# Phyre$^2$

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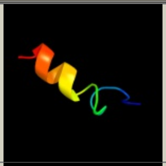
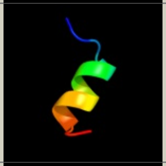
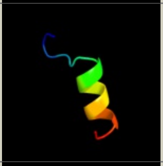
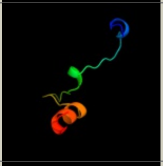
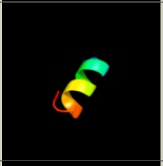
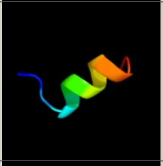
| Email | l.a.kelley@imperial.ac.uk |
| Description | P58094 |
| Date | Thu Jan 5 12:06:38 GMT 2012 |
| Unique Job ID | 9be46d66b3ac865b |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c3r7kB_ | Alignment |  | 32.0 | 22 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**probable acyl coa dehydrogenase;<br>**PDBTitle:** crystal structure of a probable acyl coa dehydrogenase from2 mycobacterium abscessus atcc 19977 / dsm 44196 |
| 2 | d1vlba1 | Alignment |  | 30.1 | 21 | **Fold:**CO dehydrogenase ISP C-domain like<br>**Superfamily:**CO dehydrogenase ISP C-domain like<br>**Family:**CO dehydrogenase ISP C-domain like |
| 3 | d1v97a1 | Alignment |  | 28.9 | 14 | **Fold:**CO dehydrogenase ISP C-domain like<br>**Superfamily:**CO dehydrogenase ISP C-domain like<br>**Family:**CO dehydrogenase ISP C-domain like |
| 4 | d1ffva1 | Alignment |  | 28.6 | 18 | **Fold:**CO dehydrogenase ISP C-domain like<br>**Superfamily:**CO dehydrogenase ISP C-domain like<br>**Family:**CO dehydrogenase ISP C-domain like |
| 5 | c2cmpA_ | Alignment |  | 26.4 | 38 | **PDB header:**terminase<br>**Chain:** A: **PDB Molecule:**terminase small subunit;<br>**PDBTitle:** crystal structure of the dna binding domain of g1p small2 terminase subunit from bacteriophage sf6 |
| 6 | c1ffuA_ | Alignment |  | 23.4 | 17 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**cuts, iron-sulfur protein of carbon monoxide<br>**PDBTitle:** carbon monoxide dehydrogenase from hydrogenophaga2 pseudoflava which lacks the mo-pyranopterin moiety of the3 molybdenum cofactor |
| 7 | d1jroa1 | Alignment |  | 20.5 | 36 | **Fold:**CO dehydrogenase ISP C-domain like<br>**Superfamily:**CO dehydrogenase ISP C-domain like<br>**Family:**CO dehydrogenase ISP C-domain like |
| 8 | d1dgja1 | Alignment |  | 20.4 | 36 | **Fold:**CO dehydrogenase ISP C-domain like<br>**Superfamily:**CO dehydrogenase ISP C-domain like<br>**Family:**CO dehydrogenase ISP C-domain like |
| 9 | d1zxia1 | Alignment |  | 19.1 | 21 | **Fold:**CO dehydrogenase ISP C-domain like<br>**Superfamily:**CO dehydrogenase ISP C-domain like<br>**Family:**CO dehydrogenase ISP C-domain like |
| 10 | d1rm6c1 | Alignment |  | 17.5 | 36 | **Fold:**CO dehydrogenase ISP C-domain like<br>**Superfamily:**CO dehydrogenase ISP C-domain like<br>**Family:**CO dehydrogenase ISP C-domain like |
| 11 | c3b9jI_ | Alignment |  | 16.8 | 14 | **PDB header:**oxidoreductase<br>**Chain:** I: **PDB Molecule:**xanthine oxidase;<br>**PDBTitle:** structure of xanthine oxidase with 2-hydroxy-6-methylpurine |

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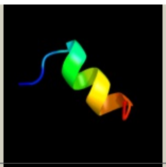
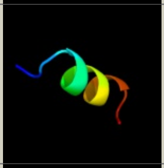
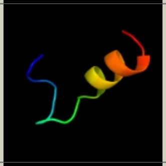
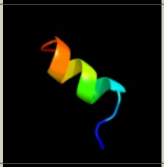
| 12 | d1t3qa1 | Alignment |  | 15.4 | 29 | **Fold:**CO dehydrogenase ISP C-domain like<br>**Superfamily:**CO dehydrogenase ISP C-domain like<br>**Family:**CO dehydrogenase ISP C-domain like |
| 13 | c1t3qD_ | Alignment |  | 14.7 | 29 | **PDB header:**oxidoreductase<br>**Chain:** D: **PDB Molecule:**quinoline 2-oxidoreductase small subunit;<br>**PDBTitle:** crystal structure of quinoline 2-oxidoreductase from pseudomonas2 putida 86 |
| 14 | c3hrdH_ | Alignment |  | 13.8 | 36 | **PDB header:**oxidoreductase<br>**Chain:** H: **PDB Molecule:**nicotinate dehydrogenase small fes subunit;<br>**PDBTitle:** crystal structure of nicotinate dehydrogenase |
| 15 | c1rm6F_ | Alignment |  | 13.6 | 23 | **PDB header:**oxidoreductase<br>**Chain:** F: **PDB Molecule:**4-hydroxybenzoyl-coa reductase gamma subunit;<br>**PDBTitle:** structure of 4-hydroxybenzoyl-coa reductase from thauera2 aromatica |
| 16 | c1lj2B_ | Alignment |  | 13.5 | 50 | **PDB header:**viral protein/ translation<br>**Chain:** B: **PDB Molecule:**nonstructural rna-binding protein 34;<br>**PDBTitle:** recognition of eif4g by rotavirus nsp3 reveals a basis for2 mrna circularization |
| 17 | c2jp7A_ | Alignment |  | 13.2 | 13 | **PDB header:**translation<br>**Chain:** A: **PDB Molecule:**mrna export factor mex67;<br>**PDBTitle:** nmr structure of the mex67 uba domain |
| 18 | d1n62a1 | Alignment |  | 12.0 | 21 | **Fold:**CO dehydrogenase ISP C-domain like<br>**Superfamily:**CO dehydrogenase ISP C-domain like<br>**Family:**CO dehydrogenase ISP C-domain like |
| 19 | c1n60D_ | Alignment |  | 10.5 | 21 | **PDB header:**oxidoreductase<br>**Chain:** D: **PDB Molecule:**carbon monoxide dehydrogenase small chain;<br>**PDBTitle:** crystal structure of the cu,mo-co dehydrogenase (codh); cyanide-2 inactivated form |
| 20 | c3eubJ_ | Alignment |  | 9.8 | 14 | **PDB header:**oxidoreductase<br>**Chain:** J: **PDB Molecule:**xanthine dehydrogenase/oxidase;<br>**PDBTitle:** crystal structure of desulfo-xanthine oxidase with xanthine |
| 21 | c2qguA_ | Alignment | not modelled | 8.8 | 33 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**probable signal peptide protein;<br>**PDBTitle:** three-dimensional structure of the phospholipid-binding protein from2 ralstonia solanacearum q8xv73_ralsq in complex with a phospholipid at3 the resolution 1.53 a. northeast structural genomics consortium4 target rsr89 |
| 22 | c3t97B_ | Alignment | not modelled | 8.5 | 36 | **PDB header:**protein transport<br>**Chain:** B: **PDB Molecule:**nuclear pore complex protein nup54;<br>**PDBTitle:** molecular architecture of the transport channel of the nuclear pore2 complex: nup62/nup54 |
| 23 | d1hd6a_ | Alignment | not modelled | 8.1 | 25 | **Fold:**Protozoan pheromone-like<br>**Superfamily:**Protozoan pheromone proteins<br>**Family:**Protozoan pheromone proteins |
| 24 | d1mzba_ | Alignment | not modelled | 7.0 | 5 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**"Winged helix" DNA-binding domain<br>**Family:**FUR-like |
| 25 | c3i38F_ | Alignment | not modelled | 6.9 | 22 | **PDB header:**chaperone<br>**Chain:** F: **PDB Molecule:**putative chaperone dnaj;<br>**PDBTitle:** structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578 |
| 26 | d1al3a_ | Alignment | not modelled | 6.8 | 22 | **Fold:**Periplasmic binding protein-like II<br>**Superfamily:**Periplasmic binding protein-like II<br>**Family:**Phosphate binding protein-like |
| 27 | c1al3A_ | Alignment | not modelled | 6.8 | 22 | **PDB header:**transcription regulation<br>**Chain:** A: **PDB Molecule:**cys regulon transcriptional activator cysb;<br>**PDBTitle:** cofactor binding fragment of cysb from klebsiella aerogenes |
| | | | | | | **PDB header:**ribosome<br>**Chain:** T: **PDB Molecule:**rps19e; |

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| 28 | c2xznT_ | Alignment | not modelled | 6.8 | 19 | **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2 |
| 29 | c3fiaA_ | Alignment | not modelled | 6.0 | 19 | **PDB header:**protein binding<br>**Chain:** A: **PDB Molecule:**intersectin-1;<br>**PDBTitle:** crystal structure of the eh 1 domain from human intersectin-2 1 protein. northeast structural genomics consortium target3 hr3646e. |
| 30 | c3kxeD_ | Alignment | not modelled | 5.9 | 50 | **PDB header:**protein binding<br>**Chain:** D: **PDB Molecule:**antitoxin protein pard-1;<br>**PDBTitle:** a conserved mode of protein recognition and binding in a2 pard-pare toxin-antitoxin complex |