# Phyre2

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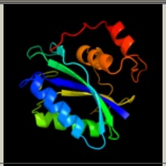
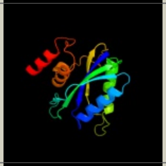
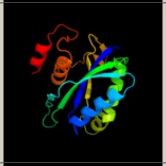
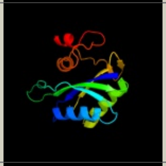
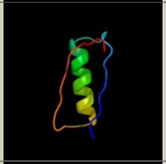
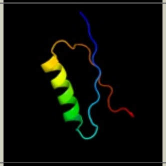
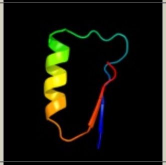
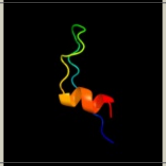
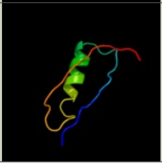
| Email | l.a.kelley@imperial.ac.uk |
| Description | P26281 |
| Date | Thu Jan 5 11:42:51 GMT 2012 |
| Unique Job ID | 65164d545bfb16c3 |

## Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | d1f9ya_ | Alignment |  | 100.0 | 100 | **Fold:**Ferredoxin-like<br>**Superfamily:**6-hydroxymethyl-7,8-dihydropterin pyrophosphokinase, HPPK<br>**Family:**6-hydroxymethyl-7,8-dihydropterin pyrophosphokinase, HPPK |
| 2 | d1cbka_ | Alignment |  | 100.0 | 57 | **Fold:**Ferredoxin-like<br>**Superfamily:**6-hydroxymethyl-7,8-dihydropterin pyrophosphokinase, HPPK<br>**Family:**6-hydroxymethyl-7,8-dihydropterin pyrophosphokinase, HPPK |
| 3 | c2qx0A_ | Alignment |  | 100.0 | 63 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**7,8-dihydro-6-hydroxymethylpterin-<br>**PDBTitle:** crystal structure of yersinia pestis hppk (ternary complex) |
| 4 | c2bmbA_ | Alignment |  | 100.0 | 33 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**folic acid synthesis protein fol1;<br>**PDBTitle:** x-ray structure of the bifunctional 6-hydroxymethyl-7,8-2 dihydroxypterin pyrophosphokinase dihydropteroate synthase3 from saccharomyces cerevisiae |
| 5 | c3mcnA_ | Alignment |  | 100.0 | 36 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**2-amino-4-hydroxy-6-hydroxymethyldihydropteridine<br>**PDBTitle:** crystal structure of the 6-hyroxymethyl-7,8-dihydropterin2 pyrophosphokinase dihydropteroate synthase bifunctional enzyme from3 francisella tularensis |
| 6 | c2cg8B_ | Alignment |  | 100.0 | 34 | **PDB header:**lyase/transferase<br>**Chain:** B: **PDB Molecule:**dihydroneopterin aldolase 6-hydroxymethyl-7,8-<br>**PDBTitle:** the bifunctional dihydroneopterin aldolase 6-hydroxymethyl-2 7,8-dihydropterin synthase from streptococcus pneumoniae |
| 7 | c3r3tA_ | Alignment |  | 31.1 | 15 | **PDB header:**rna binding protein<br>**Chain:** A: **PDB Molecule:**30s ribosomal protein s6;<br>**PDBTitle:** crystal structure of 30s ribosomal protein s from bacillus anthracis |
| 8 | d2j5aa1 | Alignment |  | 28.1 | 28 | **Fold:**Ferredoxin-like<br>**Superfamily:**Ribosomal protein S6<br>**Family:**Ribosomal protein S6 |
| 9 | c2o6lA_ | Alignment |  | 24.9 | 25 | **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 |
| 10 | c3ndcB_ | Alignment |  | 23.0 | 19 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**precorrin-4 c(11)-methyltransferase;<br>**PDBTitle:** crystal structure of precorrin-4 c11-methyltransferase from2 rhodobacter capsulatus |
| 11 | d1qjha_ | Alignment |  | 22.8 | 23 | **Fold:**Ferredoxin-like<br>**Superfamily:**Ribosomal protein S6<br>**Family:**Ribosomal protein S6 |

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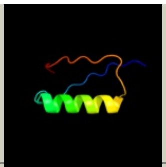
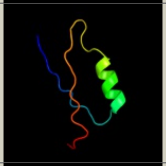
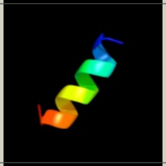
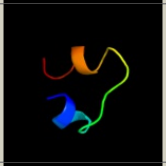
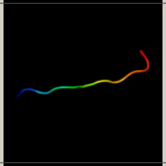
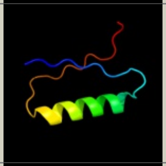
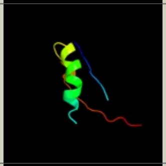
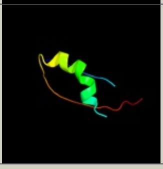
|---|---|---|---|---|---|---|
| 12 | d1loua_ | Alignment |  | 20.0 | 26 | **Fold:**Ferredoxin-like<br>**Superfamily:**Ribosomal protein S6<br>**Family:**Ribosomal protein S6 |
| 13 | c3bbnF_ | Alignment |  | 15.0 | 19 | **PDB header:**ribosome<br>**Chain:** F: **PDB Molecule:**ribosomal protein s6;<br>**PDBTitle:** homology model for the spinach chloroplast 30s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome. |
| 14 | c3idwA_ | Alignment |  | 13.7 | 13 | **PDB header:**endocytosis<br>**Chain:** A: **PDB Molecule:**actin cytoskeleton-regulatory complex protein sla1;<br>**PDBTitle:** crystal structure of sla1 homology domain 2 |
| 15 | c2inpD_ | Alignment |  | 13.4 | 19 | **PDB header:**oxidoreductase<br>**Chain:** D: **PDB Molecule:**phenol hydroxylase component phl;<br>**PDBTitle:** structure of the phenol hydroxylase-regulatory protein2 complex |
| 16 | d1t6ca1 | Alignment |  | 12.3 | 64 | **Fold:**Ribonuclease H-like motif<br>**Superfamily:**Actin-like ATPase domain<br>**Family:**Ppx/GppA phosphatase |
| 17 | d1vmba_ | Alignment |  | 12.3 | 24 | **Fold:**Ferredoxin-like<br>**Superfamily:**Ribosomal protein S6<br>**Family:**Ribosomal protein S6 |
| 18 | c1vmbA_ | Alignment |  | 12.3 | 24 | **PDB header:**translation<br>**Chain:** A: **PDB Molecule:**30s ribosomal protein s6;<br>**PDBTitle:** crystal structure of 30s ribosomal protein s6 (tm0603) from thermotoga2 maritima at 1.70 a resolution |
| 19 | d2bcgg3 | Alignment |  | 11.8 | 29 | **Fold:**FAD-linked reductases, C-terminal domain<br>**Superfamily:**FAD-linked reductases, C-terminal domain<br>**Family:**GDI-like |
| 20 | d1d5ta2 | Alignment |  | 10.9 | 34 | **Fold:**FAD-linked reductases, C-terminal domain<br>**Superfamily:**FAD-linked reductases, C-terminal domain<br>**Family:**GDI-like |
| 21 | c1u9gA_ | Alignment | not modelled | 10.9 | 37 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**general control protein gcn4;<br>**PDBTitle:** heterocyclic peptide backbone modification in gcn4-pli based coiled2 coils: replacement of k(8)l(9) |
| 22 | c2wc1A_ | Alignment | not modelled | 10.0 | 15 | **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 |
| 23 | c1w5kD_ | Alignment | not modelled | 9.6 | 32 | **PDB header:**four helix bundle<br>**Chain:** D: **PDB Molecule:**general control protein gcn4;<br>**PDBTitle:** an anti-parallel four helix bundle |
| 24 | c1w5kC_ | Alignment | not modelled | 9.6 | 32 | **PDB header:**four helix bundle<br>**Chain:** C: **PDB Molecule:**general control protein gcn4;<br>**PDBTitle:** an anti-parallel four helix bundle |
| 25 | c1w5kB_ | Alignment | not modelled | 9.6 | 32 | **PDB header:**four helix bundle<br>**Chain:** B: **PDB Molecule:**general control protein gcn4;<br>**PDBTitle:** an anti-parallel four helix bundle |
| 26 | c1w5kA_ | Alignment | not modelled | 9.6 | 32 | **PDB header:**four helix bundle<br>**Chain:** A: **PDB Molecule:**general control protein gcn4;<br>**PDBTitle:** an anti-parallel four helix bundle |
| 27 | c1yzvA_ | Alignment | not modelled | 9.4 | 7 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**hypothetical protein;<br>**PDBTitle:** hypothetical protein from trypanosoma cruzi |
| 28 | c1unyA_ | Alignment | not modelled | 8.7 | 38 | **PDB header:**four helix bundle<br>**Chain:** A: **PDB Molecule:**general control protein gcn4;<br>**PDBTitle:** structure based engineering of internal molecular surfaces2 of four helix bundles |
| 29 | c1unyB_ | Alignment | not modelled | 8.6 | 38 | **PDB header:**four helix bundle<br>**Chain:** B: **PDB Molecule:**general control protein gcn4; |

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|---|---|---|---|---|---|---|
| 29 | c1unvB_ | Alignment | not modelled | 8.6 | 38 | **PDBTitle:** structure based engineering of internal molecular surfaces2 of four helix bundles |
| 30 | c1unvA_ | Alignment | not modelled | 8.5 | 38 | **PDB header:**four helix bundle<br>**Chain:** A: **PDB Molecule:**general control protein gcn4;<br>**PDBTitle:** structure based engineering of internal molecular surfaces2 of four helix bundles |
| 31 | c2ehbD_ | Alignment | not modelled | 8.3 | 14 | **PDB header:**signalling protein/transferase<br>**Chain:** D: **PDB Molecule:**cbl-interacting serine/threonine-protein kinase 24;<br>**PDBTitle:** the structure of the c-terminal domain of the protein kinase atsos22 bound to the calcium sensor atsos3 |
| 32 | c2q4dB_ | Alignment | not modelled | 8.2 | 15 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**lysine decarboxylase-like protein at5g11950;<br>**PDBTitle:** ensemble refinement of the crystal structure of a lysine2 decarboxylase-like protein from arabidopsis thaliana gene at5g11950 |
| 33 | c2kjwA_ | Alignment | not modelled | 7.9 | 26 | **PDB header:**ribosomal protein<br>**Chain:** A: **PDB Molecule:**30s ribosomal protein s6;<br>**PDBTitle:** solution structure and backbone dynamics of the permutant2 p54-55 |
| 34 | c1u9gB_ | Alignment | not modelled | 7.9 | 38 | **PDB header:**transcription<br>**Chain:** B: **PDB Molecule:**general control protein gcn4;<br>**PDBTitle:** heterocyclic peptide backbone modification in gcn4-pli based coiled2 coils: replacement of k(8)l(9) |
| 35 | c2la3A_ | Alignment | not modelled | 7.8 | 33 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** the nmr structure of the protein np_344798.1 reveals a cca-adding2 enzyme head domain |
| 36 | c1unzA_ | Alignment | not modelled | 7.5 | 38 | **PDB header:**four helix bundle<br>**Chain:** A: **PDB Molecule:**general control protein gcn4;<br>**PDBTitle:** structure based engineering of internal molecular surfaces2 of four helix bundles |
| 37 | c1unzB_ | Alignment | not modelled | 7.5 | 38 | **PDB header:**four helix bundle<br>**Chain:** B: **PDB Molecule:**general control protein gcn4;<br>**PDBTitle:** structure based engineering of internal molecular surfaces2 of four helix bundles |
| 38 | c3a4cA_ | Alignment | not modelled | 7.5 | 33 | **PDB header:**cell cycle, replication<br>**Chain:** A: **PDB Molecule:**dna replication factor cdt1;<br>**PDBTitle:** crystal structure of cdt1 c terminal domain |
| 39 | c2qikA_ | Alignment | not modelled | 7.1 | 27 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**upf0131 protein ykqa;<br>**PDBTitle:** crystal structure of ykqa from bacillus subtilis. northeast2 structural genomics target sr631 |
| 40 | c2qbbF_ | Alignment | not modelled | 7.0 | 19 | **PDB header:**ribosome<br>**Chain:** F: **PDB Molecule:**30s ribosomal protein s6;<br>**PDBTitle:** crystal structure of the bacterial ribosome from2 escherichia coli in complex with gentamicin. this file3 contains the 30s subunit of the second 70s ribosome, with4 gentamicin bound. the entire crystal structure contains5 two 70s ribosomes and is described in remark 400. |
| 41 | d2qalf1 | Alignment | not modelled | 7.0 | 19 | **Fold:**Ferredoxin-like<br>**Superfamily:**Ribosomal protein S6<br>**Family:**Ribosomal protein S6 |
| 42 | d1dd3a1 | Alignment | not modelled | 7.0 | 26 | **Fold:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain<br>**Superfamily:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain<br>**Family:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain |
| 43 | c2zdiC_ | Alignment | not modelled | 6.6 | 19 | **PDB header:**chaperone<br>**Chain:** C: **PDB Molecule:**prefoldin subunit alpha;<br>**PDBTitle:** crystal structure of prefoldin from pyrococcus horikoshii2 ot3 |
| 44 | c3s7xC_ | Alignment | not modelled | 6.5 | 25 | **PDB header:**viral protein<br>**Chain:** C: **PDB Molecule:**major capsid protein vp1;<br>**PDBTitle:** unassembled washington university polyomavirus vp1 pentamer r198k2 mutant |
| 45 | c2dboA_ | Alignment | not modelled | 6.3 | 22 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**d-tyrosyl-trna(tyr) deacylase;<br>**PDBTitle:** crystal structure of d-tyr-trna(tyr) deacylase from aquifex aeolicus |
| 46 | d1tjna_ | Alignment | not modelled | 5.9 | 16 | **Fold:**Chelatase-like<br>**Superfamily:**Chelatase<br>**Family:**CbiX-like |
| 47 | c1tjnA_ | Alignment | not modelled | 5.9 | 16 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**sirohydrochlorin cobaltochelatase;<br>**PDBTitle:** crystal structure of hypothetical protein af0721 from archaeoglobus2 fulgidus |
| 48 | c1zawV_ | Alignment | not modelled | 5.8 | 26 | **PDB header:**structural protein<br>**Chain:** V: **PDB Molecule:**50s ribosomal protein l7/l12;<br>**PDBTitle:** ribosomal protein l10-l12(ntd) complex, space group p212121,2 form a |
| 49 | c1zawU_ | Alignment | not modelled | 5.8 | 26 | **PDB header:**structural protein<br>**Chain:** U: **PDB Molecule:**50s ribosomal protein l7/l12;<br>**PDBTitle:** ribosomal protein l10-l12(ntd) complex, space group p212121,2 form a |
| 50 | c1zawW_ | Alignment | not modelled | 5.8 | 26 | **PDB header:**structural protein<br>**Chain:** W: **PDB Molecule:**50s ribosomal protein l7/l12;<br>**PDBTitle:** ribosomal protein l10-l12(ntd) complex, space group p212121,2 form a |
| 51 | c1zaxV_ | Alignment | not modelled | 5.6 | 26 | **PDB header:**structural protein<br>**Chain:** V: **PDB Molecule:**50s ribosomal protein l7/l12;<br>**PDBTitle:** ribosomal protein l10-l12(ntd) complex, space group p212121,2 form b |
| 52 | c1zavW_ | Alignment | not modelled | 5.6 | 26 | **PDB header:**structural protein<br>**Chain:** W: **PDB Molecule:**50s ribosomal protein l7/l12;<br>**PDBTitle:** ribosomal protein l10-l12(ntd) complex, space group p21 |
| 53 | c1zaxW_ | Alignment | not modelled | 5.6 | 26 | **PDB header:**structural protein<br>**Chain:** W: **PDB Molecule:**50s ribosomal protein l7/l12; |

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|---|---|---|---|---|---|---|
| 53 | c1zaxW_ | Alignment | not modelled | 5.6 | 26 | **PDBTitle:** ribosomal protein l10-l12(ntd) complex, space group p212121,2 form b |
| 54 | c1zavV_ | Alignment | not modelled | 5.6 | 26 | **PDB header:**structural protein<br>**Chain:** V: **PDB Molecule:**50s ribosomal protein l7/l12;<br>**PDBTitle:** ribosomal protein l10-l12(ntd) complex, space group p21 |
| 55 | d1hn0a4 | Alignment | not modelled | 5.6 | 56 | **Fold:**Supersandwich<br>**Superfamily:**Galactose mutarotase-like<br>**Family:**Hyaluronate lyase-like, central domain |
| 56 | d1fxkc_ | Alignment | not modelled | 5.6 | 8 | **Fold:**Long alpha-hairpin<br>**Superfamily:**Prefoldin<br>**Family:**Prefoldin |
| 57 | c1dd3C_ | Alignment | not modelled | 5.4 | 26 | **PDB header:**ribosome<br>**Chain:** C: **PDB Molecule:**50s ribosomal protein l7/l12;<br>**PDBTitle:** crystal structure of ribosomal protein l12 from thermotoga maritima |
| 58 | c1dd3D_ | Alignment | not modelled | 5.4 | 26 | **PDB header:**ribosome<br>**Chain:** D: **PDB Molecule:**50s ribosomal protein l7/l12;<br>**PDBTitle:** crystal structure of ribosomal protein l12 from thermotoga maritima |
| 59 | d1dd4c_ | Alignment | not modelled | 5.3 | 26 | **Fold:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain<br>**Superfamily:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain<br>**Family:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain |
| 60 | c3g9rF_ | Alignment | not modelled | 5.3 | 42 | **PDB header:**viral protein<br>**Chain:** F: **PDB Molecule:**fusion complex of hiv-1 envelope glycoprotein<br>**PDBTitle:** structure of the hiv-1 gp41 membrane-proximal ectodomain2 region in a putative prefusion conformation |
| 61 | c2rbhA_ | Alignment | not modelled | 5.3 | 38 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**gamma-glutamyl cyclotransferase;<br>**PDBTitle:** gamma-glutamyl cyclotransferase |
| 62 | c1zaxZ_ | Alignment | not modelled | 5.1 | 28 | **PDB header:**structural protein<br>**Chain:** Z: **PDB Molecule:**50s ribosomal protein l7/l12;<br>**PDBTitle:** ribosomal protein l10-l12(ntd) complex, space group p212121,2 form b |