein ZipA, C-terminal domain |
| 75 | c3ha2B_ | Alignment | not modelled | 28.8 | 14 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**nadph-quinone reductase;<br>**PDBTitle:** crystal structure of protein (nadph-quinone reductase) from2 p.pentosaceus, northeast structural genomics consortium target ptr24a |
| 76 | c2iz6A_ | Alignment | not modelled | 25.5 | 17 | **PDB header:**metal transport<br>**Chain:** A: **PDB Molecule:**molybdenum cofactor carrier protein;<br>**PDBTitle:** structure of the chlamydomonas rheinhardtii moco carrier2 protein |
| 77 | c1tvmA_ | Alignment | not modelled | 24.4 | 9 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**pts system, galactitol-specific iib component;<br>**PDBTitle:** nmr structure of enzyme gatb of the galactitol-specific2 phosphoenolpyruvate-dependent phosphotransferase system |
| 78 | c1vjqB_ | Alignment | not modelled | 23.7 | 19 | **PDB header:**structural genomics, de novo protein<br>**Chain:** B: **PDB Molecule:**designed protein;<br>**PDBTitle:** designed protein based on backbone conformation of2 procarboxypeptidase-a (1aye) with sidechains chosen for maximal3 |

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| | | | | | | predicted stability. |
| 79 | c3ju3A_ | Alignment | not modelled | 18.5 | 18 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**probable 2-oxoacid ferredoxin oxidoreductase, alpha chain;<br>**PDBTitle:** crystal structure of alpha chain of probable 2-oxoacid ferredoxin2 oxidoreductase from thermoplasma acidophilum |
| 80 | d1iowa1 | Alignment | not modelled | 17.7 | 11 | **Fold:**PreATP-grasp domain<br>**Superfamily:**PreATP-grasp domain<br>**Family:**D-Alanine ligase N-terminal domain |
| 81 | c1u6tA_ | Alignment | not modelled | 16.4 | 46 | **PDB header:**protein binding, signaling protein<br>**Chain:** A: **PDB Molecule:**sh3 domain-binding glutamic acid-rich-like<br>**PDBTitle:** crystal structure of the human sh3 binding glutamic-rich2 protein like |
| 82 | c2kglA_ | Alignment | not modelled | 16.0 | 14 | **PDB header:**chaperone<br>**Chain:** A: **PDB Molecule:**mesoderm development candidate 2;<br>**PDBTitle:** nmr solution structure of mesd |
| 83 | c3dnfB_ | Alignment | not modelled | 15.4 | 14 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**4-hydroxy-3-methylbut-2-enyl diphosphate reductase;<br>**PDBTitle:** structure of (e)-4-hydroxy-3-methyl-but-2-enyl diphosphate reductase,2 the terminal enzyme of the non-mevalonate pathway |
| 84 | d1pzxa_ | Alignment | not modelled | 14.7 | 10 | **Fold:**DAK1/DegV-like<br>**Superfamily:**DAK1/DegV-like<br>**Family:**DegV-like |
| 85 | d1k9vf_ | Alignment | not modelled | 13.1 | 17 | **Fold:**Flavodoxin-like<br>**Superfamily:**Class I glutamine amidotransferase-like<br>**Family:**Class I glutamine amidotransferases (GAT) |
| 86 | c3ke8A_ | Alignment | not modelled | 12.9 | 16 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**4-hydroxy-3-methylbut-2-enyl diphosphate<br>**PDBTitle:** crystal structure of isph:hmbpp-complex |
| 87 | c2r47C_ | Alignment | not modelled | 12.7 | 13 | **PDB header:**structural genomics, unknown function<br>**Chain:** C: **PDB Molecule:**uncharacterized protein mth_862;<br>**PDBTitle:** crystal structure of mth_862 protein of unknown function from2 methanothermobacter thermautotrophicus |
| 88 | c2o6lA_ | Alignment | not modelled | 12.5 | 14 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**udp-glucuronosyltransferase 2b7;<br>**PDBTitle:** crystal structure of the udp-glucuronic acid binding domain2 of the human drug metabolizing udp-glucuronosyltransferase3 2b7 |
| 89 | c3i0zB_ | Alignment | not modelled | 12.5 | 14 | **PDB header:**isomerase<br>**Chain:** B: **PDB Molecule:**putative tagatose-6-phosphate ketose/aldose isomerase;<br>**PDBTitle:** crystal structure of putative putative tagatose-6-phosphate2 ketose/aldose isomerase (np_344614.1) from streptococcus pneumoniae3 tigr4 at 1.70 a resolution |
| 90 | d1vkra_ | Alignment | not modelled | 11.8 | 9 | **Fold:**Phosphotyrosine protein phosphatases I-like<br>**Superfamily:**PTS system IIB component-like<br>**Family:**PTS system, Lactose/Cellobiose specific IIB subunit |
| 91 | c1vkrA_ | Alignment | not modelled | 11.8 | 9 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**mannitol-specific pts system enzyme iiabc components;<br>**PDBTitle:** structure of iib domain of the mannitol-specific permease enzyme ii |
| 92 | d1o1ya_ | Alignment | not modelled | 11.7 | 6 | **Fold:**Flavodoxin-like<br>**Superfamily:**Class I glutamine amidotransferase-like<br>**Family:**Class I glutamine amidotransferases (GAT) |
| 93 | d1fs0g_ | Alignment | not modelled | 11.4 | 10 | **Fold:**Pyruvate kinase C-terminal domain-like<br>**Superfamily:**ATP synthase (F1-ATPase), gamma subunit<br>**Family:**ATP synthase (F1-ATPase), gamma subunit |
| 94 | d1t35a_ | Alignment | not modelled | 10.9 | 24 | **Fold:**MCP/YpsA-like<br>**Superfamily:**MCP/YpsA-like<br>**Family:**MoCo carrier protein-like |
| 95 | c3siiA_ | Alignment | not modelled | 10.1 | 24 | **PDB header:**hydrolase/hydrolase inhibitor<br>**Chain:** A: **PDB Molecule:**poly(adp-ribose) glycohydrolase;<br>**PDBTitle:** the x-ray crystal structure of poly(adp-ribose) glycohydrolase bound2 to the inhibitor adp-hpd from thermomonospora curvata |
| 96 | d1jkea_ | Alignment | not modelled | 10.0 | 18 | **Fold:**DTD-like<br>**Superfamily:**DTD-like<br>**Family:**DTD-like |
| 97 | c3c3jA_ | Alignment | not modelled | 10.0 | 18 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**putative tagatose-6-phosphate ketose/aldose isomerase;<br>**PDBTitle:** crystal structure of tagatose-6-phosphate ketose/aldose isomerase from2 escherichia coli |
| 98 | c3quaA_ | Alignment | not modelled | 9.6 | 7 | **PDB header:**unknown function<br>**Chain:** A: **PDB Molecule:**putative uncharacterized protein;<br>**PDBTitle:** crystal structure of a putative uncharacterized protein and possible2 molybdenum cofactor protein from mycobacterium smegmatis |
| 99 | d1jvna2 | Alignment | not modelled | 9.1 | 17 | **Fold:**Flavodoxin-like<br>**Superfamily:**Class I glutamine amidotransferase-like<br>**Family:**Class I glutamine amidotransferases (GAT) |