Phyre2

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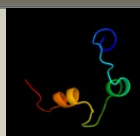
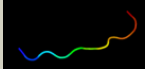
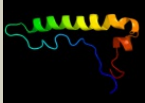
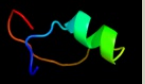
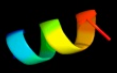
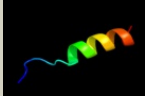
|---|---|
| Email | l.a.kelley@imperial.ac.uk |
| Description | Q4QQM4 |
| Date | Tue Jul 30 13:10:26 BST 2013 |
| Unique Job ID | 24c8b9f7d2ca641e |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c3zf7S_ | Alignment |  | 22.9 | 34 | **PDB header:**ribosome<br>**Chain:** S: **PDB Molecule:**60s ribosomal protein l18a;<br>**PDBTitle:** high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome |
| 2 | c3qoqC_ | Alignment |  | 20.2 | 54 | **PDB header:**transcription/dna<br>**Chain:** C: **PDB Molecule:**alginate and motility regulator z;<br>**PDBTitle:** crystal structure of the transcription factor amrz in complex with the2 18 base pair amrz1 binding site |
| 3 | c2hjnA_ | Alignment |  | 17.1 | 13 | **PDB header:**cell cycle<br>**Chain:** A: **PDB Molecule:**maintenance of ploidy protein mob1;<br>**PDBTitle:** structural and functional analysis of saccharomyces2 cerevisiae mob1 |
| 4 | d1ixrc1 | Alignment |  | 17.0 | 30 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**"Winged helix" DNA-binding domain<br>**Family:**Helicase DNA-binding domain |
| 5 | d1in4a1 | Alignment |  | 15.4 | 30 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**"Winged helix" DNA-binding domain<br>**Family:**Helicase DNA-binding domain |
| 6 | c3j39S_ | Alignment |  | 15.2 | 26 | **PDB header:**ribosome<br>**Chain:** S: **PDB Molecule:**60s ribosomal protein l18a;<br>**PDBTitle:** structure of the d. melanogaster 60s ribosomal proteins |
| 7 | c2v6xB_ | Alignment |  | 14.3 | 55 | **PDB header:**protein transport<br>**Chain:** B: **PDB Molecule:**doa4-independent degradation protein 4;<br>**PDBTitle:** structural insight into the interaction between escrt-iii2 and vps4 |
| 8 | c3nr5A_ | Alignment |  | 14.2 | 41 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**repressor of rna polymerase iii transcription maf1 homolog;<br>**PDBTitle:** crystal structure of human maf1 |
| 9 | d1rk8b_ | Alignment |  | 13.8 | 40 | **Fold:**Mago nashi protein<br>**Superfamily:**Mago nashi protein<br>**Family:**Mago nashi protein |
| 10 | c1t0fC_ | Alignment |  | 13.7 | 24 | **PDB header:**dna binding protein<br>**Chain:** C: **PDB Molecule:**transposon tn7 transposition protein tnsc;<br>**PDBTitle:** crystal structure of the tnsa/tnsc(504-555) complex |
| 11 | d1mnta_ | Alignment |  | 13.1 | 31 | **Fold:**Ribbon-helix-helix<br>**Superfamily:**Ribbon-helix-helix<br>**Family:**Arc/Mnt-like phage repressors |

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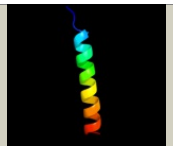
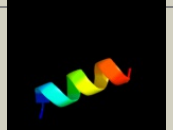
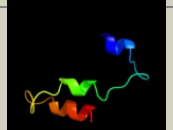
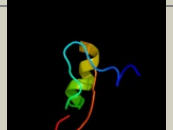
| 12 | c3pcqX_ | Alignment |  | 12.7 | 15 | **PDB header:**photosynthesis<br>**Chain:** X: **PDB Molecule:**photosystem i 4.8k protein;<br>**PDBTitle:** femtosecond x-ray protein nanocrystallography |
| 13 | c1yewF_ | Alignment |  | 12.6 | 15 | **PDB header:**oxidoreductase, membrane protein<br>**Chain:** F: **PDB Molecule:**particulate methane monooxygenase, a subunit;<br>**PDBTitle:** crystal structure of particulate methane monooxygenase |
| 14 | c3di3A_ | Alignment |  | 12.4 | 26 | **PDB header:**cytokine/cytokine receptor<br>**Chain:** A: **PDB Molecule:**interleukin-7;<br>**PDBTitle:** crystal structure of the complex of human interleukin-7 with2 glycosylated human interleukin-7 receptor alpha ectodomain |
| 15 | c3j3bS_ | Alignment |  | 12.4 | 29 | **PDB header:**ribosome<br>**Chain:** S: **PDB Molecule:**60s ribosomal protein l18a;<br>**PDBTitle:** structure of the human 60s ribosomal proteins |
| 16 | c1u9pA_ | Alignment |  | 12.2 | 27 | **PDB header:**unknown function<br>**Chain:** A: **PDB Molecule:**parc;<br>**PDBTitle:** permuted single-chain arc |
| 17 | c3izcS_ | Alignment |  | 12.1 | 26 | **PDB header:**ribosome<br>**Chain:** S: **PDB Molecule:**60s ribosomal protein rpl20 (l18ae);<br>**PDBTitle:** localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome |
| 18 | c3twfA_ | Alignment |  | 11.7 | 60 | **PDB header:**unknown function<br>**Chain:** A: **PDB Molecule:**alpha4f3a;<br>**PDBTitle:** crystal structure of the de novo designed fluorinated peptide2 alpha4f3a |
| 19 | c3twfB_ | Alignment |  | 11.7 | 60 | **PDB header:**unknown function<br>**Chain:** B: **PDB Molecule:**alpha4f3a;<br>**PDBTitle:** crystal structure of the de novo designed fluorinated peptide2 alpha4f3a |
| 20 | d1ixsb1 | Alignment |  | 11.3 | 30 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**"Winged helix" DNA-binding domain<br>**Family:**Helicase DNA-binding domain |
| 21 | c3chxF_ | Alignment | not modelled | 10.8 | 15 | **PDB header:**membrane protein<br>**Chain:** F: **PDB Molecule:**pmoa;<br>**PDBTitle:** crystal structure of methylosinus trichosporium ob3b2 particulate methane monooxygenase (pmmo) |
| 22 | c3tweA_ | Alignment | not modelled | 9.9 | 67 | **PDB header:**unknown function<br>**Chain:** A: **PDB Molecule:**alpha4h;<br>**PDBTitle:** crystal structure of the de novo designed peptide alpha4h |
| 23 | c1ho7A_ | Alignment | not modelled | 9.8 | 47 | **PDB header:**membrane protein<br>**Chain:** A: **PDB Molecule:**voltage-gated potassium channel protein;<br>**PDBTitle:** nmr structure of the potassium channel fragment l45 in tfe |
| 24 | c1ho2A_ | Alignment | not modelled | 9.8 | 47 | **PDB header:**membrane protein<br>**Chain:** A: **PDB Molecule:**voltage-gated potassium channel protein;<br>**PDBTitle:** nmr structure of the potassium channel fragment l45 in2 micelles |
| 25 | c3tweB_ | Alignment | not modelled | 9.6 | 67 | **PDB header:**unknown function<br>**Chain:** B: **PDB Molecule:**alpha4h;<br>**PDBTitle:** crystal structure of the de novo designed peptide alpha4h |
| 26 | d2gaxa1 | Alignment | not modelled | 9.5 | 34 | **Fold:**Peptidyl-tRNA hydrolase II<br>**Superfamily:**Peptidyl-tRNA hydrolase II<br>**Family:**Peptidyl-tRNA hydrolase II |
| 27 | c3o27B_ | Alignment | not modelled | 9.5 | 29 | **PDB header:**dna binding protein<br>**Chain:** B: **PDB Molecule:**putative uncharacterized protein;<br>**PDBTitle:** the crystal structure of c68 from the hybrid virus-plasmid pssvx |
| 28 | c4a19X_ | Alignment | not modelled | 9.3 | 13 | **PDB header:**ribosome<br>**Chain:** X: **PDB Molecule:**rpl18a;<br>**PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 26s rrna and3 proteins of molecule 2. |

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| 29 | c3jtgA_ | Alignment | not modelled | 9.1 | 33 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**ets-related transcription factor elf-3;<br>**PDBTitle:** crystal structure of mouse elf3 c-terminal dna-binding domain in2 complex with type ii tgf-beta receptor promoter dna |
| 30 | d2j0sc1 | Alignment | not modelled | 8.9 | 45 | **Fold:**Mago nashi protein<br>**Superfamily:**Mago nashi protein<br>**Family:**Mago nashi protein |
| 31 | c4fe1X_ | Alignment | not modelled | 8.8 | 15 | **PDB header:**photosynthesis<br>**Chain:** X: **PDB Molecule:**photosystem i 4.8k protein;<br>**PDBTitle:** improving the accuracy of macromolecular structure refinement at 7 a2 resolution |
| 32 | c1jb0X_ | Alignment | not modelled | 8.8 | 15 | **PDB header:**photosynthesis<br>**Chain:** X: **PDB Molecule:**photosystem i subunit psax;<br>**PDBTitle:** crystal structure of photosystem i: a photosynthetic reaction center2 and core antenna system from cyanobacteria |
| 33 | d1jb0x_ | Alignment | not modelled | 8.8 | 15 | **Fold:**Single transmembrane helix<br>**Superfamily:**Subunit PsaX of photosystem I reaction centre<br>**Family:**Subunit PsaX of photosystem I reaction centre |
| 34 | c2bbdA_ | Alignment | not modelled | 8.8 | 40 | **PDB header:**viral protein<br>**Chain:** A: **PDB Molecule:**coat protein;<br>**PDBTitle:** crystal structure of the stiv mcp |
| 35 | c1kyqC_ | Alignment | not modelled | 8.7 | 31 | **PDB header:**oxidoreductase, lyase<br>**Chain:** C: **PDB Molecule:**siroheme biosynthesis protein met8;<br>**PDBTitle:** met8p: a bifunctional nad-dependent dehydrogenase and2 ferrochelatase involved in siroheme synthesis. |
| 36 | c3zpyB_ | Alignment | not modelled | 8.5 | 24 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**alginate lyase, family pl7;<br>**PDBTitle:** crystal structure of the marine pl7 alginate lyase alya12 from zobellia galactanivorans |
| 37 | c4gd3B_ | Alignment | not modelled | 8.4 | 12 | **PDB header:**oxidoreductase/electron transport<br>**Chain:** B: **PDB Molecule:**ni/fe-hydrogenase 1 b-type cytochrome subunit;<br>**PDBTitle:** structure of e. coli hydrogenase-1 in complex with cytochrome b |
| 38 | c4gd3A_ | Alignment | not modelled | 8.4 | 12 | **PDB header:**oxidoreductase/electron transport<br>**Chain:** A: **PDB Molecule:**ni/fe-hydrogenase 1 b-type cytochrome subunit;<br>**PDBTitle:** structure of e. coli hydrogenase-1 in complex with cytochrome b |
| 39 | c3izci_ | Alignment | not modelled | 8.4 | 38 | **PDB header:**ribosome<br>**Chain:** l: **PDB Molecule:**60s ribosomal protein rpl10 (l10e);<br>**PDBTitle:** localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome |
| 40 | c2islB_ | Alignment | not modelled | 8.1 | 29 | **PDB header:**flavoprotein<br>**Chain:** B: **PDB Molecule:**blub;<br>**PDBTitle:** blub bound to reduced flavin (fmnh2) and molecular oxygen.2 (clear crystal form) |
| 41 | c3iz5i_ | Alignment | not modelled | 8.0 | 38 | **PDB header:**ribosome<br>**Chain:** l: **PDB Molecule:**60s ribosomal protein l10 (l10e);<br>**PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome |
| 42 | c1nybA_ | Alignment | not modelled | 7.9 | 36 | **PDB header:**transcription/rna<br>**Chain:** A: **PDB Molecule:**probable regulatory protein n;<br>**PDBTitle:** solution structure of the bacteriophage phi21 n peptide-boxb2 rna complex |
| 43 | c3lw6A_ | Alignment | not modelled | 7.8 | 63 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**beta-4-galactosyltransferase 7;<br>**PDBTitle:** crystal structure of drosophila beta1,4-galactosyltransferase-7 |
| 44 | d1b9ha_ | Alignment | not modelled | 7.4 | 17 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**GABA-aminotransferase-like |
| 45 | d1oe4a_ | Alignment | not modelled | 6.8 | 26 | **Fold:**Uracil-DNA glycosylase-like<br>**Superfamily:**Uracil-DNA glycosylase-like<br>**Family:**Single-strand selective monofunctional uracil-DNA glycosylase SMUG1 |
| 46 | d1kqfc_ | Alignment | not modelled | 6.8 | 18 | **Fold:**Heme-binding four-helical bundle<br>**Superfamily:**Transmembrane di-heme cytochromes<br>**Family:**Formate dehydrogenase N, cytochrome (gamma) subunit |
| 47 | d2frea1 | Alignment | not modelled | 6.8 | 25 | **Fold:**FMN-dependent nitroreductase-like<br>**Superfamily:**FMN-dependent nitroreductase-like<br>**Family:**NADH oxidase/flavin reductase |
| 48 | d1jvra_ | Alignment | not modelled | 6.8 | 23 | **Fold:**Retroviral matrix proteins<br>**Superfamily:**Retroviral matrix proteins<br>**Family:**HTLV-II matrix protein |
| 49 | c3a0hJ_ | Alignment | not modelled | 6.7 | 21 | **PDB header:**electron transport<br>**Chain:** J: **PDB Molecule:**photosystem ii reaction center protein j;<br>**PDBTitle:** crystal structure of i-substituted photosystem ii complex |
| 50 | d2axtj1 | Alignment | not modelled | 6.7 | 21 | **Fold:**Single transmembrane helix<br>**Superfamily:**Photosystem II reaction center protein J, PsbJ<br>**Family:**PsbJ-like |
| 51 | c3j3bg_ | Alignment | not modelled | 6.6 | 25 | **PDB header:**ribosome<br>**Chain:** G: **PDB Molecule:**60s ribosomal protein l7a;<br>**PDBTitle:** structure of the human 60s ribosomal proteins |
| 52 | d2iu5a2 | Alignment | not modelled | 6.5 | 25 | **Fold:**Tetracyclin repressor-like, C-terminal domain<br>**Superfamily:**Tetracyclin repressor-like, C-terminal domain<br>**Family:**Tetracyclin repressor-like, C-terminal domain |
| 53 | d3cx5d2 | Alignment | not modelled | 6.4 | 50 | **Fold:**Single transmembrane helix<br>**Superfamily:**Cytochrome c1 subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase), transmembrane anchor<br>**Family:**Cytochrome c1 subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase), transmembrane anchor |
| | | | | | | **Fold:**Single transmembrane helix<br>**Superfamily:**Cytochrome c1 subunit of cytochrome bc1 complex |

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| 54 | d1ppjd2 | Alignment | not modelled | 6.2 | 63 | (Ubiquinol-cytochrome c reductase), transmembrane anchor<br>**Family:**Cytochrome c1 subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase), transmembrane anchor |
| 55 | c2zkrq_ | Alignment | not modelled | 6.1 | 20 | **PDB header:**ribosomal protein/rna<br>**Chain:** Q: **PDB Molecule:**rna expansion segment es31 part ii;<br>**PDBTitle:** structure of a mammalian ribosomal 60s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map |
| 56 | c3ge5A_ | Alignment | not modelled | 6.1 | 18 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**putative nad(p)h:fmn oxidoreductase;<br>**PDBTitle:** crystal structure of a putative nad(p)h:fmn oxidoreductase (pg0310)2 from porphyromonas gingivalis w83 at 1.70 a resolution |
| 57 | c1ckkB_ | Alignment | not modelled | 6.1 | 25 | **PDB header:**calmodulin-peptide complex<br>**Chain:** B: **PDB Molecule:**protein (rat ca2+/calmodulin dependent protein<br>**PDBTitle:** calmodulin/rat ca2+/calmodulin dependent protein kinase2 fragment |
| 58 | d1pv0a_ | Alignment | not modelled | 6.0 | 27 | **Fold:**Long alpha-hairpin<br>**Superfamily:**Sporulation inhibitor Sda<br>**Family:**Sporulation inhibitor Sda |
| 59 | d2e74f1 | Alignment | not modelled | 5.9 | 46 | **Fold:**Single transmembrane helix<br>**Superfamily:**PetM subunit of the cytochrome b6f complex<br>**Family:**PetM subunit of the cytochrome b6f complex |
| 60 | c3u5eS_ | Alignment | not modelled | 5.9 | 37 | **PDB header:**ribosome<br>**Chain:** S: **PDB Molecule:**60s ribosomal protein l20-a;<br>**PDBTitle:** the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 60s subunit, ribosome a |
| 61 | c3j21d_ | Alignment | not modelled | 5.9 | 36 | **PDB header:**ribosome<br>**Chain:** D: **PDB Molecule:**50s ribosomal protein l4p;<br>**PDBTitle:** promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins) |
| 62 | c3bemA_ | Alignment | not modelled | 5.9 | 14 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**putative nad(p)h nitroreductase ydfn;<br>**PDBTitle:** crystal structure of putative nitroreductase ydfn (2632848) from2 bacillus subtilis at 1.65 a resolution |
| 63 | c1q2iA_ | Alignment | not modelled | 5.8 | 40 | **PDB header:**antitumor protein<br>**Chain:** A: **PDB Molecule:**pnc27;<br>**PDBTitle:** nmr solution structure of a peptide from the mdm-2 binding2 domain of the p53 protein that is selectively cytotoxic to3 cancer cells |
| 64 | c3ho5B_ | Alignment | not modelled | 5.8 | 69 | **PDB header:**signaling protein<br>**Chain:** B: **PDB Molecule:**hedgehog-interacting protein;<br>**PDBTitle:** crystal structure of hedgehog-interacting protein (hhip) and sonic2 hedgehog (shh) complex |
| 65 | d1dp7p_ | Alignment | not modelled | 5.7 | 15 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**"Winged helix" DNA-binding domain<br>**Family:**P4 origin-binding domain-like |
| 66 | d1ef5a_ | Alignment | not modelled | 5.6 | 40 | **Fold:**beta-Grasp (ubiquitin-like)<br>**Superfamily:**Ubiquitin-like<br>**Family:**Ras-binding domain, RBD |
| 67 | d1k8ib2 | Alignment | not modelled | 5.6 | 32 | **Fold:**MHC antigen-recognition domain<br>**Superfamily:**MHC antigen-recognition domain<br>**Family:**MHC antigen-recognition domain |
| 68 | c2ebyA_ | Alignment | not modelled | 5.6 | 12 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**putative hth-type transcriptional regulator ybaq;<br>**PDBTitle:** crystal structure of a hypothetical protein from e. coli |
| 69 | c4a19L_ | Alignment | not modelled | 5.2 | 44 | **PDB header:**ribosome<br>**Chain:** L: **PDB Molecule:**rpl34;<br>**PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 26s rrna and3 proteins of molecule 2. |
| 70 | c2kpmA_ | Alignment | not modelled | 5.2 | 19 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** solution nmr structure of uncharacterized protein from gene2 locus ne0665 of nitrosomonas europaea. northeast structural3 genomics target ner103a |
| 71 | c3j39g_ | Alignment | not modelled | 5.1 | 58 | **PDB header:**ribosome<br>**Chain:** G: **PDB Molecule:**60s ribosomal protein l7a;<br>**PDBTitle:** structure of the d. melanogaster 60s ribosomal proteins |
| 72 | d2jxta1 | Alignment | not modelled | 5.1 | 21 | **Fold:**RplX-like<br>**Superfamily:**RplX-like<br>**Family:**RplX-like |
| 73 | c2zuuA_ | Alignment | not modelled | 5.1 | 38 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**lacto-n-biose phosphorylase;<br>**PDBTitle:** crystal structure of galacto-n-biose/lacto-n-biose i phosphorylase in2 complex with glcnac |
| 74 | c3mtvA_ | Alignment | not modelled | 5.1 | 22 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**papain-like cysteine protease;<br>**PDBTitle:** the crystal structure of the prrsv nonstructural protein nsp1 |
| 75 | c1ujwB_ | Alignment | not modelled | 5.1 | 44 | **PDB header:**transport protein/hydrolase<br>**Chain:** B: **PDB Molecule:**colicin e3;<br>**PDBTitle:** structure of the complex between btub and colicin e3 receptor binding2 domain |