Phyre2

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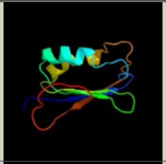
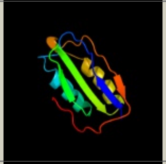
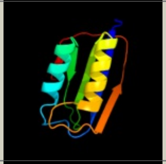
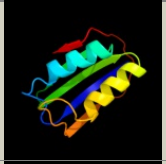
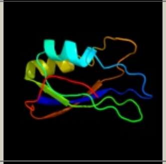
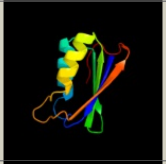
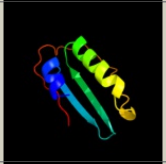
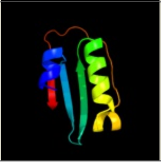
| Email | l.a.kelley@imperial.ac.uk |
| Description | P0AB65 |
| Date | Thu Jan 5 11:14:44 GMT 2012 |
| Unique Job ID | d1b2736c613b643f |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c2gv1A_ | Alignment |  | 100.0 | 100 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**probable acylphosphatase;<br>**PDBTitle:** nmr solution structure of the acylphosphatase from2 eschaerichia coli |
| 2 | c3br8A_ | Alignment |  | 100.0 | 36 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**probable acylphosphatase;<br>**PDBTitle:** crystal structure of acylphosphatase from bacillus subtilis |
| 3 | c2bjeA_ | Alignment |  | 100.0 | 51 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**acylphosphatase;<br>**PDBTitle:** acylphosphatase from sulfolobus solfataricus. monclinic p212 space group |
| 4 | d2acya_ | Alignment |  | 100.0 | 32 | **Fold:**Ferredoxin-like<br>**Superfamily:**Acylphosphatase/BLUF domain-like<br>**Family:**Acylphosphatase-like |
| 5 | d1urra_ | Alignment |  | 100.0 | 30 | **Fold:**Ferredoxin-like<br>**Superfamily:**Acylphosphatase/BLUF domain-like<br>**Family:**Acylphosphatase-like |
| 6 | d1w2ia_ | Alignment |  | 100.0 | 48 | **Fold:**Ferredoxin-like<br>**Superfamily:**Acylphosphatase/BLUF domain-like<br>**Family:**Acylphosphatase-like |
| 7 | d1apsa_ | Alignment |  | 100.0 | 33 | **Fold:**Ferredoxin-like<br>**Superfamily:**Acylphosphatase/BLUF domain-like<br>**Family:**Acylphosphatase-like |
| 8 | d1ulra_ | Alignment |  | 100.0 | 49 | **Fold:**Ferredoxin-like<br>**Superfamily:**Acylphosphatase/BLUF domain-like<br>**Family:**Acylphosphatase-like |
| 9 | d1gxua_ | Alignment |  | 100.0 | 36 | **Fold:**Ferredoxin-like<br>**Superfamily:**Acylphosphatase/BLUF domain-like<br>**Family:**Acylphosphatase-like |
| 10 | d2buna1 | Alignment |  | 91.2 | 19 | **Fold:**Ferredoxin-like<br>**Superfamily:**Acylphosphatase/BLUF domain-like<br>**Family:**BLUF domain |
| 11 | d1yrxa1 | Alignment |  | 90.6 | 21 | **Fold:**Ferredoxin-like<br>**Superfamily:**Acylphosphatase/BLUF domain-like<br>**Family:**BLUF domain |

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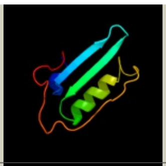
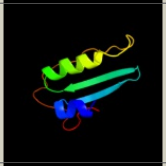
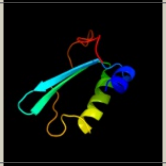
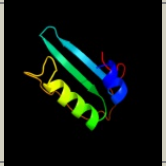
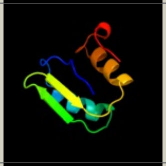
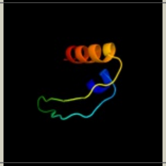
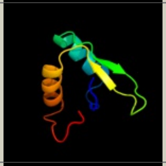
|---|---|---|---|---|---|---|
| 12 | c2hfnJ_ | Alignment |  | 89.6 | 16 | **PDB header:**electron transport<br>**Chain:** J: **PDB Molecule:**synechocystis photoreceptor (slr1694);<br>**PDBTitle:** crystal structures of the synechocystis photoreceptor slr1694 reveal2 distinct structural states related to signaling |
| 13 | c2kb2A_ | Alignment |  | 89.5 | 21 | **PDB header:**signaling protein, hydrolase regulator<br>**Chain:** A: **PDB Molecule:**blrp1;<br>**PDBTitle:** blrp1 bluf |
| 14 | d2byca1 | Alignment |  | 88.1 | 18 | **Fold:**Ferredoxin-like<br>**Superfamily:**Acylphosphatase/BLUF domain-like<br>**Family:**BLUF domain |
| 15 | d1x0pa1 | Alignment |  | 87.5 | 18 | **Fold:**Ferredoxin-like<br>**Superfamily:**Acylphosphatase/BLUF domain-like<br>**Family:**BLUF domain |
| 16 | c2xznF_ | Alignment |  | 85.8 | 14 | **PDB header:**ribosome<br>**Chain:** F: **PDB Molecule:**eif1;<br>**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 |
| 17 | d2qswa1 | Alignment |  | 85.4 | 15 | **Fold:**Ferredoxin-like<br>**Superfamily:**ACT-like<br>**Family:**NIL domain-like |
| 18 | c2oghA_ | Alignment |  | 81.2 | 11 | **PDB header:**translation<br>**Chain:** A: **PDB Molecule:**eukaryotic translation initiation factor eif-1;<br>**PDBTitle:** solution structure of yeast eif1 |
| 19 | d2if1a_ | Alignment |  | 79.7 | 9 | **Fold:**eIF1-like<br>**Superfamily:**eIF1-like<br>**Family:**eIF1-like |
| 20 | d2f1fa2 | Alignment |  | 78.2 | 12 | **Fold:**Ferredoxin-like<br>**Superfamily:**ACT-like<br>**Family:**IlvH-like |
| 21 | d2fgca1 | Alignment | not modelled | 76.4 | 12 | **Fold:**Ferredoxin-like<br>**Superfamily:**ACT-like<br>**Family:**IlvH-like |
| 22 | d2pc6a1 | Alignment | not modelled | 74.9 | 12 | **Fold:**Ferredoxin-like<br>**Superfamily:**ACT-like<br>**Family:**IlvH-like |
| 23 | c2fgcA_ | Alignment | not modelled | 64.8 | 12 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**acetolactate synthase, small subunit;<br>**PDBTitle:** crystal structure of acetolactate synthase- small subunit from2 thermotoga maritima |
| 24 | c3c5tB_ | Alignment | not modelled | 64.5 | 53 | **PDB header:**signaling protein/signaling protein<br>**Chain:** B: **PDB Molecule:**exendin-4;<br>**PDBTitle:** crystal structure of the ligand-bound glucagon-like peptide-1 receptor2 extracellular domain |
| 25 | c2pc6C_ | Alignment | not modelled | 61.8 | 11 | **PDB header:**lyase<br>**Chain:** C: **PDB Molecule:**probable acetolactate synthase isozyme iii (small subunit);<br>**PDBTitle:** crystal structure of putative acetolactate synthase- small subunit2 from nitrosomonas europaea |
| 26 | c2f1fA_ | Alignment | not modelled | 61.0 | 12 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**acetolactate synthase isozyme iii small subunit;<br>**PDBTitle:** crystal structure of the regulatory subunit of2 acetohydroxyacid synthase isozyme iii from e. coli |
| 27 | c2rjzA_ | Alignment | not modelled | 58.3 | 14 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**pilo protein;<br>**PDBTitle:** crystal structure of the type 4 fimbrial biogenesis protein pilo from2 pseudomonas aeruginosa |
| 28 | d3dhxa1 | Alignment | not modelled | 56.6 | 15 | **Fold:**Ferredoxin-like<br>**Superfamily:**ACT-like<br>**Family:**NIL domain-like |

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| 29 | d2qrra1 | Alignment | not modelled | 56.1 | 13 | **Fold:**Ferredoxin-like<br>**Superfamily:**ACT-like<br>**Family:**NIL domain-like |
| 30 | d1a0ia1 | Alignment | not modelled | 40.6 | 16 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**DNA ligase/mRNA capping enzyme postcatalytic domain |
| 31 | d2zjre1 | Alignment | not modelled | 25.1 | 16 | **Fold:**Ribosomal protein L6<br>**Superfamily:**Ribosomal protein L6<br>**Family:**Ribosomal protein L6 |
| 32 | c3fhaD_ | Alignment | not modelled | 23.6 | 18 | **PDB header:**hydrolase<br>**Chain:** D: **PDB Molecule:**endo-beta-n-acetylglucosaminidase;<br>**PDBTitle:** structure of endo-beta-n-acetylglucosaminidase a |
| 33 | c2yy3B_ | Alignment | not modelled | 22.7 | 21 | **PDB header:**translation<br>**Chain:** B: **PDB Molecule:**elongation factor 1-beta;<br>**PDBTitle:** crystal structure of translation elongation factor ef-1 beta from2 pyrococcus horikoshii |
| 34 | d3ceda1 | Alignment | not modelled | 22.6 | 13 | **Fold:**Ferredoxin-like<br>**Superfamily:**ACT-like<br>**Family:**NIL domain-like |
| 35 | c2zkre_ | Alignment | not modelled | 21.8 | 11 | **PDB header:**ribosomal protein/rna<br>**Chain:** E: **PDB Molecule:**rna expansion segment es7 part ii;<br>**PDBTitle:** structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map |
| 36 | d1fx0a2 | Alignment | not modelled | 17.0 | 36 | **Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like<br>**Superfamily:**N-terminal domain of alpha and beta subunits of F1 ATP synthase<br>**Family:**N-terminal domain of alpha and beta subunits of F1 ATP synthase |
| 37 | d2jdia2 | Alignment | not modelled | 16.0 | 36 | **Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like<br>**Superfamily:**N-terminal domain of alpha and beta subunits of F1 ATP synthase<br>**Family:**N-terminal domain of alpha and beta subunits of F1 ATP synthase |
| 38 | c3gwpA_ | Alignment | not modelled | 15.9 | 19 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**carbon-sulfur lyase involved in aluminum resistance;<br>**PDBTitle:** crystal structure of carbon-sulfur lyase involved in aluminum2 resistance (yp_878183.1) from clostridium novyi nt at 2.90 a3 resolution |
| 39 | c3ucoB_ | Alignment | not modelled | 15.2 | 18 | **PDB header:**lyase/lyase inhibitor<br>**Chain:** B: **PDB Molecule:**carbonic anhydrase;<br>**PDBTitle:** coccomyxa beta-carbonic anhydrase in complex with iodide |
| 40 | c1jrjA_ | Alignment | not modelled | 14.3 | 53 | **PDB header:**hormone/growth factor<br>**Chain:** A: **PDB Molecule:**exendin-4;<br>**PDBTitle:** solution structure of exendin-4 in 30-vol% trifluoroethanol |
| 41 | c2dclB_ | Alignment | not modelled | 12.8 | 14 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**hypothetical upf0166 protein ph1503;<br>**PDBTitle:** structure of ph1503 protein from pyrococcus horikoshii ot3 |
| 42 | c2a5vB_ | Alignment | not modelled | 12.2 | 27 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**carbonic anhydrase (carbonate dehydratase) (carbonic<br>**PDBTitle:** crystal structure of m. tuberculosis beta carbonic anhydrase, rv3588c,2 tetrameric form |
| 43 | d2cz4a1 | Alignment | not modelled | 11.8 | 19 | **Fold:**Ferredoxin-like<br>**Superfamily:**GlnB-like<br>**Family:**Prokaryotic signal transducing protein |
| 44 | d1d1ra_ | Alignment | not modelled | 11.7 | 16 | **Fold:**eIF1-like<br>**Superfamily:**eIF1-like<br>**Family:**eIF1-like |
| 45 | c1d1rA_ | Alignment | not modelled | 11.7 | 16 | **PDB header:**structural genomics<br>**Chain:** A: **PDB Molecule:**hypothetical 11.4 kd protein ycih in pyrf-osmb<br>**PDBTitle:** nmr solution structure of the product of the e. coli ycih2 gene. |
| 46 | c2jz2A_ | Alignment | not modelled | 10.6 | 19 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**ssl0352 protein;<br>**PDBTitle:** solution nmr structure of ssl0352 protein from synechocystis sp. pcc2 6803. northeast structural genomics consortium target sgr42 |
| 47 | d1vqoh1 | Alignment | not modelled | 8.6 | 16 | **Fold:**alpha/beta-Hammerhead<br>**Superfamily:**Ribosomal protein L16p/L10e<br>**Family:**Ribosomal protein L10e |
| 48 | c2qv6D_ | Alignment | not modelled | 8.3 | 10 | **PDB header:**hydrolase<br>**Chain:** D: **PDB Molecule:**gtp cyclohydrolase iii;<br>**PDBTitle:** gtp cyclohydrolase iii from m. jannaschii (mj0145)2 complexed with gtp and metal ions |
| 49 | d1maba2 | Alignment | not modelled | 7.8 | 36 | **Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like<br>**Superfamily:**N-terminal domain of alpha and beta subunits of F1 ATP synthase<br>**Family:**N-terminal domain of alpha and beta subunits of F1 ATP synthase |
| 50 | c3eyxB_ | Alignment | not modelled | 7.6 | 25 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**carbonic anhydrase;<br>**PDBTitle:** crystal structure of carbonic anhydrase nce103 from2 saccharomyces cerevisiae |
| 51 | d2fyxa1 | Alignment | not modelled | 7.5 | 15 | **Fold:**Ferredoxin-like<br>**Superfamily:**Transposase IS200-like<br>**Family:**Transposase IS200-like |
| 52 | c3qm2A_ | Alignment | not modelled | 7.4 | 14 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**phosphoserine aminotransferase;<br>**PDBTitle:** 2.25 angstrom crystal structure of phosphoserine aminotransferase2 (serc) from salmonella enterica subsp. enterica |

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| | | | | | | serovar typhimurium |
| 53 | c1iq8B_ | Alignment | not modelled | 7.2 | 13 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**archaeosine trna-guanine transglycosylase;<br>**PDBTitle:** crystal structure of archaeosine trna-guanine2 transglycosylase from pyrococcus horikoshii |
| 54 | d2vjva1 | Alignment | not modelled | 7.2 | 20 | **Fold:**Ferredoxin-like<br>**Superfamily:**Transposase IS200-like<br>**Family:**Transposase IS200-like |
| 55 | c1vi7A_ | Alignment | not modelled | 6.9 | 9 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**hypothetical protein yigz;<br>**PDBTitle:** crystal structure of an hypothetical protein |
| 56 | d1nvma1 | Alignment | not modelled | 6.8 | 19 | **Fold:**RuvA C-terminal domain-like<br>**Superfamily:**post-HMGL domain-like<br>**Family:**DmpG/LeuA communication domain-like |
| 57 | c1d0rA_ | Alignment | not modelled | 6.7 | 27 | **PDB header:**hormone/growth factor<br>**Chain:** A: **PDB Molecule:**glucagon-like peptide-1-(7-36)-amide;<br>**PDBTitle:** solution structure of glucagon-like peptide-1-(7-36)-amide2 in trifluoroethanol/water |
| 58 | c3c9gB_ | Alignment | not modelled | 6.6 | 3 | **PDB header:**nucleotide binding protein<br>**Chain:** B: **PDB Molecule:**upf0200/upf0201 protein af_1395;<br>**PDBTitle:** crystal structure of uncharacterized upf0201 protein af_135 |
| 59 | d1ddza1 | Alignment | not modelled | 6.5 | 19 | **Fold:**Resolvase-like<br>**Superfamily:**beta-carbonic anhydrase, cab<br>**Family:**beta-carbonic anhydrase, cab |
| 60 | c2zkrh_ | Alignment | not modelled | 6.4 | 16 | **PDB header:**ribosomal protein/rna<br>**Chain:** H: **PDB Molecule:**rna expansion segment es12;<br>**PDBTitle:** structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map |
| 61 | d2zgwa1 | Alignment | not modelled | 6.3 | 47 | **Fold:**SH3-like barrel<br>**Superfamily:**C-terminal domain of transcriptional repressors<br>**Family:**Biotin repressor (BirA) |
| 62 | c3lasA_ | Alignment | not modelled | 6.2 | 31 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**putative carbonic anhydrase;<br>**PDBTitle:** crystal structure of carbonic anhydrase from streptococcus mutans to2 1.4 angstrom resolution |
| 63 | d1whra_ | Alignment | not modelled | 5.9 | 14 | **Fold:**IF3-like<br>**Superfamily:**R3H domain<br>**Family:**R3H domain |
| 64 | c2ldiA_ | Alignment | not modelled | 5.9 | 9 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**zinc-transporting atpase;<br>**PDBTitle:** nmr solution structure of ziaan sub mutant |
| 65 | c2qz4A_ | Alignment | not modelled | 5.8 | 18 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**paraplegin;<br>**PDBTitle:** human paraplegin, aaa domain in complex with adp |
| 66 | c2ju5A_ | Alignment | not modelled | 5.7 | 20 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**thioredoxin disulfide isomerase;<br>**PDBTitle:** dsbh oxidoreductase |
| 67 | c2a8cE_ | Alignment | not modelled | 5.6 | 24 | **PDB header:**lyase<br>**Chain:** E: **PDB Molecule:**carbonic anhydrase 2;<br>**PDBTitle:** haemophilus influenzae beta-carbonic anhydrase |
| 68 | d1ddza2 | Alignment | not modelled | 5.5 | 20 | **Fold:**Resolvase-like<br>**Superfamily:**beta-carbonic anhydrase, cab<br>**Family:**beta-carbonic anhydrase, cab |
| 69 | d2hh8a1 | Alignment | not modelled | 5.4 | 26 | **Fold:**YdfO-like<br>**Superfamily:**YdfO-like<br>**Family:**YdfO-like |
| 70 | d1skyb2 | Alignment | not modelled | 5.3 | 33 | **Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like<br>**Superfamily:**N-terminal domain of alpha and beta subunits of F1 ATP synthase<br>**Family:**N-terminal domain of alpha and beta subunits of F1 ATP synthase |