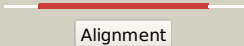

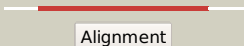

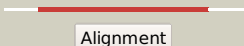







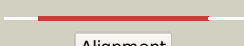




















# Phyre2

Email [mdejesus@rockefeller.edu](mailto:mdejesus@rockefeller.edu)  
 Description RVBD3339c\_(icd1)\_3724786\_3726015  
 Date Thu Aug 8 16:20:55 BST 2019  
 Unique Job ID 2a119fb680d34ac4

Detailed template information

| #  | Template                | Alignment Coverage  | 3D Model  | Confidence | % i.d. | Template Information  |
|----|-------------------------|---|---|------------|--------|---|
| 1  | <a href="#">c3us8A_</a> |  Alignment   |    | 100.0      | 72     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> isocitrate dehydrogenase [nadp];<br><b>PDBTitle:</b> crystal structure of an isocitrate dehydrogenase from sinorhizobium2 meliloti 1021  |
| 2  | <a href="#">c2qfyE_</a> |  Alignment   |    | 100.0      | 62     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> E: <b>PDB Molecule:</b> isocitrate dehydrogenase [nadp];<br><b>PDBTitle:</b> crystal structure of saccharomyces cerevesiae mitochondrial nadp(+)-2 dependent isocitrate dehydrogenase in complex with a-ketoglutarate                                  |
| 3  | <a href="#">d1t0la_</a> |  Alignment   |    | 100.0      | 66     | <b>Fold:</b> Isocitrate/Isopropylmalate dehydrogenase-like<br><b>Superfamily:</b> Isocitrate/Isopropylmalate dehydrogenase-like<br><b>Family:</b> Dimeric isocitrate & isopropylmalate dehydrogenases   |
| 4  | <a href="#">d1lwda_</a> |  Alignment   |    | 100.0      | 66     | <b>Fold:</b> Isocitrate/Isopropylmalate dehydrogenase-like<br><b>Superfamily:</b> Isocitrate/Isopropylmalate dehydrogenase-like<br><b>Family:</b> Dimeric isocitrate & isopropylmalate dehydrogenases   |
| 5  | <a href="#">c2uxqB_</a> |  Alignment |  | 100.0      | 51     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> isocitrate dehydrogenase native;<br><b>PDBTitle:</b> isocitrate dehydrogenase from the psychrophilic bacterium2 desulfotalea psychrophila: biochemical properties and3 crystal structure analysis                              |
| 6  | <a href="#">c1zorB_</a> |  Alignment |  | 100.0      | 55     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> isocitrate dehydrogenase;<br><b>PDBTitle:</b> isocitrate dehydrogenase from the hyperthermophile thermotoga maritima   |
| 7  | <a href="#">c4aoyD_</a> |  Alignment |  | 100.0      | 53     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> D: <b>PDB Molecule:</b> isocitrate dehydrogenase [nadp];<br><b>PDBTitle:</b> open ctidh. the complex structures of isocitrate dehydrogenase from2 clostridium thermocellum and desulfotalea psychrophila, support a new3 active site locking mechanism |
| 8  | <a href="#">d1hqsa_</a> |  Alignment |  | 100.0      | 23     | <b>Fold:</b> Isocitrate/Isopropylmalate dehydrogenase-like<br><b>Superfamily:</b> Isocitrate/Isopropylmalate dehydrogenase-like<br><b>Family:</b> Dimeric isocitrate & isopropylmalate dehydrogenases   |
| 9  | <a href="#">c2d4vD_</a> |  Alignment |  | 100.0      | 24     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> D: <b>PDB Molecule:</b> isocitrate dehydrogenase;<br><b>PDBTitle:</b> crystal structure of nad dependent isocitrate dehydrogenase2 from acidithiobacillus thiooxidans  |
| 10 | <a href="#">c2d1cB_</a> |  Alignment |  | 100.0      | 23     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> isocitrate dehydrogenase;<br><b>PDBTitle:</b> crystal structure of tt0538 protein from thermus thermophilus hb8  |
| 11 | <a href="#">c3fmxX_</a> |  Alignment |  | 100.0      | 17     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> X: <b>PDB Molecule:</b> tartrate dehydrogenase/decarboxylase;<br><b>PDBTitle:</b> crystal structure of tartrate dehydrogenase from pseudomonas putida2 complexed with nadh   |

|    |                         |           |   |       |    |   |
|----|-------------------------|-----------|---|-------|----|---|
| 12 | <a href="#">d1pb1a_</a> | Alignment |    | 100.0 | 22 | <b>Fold:</b> Isocitrate/Isopropylmalate dehydrogenase-like<br><b>Superfamily:</b> Isocitrate/Isopropylmalate dehydrogenase-like<br><b>Family:</b> Dimeric isocitrate & isopropylmalate dehydrogenases   |
| 13 | <a href="#">c2e0cA_</a> | Alignment |    | 100.0 | 20 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 409aa long hypothetical nadp-dependent isocitrate<br><b>PDBTitle:</b> crystal structure of isocitrate dehydrogenase from sulfobolus tokodaii2 strain7 at 2.0 a resolution          |
| 14 | <a href="#">d1v53a1</a> | Alignment |    | 100.0 | 19 | <b>Fold:</b> Isocitrate/Isopropylmalate dehydrogenase-like<br><b>Superfamily:</b> Isocitrate/Isopropylmalate dehydrogenase-like<br><b>Family:</b> Dimeric isocitrate & isopropylmalate dehydrogenases   |
| 15 | <a href="#">d1cnza_</a> | Alignment |    | 100.0 | 20 | <b>Fold:</b> Isocitrate/Isopropylmalate dehydrogenase-like<br><b>Superfamily:</b> Isocitrate/Isopropylmalate dehydrogenase-like<br><b>Family:</b> Dimeric isocitrate & isopropylmalate dehydrogenases   |
| 16 | <a href="#">d1cm7a_</a> | Alignment |    | 100.0 | 19 | <b>Fold:</b> Isocitrate/Isopropylmalate dehydrogenase-like<br><b>Superfamily:</b> Isocitrate/Isopropylmalate dehydrogenase-like<br><b>Family:</b> Dimeric isocitrate & isopropylmalate dehydrogenases   |
| 17 | <a href="#">c3uduG_</a> | Alignment |    | 100.0 | 22 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> G: <b>PDB Molecule:</b> 3-isopropylmalate dehydrogenase;<br><b>PDBTitle:</b> crystal structure of putative 3-isopropylmalate dehydrogenase from2 campylobacter jejuni                                      |
| 18 | <a href="#">c3u1hA_</a> | Alignment |  | 100.0 | 23 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 3-isopropylmalate dehydrogenase;<br><b>PDBTitle:</b> crystal structure of ipmdh from the last common ancestor of bacillus  |
| 19 | <a href="#">d1vlca_</a> | Alignment |  | 100.0 | 22 | <b>Fold:</b> Isocitrate/Isopropylmalate dehydrogenase-like<br><b>Superfamily:</b> Isocitrate/Isopropylmalate dehydrogenase-like<br><b>Family:</b> Dimeric isocitrate & isopropylmalate dehydrogenases   |
| 20 | <a href="#">c3vl3A_</a> | Alignment |  | 100.0 | 22 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 3-isopropylmalate dehydrogenase;<br><b>PDBTitle:</b> 3-isopropylmalate dehydrogenase from shewanella oneidensis mr-1 at 3402 mpa   |
| 21 | <a href="#">d1wpwa_</a> | Alignment | not modelled  | 100.0 | 20 | <b>Fold:</b> Isocitrate/Isopropylmalate dehydrogenase-like<br><b>Superfamily:</b> Isocitrate/Isopropylmalate dehydrogenase-like<br><b>Family:</b> Dimeric isocitrate & isopropylmalate dehydrogenases   |
| 22 | <a href="#">d1xaca_</a> | Alignment | not modelled  | 100.0 | 21 | <b>Fold:</b> Isocitrate/Isopropylmalate dehydrogenase-like<br><b>Superfamily:</b> Isocitrate/Isopropylmalate dehydrogenase-like<br><b>Family:</b> Dimeric isocitrate & isopropylmalate dehydrogenases   |
| 23 | <a href="#">c3ty3A_</a> | Alignment | not modelled  | 100.0 | 20 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> probable homoisocitrate dehydrogenase;<br><b>PDBTitle:</b> crystal structure of homoisocitrate dehydrogenase from2 schizosaccharomyces pombe bound to glycyL-glycyl-glycine        |
| 24 | <a href="#">c4iwHA_</a> | Alignment | not modelled  | 100.0 | 20 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 3-isopropylmalate dehydrogenase;<br><b>PDBTitle:</b> crystal structure of a 3-isopropylmalate dehydrogenase from2 burkholderia pseudomallei  |
| 25 | <a href="#">d1g2ua_</a> | Alignment | not modelled  | 100.0 | 21 | <b>Fold:</b> Isocitrate/Isopropylmalate dehydrogenase-like<br><b>Superfamily:</b> Isocitrate/Isopropylmalate dehydrogenase-like<br><b>Family:</b> Dimeric isocitrate & isopropylmalate dehydrogenases   |
| 26 | <a href="#">c3r8wC_</a> | Alignment | not modelled  | 100.0 | 17 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> C: <b>PDB Molecule:</b> 3-isopropylmalate dehydrogenase 2, chloroplastic;<br><b>PDBTitle:</b> structure of 3-isopropylmalate dehydrogenase isoform 2 from2 arabidopsis thaliana at 2.2 angstrom resolution |
| 27 | <a href="#">c1x0lB_</a> | Alignment | not modelled  | 100.0 | 21 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> homoisocitrate dehydrogenase;<br><b>PDBTitle:</b> crystal structure of tetrameric homoisocitrate dehydrogenase from an2 extreme thermophile, thermus thermophilus                  |
| 28 | <a href="#">c1tyoA_</a> | Alignment | not modelled  | 100.0 | 21 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> isocitrate dehydrogenase;<br><b>PDBTitle:</b> isocitrate dehydrogenase from the hyperthermophile   |

|    |                         |           |              |       |    |  |
|----|-------------------------|-----------|--------------|-------|----|--|
|    |                         |           |              |       |    | aeropyrum pernix in2 complex with etheno-nadp  |
| 29 | <a href="#">d1a05a_</a> | Alignment | not modelled | 100.0 | 20 | <b>Fold:</b> Isocitrate/Isopropylmalate dehydrogenase-like<br><b>Superfamily:</b> Isocitrate/Isopropylmalate dehydrogenase-like<br><b>Family:</b> Dimeric isocitrate & isopropylmalate dehydrogenases  |
| 30 | <a href="#">d1w0da_</a> | Alignment | not modelled | 100.0 | 20 | <b>Fold:</b> Isocitrate/Isopropylmalate dehydrogenase-like<br><b>Superfamily:</b> Isocitrate/Isopropylmalate dehydrogenase-like<br><b>Family:</b> Dimeric isocitrate & isopropylmalate dehydrogenases  |
| 31 | <a href="#">c5hn6A_</a> | Alignment | not modelled | 100.0 | 22 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> homoisocitrate dehydrogenase;<br><b>PDBTitle:</b> crystal structure of beta-decarboxylating dehydrogenase (tk0280) from2 thermococcus kodakarensis complexed with mn and 3-isopropylmalate        |
| 32 | <a href="#">c5grhA_</a> | Alignment | not modelled | 100.0 | 24 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> isocitrate dehydrogenase [nad] subunit alpha,<br><b>PDBTitle:</b> crystal structure of the alpha gamma heterodimer of human idh3 in2 complex with mg(2+)  |
| 33 | <a href="#">c3blxL_</a> | Alignment | not modelled | 100.0 | 28 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> L: <b>PDB Molecule:</b> isocitrate dehydrogenase [nad] subunit 2;<br><b>PDBTitle:</b> yeast isocitrate dehydrogenase (apo form)   |
| 34 | <a href="#">c5grhB_</a> | Alignment | not modelled | 100.0 | 21 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> isocitrate dehydrogenase [nad] subunit gamma,<br><b>PDBTitle:</b> crystal structure of the alpha gamma heterodimer of human idh3 in2 complex with mg(2+)  |
| 35 | <a href="#">c3blxM_</a> | Alignment | not modelled | 100.0 | 21 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> M: <b>PDB Molecule:</b> isocitrate dehydrogenase [nad] subunit 1;<br><b>PDBTitle:</b> yeast isocitrate dehydrogenase (apo form)   |
| 36 | <a href="#">c2iv0A_</a> | Alignment | not modelled | 100.0 | 22 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> isocitrate dehydrogenase;<br><b>PDBTitle:</b> thermal stability of isocitrate dehydrogenase from2 archaeoglobus fulgidus studied by crystal structure3 analysis and engineering of chimers        |
| 37 | <a href="#">c6g3uA_</a> | Alignment | not modelled | 97.9  | 16 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> isocitrate dehydrogenase;<br><b>PDBTitle:</b> structure of pseudomonas aeruginosa isocitrate dehydrogenase, idh   |
| 38 | <a href="#">d1itwa_</a> | Alignment | not modelled | 97.8  | 16 | <b>Fold:</b> Isocitrate/Isopropylmalate dehydrogenase-like<br><b>Superfamily:</b> Isocitrate/Isopropylmalate dehydrogenase-like<br><b>Family:</b> Monomeric isocitrate dehydrogenase   |
| 39 | <a href="#">c2b0tA_</a> | Alignment | not modelled | 97.6  | 14 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> nadp isocitrate dehydrogenase;<br><b>PDBTitle:</b> structure of monomeric nadp isocitrate dehydrogenase   |
| 40 | <a href="#">d1r8ka_</a> | Alignment | not modelled | 96.1  | 16 | <b>Fold:</b> Isocitrate/Isopropylmalate dehydrogenase-like<br><b>Superfamily:</b> Isocitrate/Isopropylmalate dehydrogenase-like<br><b>Family:</b> PdxA-like  |
| 41 | <a href="#">c4jqpA_</a> | Alignment | not modelled | 95.6  | 14 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 4-hydroxythreonine-4-phosphate dehydrogenase;<br><b>PDBTitle:</b> x-ray crystal structure of a 4-hydroxythreonine-4-phosphate2 dehydrogenase from burkholderia phymatum                           |
| 42 | <a href="#">c2hi1A_</a> | Alignment | not modelled | 94.6  | 21 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> 4-hydroxythreonine-4-phosphate dehydrogenase 2;<br><b>PDBTitle:</b> the structure of a putative 4-hydroxythreonine-4-phosphate2 dehydrogenase from salmonella typhimurium. |
| 43 | <a href="#">d1ptma_</a> | Alignment | not modelled | 94.3  | 16 | <b>Fold:</b> Isocitrate/Isopropylmalate dehydrogenase-like<br><b>Superfamily:</b> Isocitrate/Isopropylmalate dehydrogenase-like<br><b>Family:</b> PdxA-like  |
| 44 | <a href="#">c4atyA_</a> | Alignment | not modelled | 94.1  | 13 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> terephthalate 1,2-cis-dihydrodiol dehydrogenase;<br><b>PDBTitle:</b> crystal structure of a terephthalate 1,2-cis-2 dihydrodioldehydrogenase from burkholderia xenovorans3 lb400                  |
| 45 | <a href="#">c3tsnD_</a> | Alignment | not modelled | 93.3  | 16 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> D: <b>PDB Molecule:</b> 4-hydroxythreonine-4-phosphate dehydrogenase;<br><b>PDBTitle:</b> 4-hydroxythreonine-4-phosphate dehydrogenase from campylobacter jejuni  |
| 46 | <a href="#">c1yxoB_</a> | Alignment | not modelled | 88.5  | 16 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> 4-hydroxythreonine-4-phosphate dehydrogenase 1;<br><b>PDBTitle:</b> crystal structure of pyridoxal phosphate biosynthetic protein pdxa2 pa0593  |
| 47 | <a href="#">c5ahwC_</a> | Alignment | not modelled | 24.1  | 9  | <b>PDB header:</b> signaling protein<br><b>Chain:</b> C: <b>PDB Molecule:</b> universal stress protein;<br><b>PDBTitle:</b> crystal structure of universal stress protein msmeg_3811 in2 complex with camp   |
| 48 | <a href="#">c1p84E_</a> | Alignment | not modelled | 21.9  | 18 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> E: <b>PDB Molecule:</b> ubiquinol-cytochrome c reductase iron-sulfur subunit;<br><b>PDBTitle:</b> hdbt inhibited yeast cytochrome bc1 complex   |
| 49 | <a href="#">d1kl7a_</a> | Alignment | not modelled | 21.9  | 17 | <b>Fold:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes<br><b>Superfamily:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes<br><b>Family:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes                                    |
| 50 | <a href="#">c3fh0A_</a> | Alignment | not modelled | 21.8  | 12 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative universal stress protein kpn_01444;<br><b>PDBTitle:</b> crystal structure of putative universal stress protein kpn_01444 -2 atpase                                |
| 51 | <a href="#">c2fyuE_</a> | Alignment | not modelled | 20.6  | 18 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> E: <b>PDB Molecule:</b> ubiquinol-cytochrome c reductase iron-sulfur subunit,<br><b>PDBTitle:</b> crystal structure of bovine heart mitochondrial bc1 with jg1442 inhibitor   |

|    |                         |           |              |      |    |  |
|----|-------------------------|-----------|--------------|------|----|--|
| 52 | <a href="#">c5i0cA</a>  | Alignment | not modelled | 15.6 | 11 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein yjdj;<br><b>PDBTitle:</b> crystal structure of predicted acyltransferase yjdj with acyl-coa n-2 acyltransferase domain from escherichia coli str. k-12       |
| 53 | <a href="#">c2q62A</a>  | Alignment | not modelled | 12.4 | 13 | <b>PDB header:</b> flavoprotein<br><b>Chain:</b> A: <b>PDB Molecule:</b> arsh;<br><b>PDBTitle:</b> crystal structure of arsh from sinorhizobium meliloti   |
| 54 | <a href="#">c1nvpD</a>  | Alignment | not modelled | 11.8 | 23 | <b>PDB header:</b> transcription/dna<br><b>Chain:</b> D: <b>PDB Molecule:</b> transcription initiation factor iia gamma chain;<br><b>PDBTitle:</b> human tfiia/tbp/dna complex   |
| 55 | <a href="#">d1a0ca</a>  | Alignment | not modelled | 11.7 | 19 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Xylose isomerase-like<br><b>Family:</b> Xylose isomerase   |
| 56 | <a href="#">d2ffea1</a> | Alignment | not modelled | 11.6 | 11 | <b>Fold:</b> CofD-like<br><b>Superfamily:</b> CofD-like<br><b>Family:</b> CofD-like  |
| 57 | <a href="#">d1riea</a>  | Alignment | not modelled | 11.5 | 18 | <b>Fold:</b> ISP domain<br><b>Superfamily:</b> ISP domain<br><b>Family:</b> Rieske iron-sulfur protein (ISP)   |
| 58 | <a href="#">c2dumD</a>  | Alignment | not modelled | 11.3 | 18 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> D: <b>PDB Molecule:</b> hypothetical protein ph0823;<br><b>PDBTitle:</b> crystal structure of hypothetical protein, ph0823   |
| 59 | <a href="#">c4xkmB</a>  | Alignment | not modelled | 11.2 | 20 | <b>PDB header:</b> isomerase<br><b>Chain:</b> B: <b>PDB Molecule:</b> xylose isomerase;<br><b>PDBTitle:</b> crystal structure of xylose isomerase from an human intestinal tract2 microbe bacteroides thetaiotaomicron                                     |
| 60 | <a href="#">d1ofda1</a> | Alignment | not modelled | 10.7 | 17 | <b>Fold:</b> Single-stranded right-handed beta-helix<br><b>Superfamily:</b> Alpha subunit of glutamate synthase, C-terminal domain<br><b>Family:</b> Alpha subunit of glutamate synthase, C-terminal domain  |
| 61 | <a href="#">d1u84a</a>  | Alignment | not modelled | 10.4 | 20 | <b>Fold:</b> YugE-like<br><b>Superfamily:</b> YugE-like<br><b>Family:</b> YugE-like  |
| 62 | <a href="#">d1mn3a</a>  | Alignment | not modelled | 10.1 | 9  | <b>Fold:</b> RuvA C-terminal domain-like<br><b>Superfamily:</b> UBA-like<br><b>Family:</b> CUE domain  |
| 63 | <a href="#">c5fjsB</a>  | Alignment | not modelled | 10.1 | 7  | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> glucosylceramidase;<br><b>PDBTitle:</b> bacterial beta-glucosidase reveals the structural and functional2 basis of genetic defects in human glucocerebrosidase 2 (gba2)3 disorders   |
| 64 | <a href="#">c3wvxA</a>  | Alignment | not modelled | 10.1 | 21 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> non-reducing end beta-l-arabinofuranosidase;<br><b>PDBTitle:</b> crystal structure of gh127 beta-l-arabinofuranosidase hypba1 from2 bifidobacterium longum arabinose complex form    |
| 65 | <a href="#">d2o8ra3</a> | Alignment | not modelled | 10.0 | 8  | <b>Fold:</b> Phospholipase D/nuclease<br><b>Superfamily:</b> Phospholipase D/nuclease<br><b>Family:</b> Polyphosphate kinase C-terminal domain   |
| 66 | <a href="#">d1xmta</a>  | Alignment | not modelled | 9.5  | 11 | <b>Fold:</b> Acyl-CoA N-acyltransferases (Nat)<br><b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat)<br><b>Family:</b> N-acetyl transferase, NAT  |
| 67 | <a href="#">c2yu3A</a>  | Alignment | not modelled | 9.4  | 13 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> dna-directed rna polymerase iii 39 kda<br><b>PDBTitle:</b> solution structure of the domain swapped wingedhelix in dna-2 directed rna polymerase iii 39 kda polypeptide          |
| 68 | <a href="#">c2hb0B</a>  | Alignment | not modelled | 9.4  | 12 | <b>PDB header:</b> cell adhesion<br><b>Chain:</b> B: <b>PDB Molecule:</b> cfa/i fimbrial subunit e;<br><b>PDBTitle:</b> crystal structure of cfae, the adhesive subunit of cfa/i2 fimbria of enterotoxigenic escherichia coli                              |
| 69 | <a href="#">c6bwsA</a>  | Alignment | not modelled | 9.3  | 10 | <b>PDB header:</b> unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> glycolate utilization protein;<br><b>PDBTitle:</b> crystal structure of efga from methylobacterium extorquens   |
| 70 | <a href="#">d2d9ra1</a> | Alignment | not modelled | 9.2  | 20 | <b>Fold:</b> Double-split beta-barrel<br><b>Superfamily:</b> AF2212/PG0164-like<br><b>Family:</b> PG0164-like  |
| 71 | <a href="#">c3rhtB</a>  | Alignment | not modelled | 9.2  | 11 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> B: <b>PDB Molecule:</b> (gatase1)-like protein;<br><b>PDBTitle:</b> crystal structure of type 1 glutamine amidotransferase (gatase1)-like2 protein from planctomyces limnophilus |
| 72 | <a href="#">d1a0ea</a>  | Alignment | not modelled | 9.0  | 10 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Xylose isomerase-like<br><b>Family:</b> Xylose isomerase   |
| 73 | <a href="#">d2gana1</a> | Alignment | not modelled | 8.9  | 10 | <b>Fold:</b> Acyl-CoA N-acyltransferases (Nat)<br><b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat)<br><b>Family:</b> N-acetyl transferase, NAT  |
| 74 | <a href="#">c2pfsA</a>  | Alignment | not modelled | 8.8  | 9  | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> universal stress protein;<br><b>PDBTitle:</b> crystal structure of universal stress protein from nitrosomonas2 europaea                                  |
| 75 | <a href="#">c2j3zA</a>  | Alignment | not modelled | 8.6  | 16 | <b>PDB header:</b> toxin<br><b>Chain:</b> A: <b>PDB Molecule:</b> c2 toxin component i;<br><b>PDBTitle:</b> crystal structure of the enzymatic component c2-i of the c2-toxin from2 clostridium botulinum at ph 6.1  |
| 76 | <a href="#">c6ex6A</a>  | Alignment | not modelled | 8.6  | 21 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> six-hairpin glycosidase;<br><b>PDBTitle:</b> the gh127, beta-arabinofuranosidase, bt3674   |
| 77 | <a href="#">c1nh2D</a>  | Alignment | not modelled | 8.6  | 19 | <b>PDB header:</b> transcription/dna<br><b>Chain:</b> D: <b>PDB Molecule:</b> transcription initiation factor iia small chain;<br><b>PDBTitle:</b> crystal structure of a yeast tfiia/tbp/dna complex<br><b>PDB header:</b> oxidoreductase                 |

|    |                         |           |              |     |    |   |
|----|-------------------------|-----------|--------------|-----|----|---|
| 78 | <a href="#">c6dxdD</a>  | Alignment | not modelled | 8.4 | 16 | <b>Chain:</b> D: <b>PDB Molecule:</b> fmn-dependent nadh-azoreductase; <b>PDBTitle:</b> the crystal structure of an fmn-dependent nadh-azoreductase from <i>klebsiella pneumoniae</i>   |
| 79 | <a href="#">c2ozhA</a>  | Alignment | not modelled | 8.3 | 8  | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein xcc2953; <b>PDBTitle:</b> crystal structure of a putative acetyltransferase belonging to the <i>gnt</i> family (xcc2953) from <i>xanthomonas campestris</i> pv. <i>campestris</i> at 3.140 a resolution                      |
| 80 | <a href="#">c4wnyA</a>  | Alignment | not modelled | 8.2 | 9  | <b>PDB header:</b> signaling protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> universal stress protein; <b>PDBTitle:</b> crystal structure of a protein from the universal stress protein2 family from <i>burkholderia pseudomallei</i>   |
| 81 | <a href="#">c5m1hA</a>  | Alignment | not modelled | 8.1 | 18 | <b>PDB header:</b> viral protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> gag protein; <b>PDBTitle:</b> structure of a spumaretrovirus gag central domain reveals an ancient2 retroviral capsid   |
| 82 | <a href="#">c3f83A</a>  | Alignment | not modelled | 7.9 | 12 | <b>PDB header:</b> cell adhesion<br><b>Chain:</b> A: <b>PDB Molecule:</b> fusion of the minor pilin cfae and major pilin cfab; <b>PDBTitle:</b> structure of fusion complex of the minor pilin cfae and major pilin2 cfab of <i>cfa/i</i> pili from <i>etec</i> e. coli   |
| 83 | <a href="#">c5dniB</a>  | Alignment | not modelled | 7.9 | 13 | <b>PDB header:</b> lyase<br><b>Chain:</b> B: <b>PDB Molecule:</b> putative (+)-tartrate dehydratase subunit beta; <b>PDBTitle:</b> crystal structure of <i>methanocaldococcus jannaschii</i> fumarate hydratase2 beta subunit   |
| 84 | <a href="#">d1q77a</a>  | Alignment | not modelled | 7.8 | 3  | <b>Fold:</b> Adenine nucleotide alpha hydrolase-like<br><b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like<br><b>Family:</b> Universal stress protein-like  |
| 85 | <a href="#">d1qasa3</a> | Alignment | not modelled | 7.7 | 15 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> PLC-like phosphodiesterases<br><b>Family:</b> Mammalian PLC   |
| 86 | <a href="#">d1t9ba1</a> | Alignment | not modelled | 7.4 | 11 | <b>Fold:</b> DHS-like NAD/FAD-binding domain<br><b>Superfamily:</b> DHS-like NAD/FAD-binding domain<br><b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain   |
| 87 | <a href="#">c2p0yA</a>  | Alignment | not modelled | 7.3 | 17 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein lp_0780; <b>PDBTitle:</b> crystal structure of q88yi3_lacpl from <i>lactobacillus plantarum</i> .2 northeast structural genomics consortium target lpr6  |
| 88 | <a href="#">c4pc4B</a>  | Alignment | not modelled | 7.3 | 7  | <b>PDB header:</b> lipid binding protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> 30k lipoprotein; <b>PDBTitle:</b> bombyx mori lipoprotein 6   |
| 89 | <a href="#">d1jmva</a>  | Alignment | not modelled | 7.3 | 6  | <b>Fold:</b> Adenine nucleotide alpha hydrolase-like<br><b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like<br><b>Family:</b> Universal stress protein-like  |
| 90 | <a href="#">c2pt7G</a>  | Alignment | not modelled | 7.1 | 11 | <b>PDB header:</b> hydrolase/protein binding<br><b>Chain:</b> G: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of cag virb11 (hp0525) and an inhibitory protein2 (hp1451)   |
| 91 | <a href="#">c2jaxA</a>  | Alignment | not modelled | 7.1 | 12 | <b>PDB header:</b> protein binding<br><b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein tb31.7; <b>PDBTitle:</b> universal stress protein rv2623 from <i>mycobacterium</i> 2 tuberculosis  |
| 92 | <a href="#">c3pubA</a>  | Alignment | not modelled | 7.0 | 11 | <b>PDB header:</b> unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> 30kda protein; <b>PDBTitle:</b> crystal structure of the bombyx mori low molecular weight lipoprotein2 7 (bmlp7)   |
| 93 | <a href="#">c2kvoA</a>  | Alignment | not modelled | 6.9 | 13 | <b>PDB header:</b> photosynthesis<br><b>Chain:</b> A: <b>PDB Molecule:</b> photosystem ii reaction center psb28 protein; <b>PDBTitle:</b> solution nmr structure of photosystem ii reaction center psb28 protein2 from <i>synechocystis</i> sp.(strain pcc 6803), northeast structural3 genomics consortium target sgr171 |
| 94 | <a href="#">d1tj1a2</a> | Alignment | not modelled | 6.9 | 13 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> FAD-linked oxidoreductase<br><b>Family:</b> Proline dehydrogenase domain of bifunctional PutA protein   |
| 95 | <a href="#">d1i27a</a>  | Alignment | not modelled | 6.9 | 28 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> "Winged helix" DNA-binding domain<br><b>Family:</b> C-terminal domain of the rap74 subunit of TFIIF  |
| 96 | <a href="#">c3dddA</a>  | Alignment | not modelled | 6.8 | 13 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative acetyltransferase; <b>PDBTitle:</b> crystal structure of a putative acetyltransferase (np_142035.1) from <i>pyrococcus horikoshii</i> at 2.25 a resolution   |
| 97 | <a href="#">c3zpnD</a>  | Alignment | not modelled | 6.7 | 11 | <b>PDB header:</b> photosynthesis<br><b>Chain:</b> D: <b>PDB Molecule:</b> photosystem ii reaction center psb28 protein; <b>PDBTitle:</b> structure of psb28  |
| 98 | <a href="#">c2fynO</a>  | Alignment | not modelled | 6.6 | 16 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> O: <b>PDB Molecule:</b> ubiquinol-cytochrome c reductase iron-sulfur<br><b>PDBTitle:</b> crystal structure analysis of the double mutant <i>rhodobacter</i> 2 <i>sphaeroides</i> bc1 complex   |
| 99 | <a href="#">c6hhnA</a>  | Alignment | not modelled | 6.6 | 21 | <b>PDB header:</b> isomerase<br><b>Chain:</b> A: <b>PDB Molecule:</b> l-rhamnose mutarotase; <b>PDBTitle:</b> crystal structure of l-rhamnose mutarotase fa22100 from <i>formosa2</i> <i>agariphila</i>   |