# Phyre$^2$

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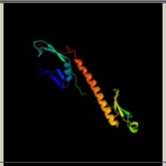
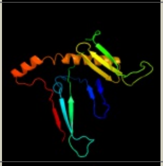
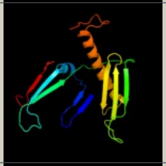
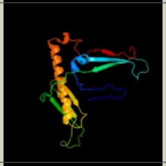
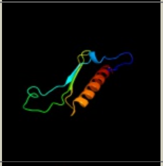
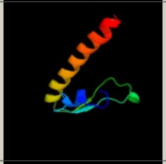
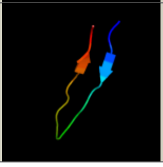
| Email | l.a.kelley@imperial.ac.uk |
| Description | P28369 |
| Date | Thu Jan 5 11:44:56 GMT 2012 |
| Unique Job ID | 40bf335e43aa607d |

## Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c3d5cX_ | Alignment |  | 100.0 | 25 | **PDB header:**ribosome<br>**Chain:** X: **PDB Molecule:**peptide chain release factor 1;<br>**PDBTitle:** structural basis for translation termination on the 70s ribosome. this2 file contains the 30s subunit, release factor 1 (rf1), two trna, and3 mrna molecules of the second 70s ribosome. the entire crystal4 structure contains two 70s ribosomes as described in remark 400. |
| 2 | c2ihr1_ | Alignment |  | 100.0 | 30 | **PDB header:**translation<br>**Chain:** 1: **PDB Molecule:**peptide chain release factor 2;<br>**PDBTitle:** rf2 of thermus thermophilus |
| 3 | d1gqea_ | Alignment |  | 100.0 | 28 | **Fold:**Release factor<br>**Superfamily:**Release factor<br>**Family:**Release factor |
| 4 | d2b3tb1 | Alignment |  | 100.0 | 28 | **Fold:**Release factor<br>**Superfamily:**Release factor<br>**Family:**Release factor |
| 5 | d1rq0a_ | Alignment |  | 100.0 | 30 | **Fold:**Release factor<br>**Superfamily:**Release factor<br>**Family:**Release factor |
| 6 | c1zbtA_ | Alignment |  | 100.0 | 16 | **PDB header:**translation<br>**Chain:** A: **PDB Molecule:**peptide chain release factor 1;<br>**PDBTitle:** crystal structure of peptide chain release factor 1 (rf-1) (smu.1085)2 from streptococcus mutans at 2.34 a resolution |
| 7 | c2jy9A_ | Alignment |  | 99.9 | 32 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**putative trna hydrolase domain;<br>**PDBTitle:** nmr structure of putative trna hydrolase domain from2 salmonella typhimurium. northeast structural genomics3 consortium target str220 |
| 8 | c2jvaA_ | Alignment |  | 99.9 | 26 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**peptidyl-trna hydrolase domain protein;<br>**PDBTitle:** nmr solution structure of peptidyl-trna hydrolase domain protein from2 pseudomonas syringae pv. tomato. northeast structural genomics3 consortium target psr211 |
| 9 | d1j26a_ | Alignment |  | 99.9 | 32 | **Fold:**dsRBD-like<br>**Superfamily:**Peptidyl-tRNA hydrolase domain-like<br>**Family:**Peptidyl-tRNA hydrolase domain |
| 10 | d2ctka1 | Alignment |  | 42.8 | 17 | **Fold:**Eukaryotic type KH-domain (KH-domain type I)<br>**Superfamily:**Eukaryotic type KH-domain (KH-domain type I)<br>**Family:**Eukaryotic type KH-domain (KH-domain type I) |
| 11 | c1s1hl_ | Alignment |  | 16.4 | 5 | **PDB header:**ribosome<br>**Chain:** I: **PDB Molecule:**40s ribosomal protein s16;<br>**PDBTitle:** structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1h,4 contains 40s subunit. the 60s ribosomal subunit is in file5 1s1i. |

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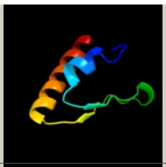
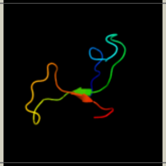
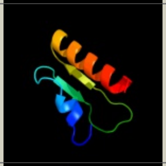
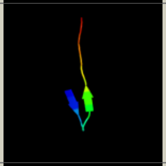
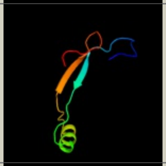
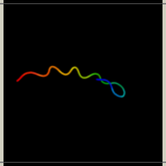
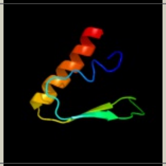
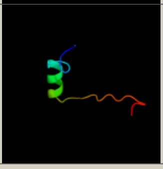
| 12 | d2ctja1 | Alignment |  | 15.9 | 15 | **Fold:**Eukaryotic type KH-domain (KH-domain type I)<br>**Superfamily:**Eukaryotic type KH-domain (KH-domain type I)<br>**Family:**Eukaryotic type KH-domain (KH-domain type I) |
| 13 | c2yrvA_ | Alignment |  | 13.4 | 10 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**at-rich interactive domain-containing protein 4a;<br>**PDBTitle:** solution structure of the rbb1nt domain of human2 rb(retinoblastoma)-binding protein 1 |
| 14 | d2axya1 | Alignment |  | 12.4 | 22 | **Fold:**Eukaryotic type KH-domain (KH-domain type I)<br>**Superfamily:**Eukaryotic type KH-domain (KH-domain type I)<br>**Family:**Eukaryotic type KH-domain (KH-domain type I) |
| 15 | c1ztgD_ | Alignment |  | 11.9 | 18 | **PDB header:**dna, rna binding protein/dna<br>**Chain:** D: **PDB Molecule:**poly(rc)-binding protein 1;<br>**PDBTitle:** human alpha polyc binding protein kh1 |
| 16 | d2vqei1 | Alignment |  | 11.0 | 14 | **Fold:**Ribosomal protein S5 domain 2-like<br>**Superfamily:**Ribosomal protein S5 domain 2-like<br>**Family:**Translational machinery components |
| 17 | d1kgia_ | Alignment |  | 10.2 | 12 | **Fold:**Prealbumin-like<br>**Superfamily:**Transthyretin (synonym: prealbumin)<br>**Family:**Transthyretin (synonym: prealbumin) |
| 18 | d2gy9i1 | Alignment |  | 10.2 | 14 | **Fold:**Ribosomal protein S5 domain 2-like<br>**Superfamily:**Ribosomal protein S5 domain 2-like<br>**Family:**Translational machinery components |
| 19 | c2jzxA_ | Alignment |  | 9.8 | 21 | **PDB header:**rna binding protein<br>**Chain:** A: **PDB Molecule:**poly(rc)-binding protein 2;<br>**PDBTitle:** pcbp2 kh1-kh2 domains |
| 20 | c2x9qA_ | Alignment |  | 9.7 | 14 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**cyclodipeptide synthetase;<br>**PDBTitle:** structure of the mycobacterium tuberculosis protein, rv2275,2 demonstrates that cyclodipeptide synthetases are related3 to type i trna-synthetases. |
| 21 | c2zkqi_ | Alignment | not modelled | 9.4 | 7 | **PDB header:**ribosomal protein/rna<br>**Chain:** I: **PDB Molecule:**<br>**PDBTitle:** structure of a mammalian ribosomal 40s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map |
| 22 | c3bbnI_ | Alignment | not modelled | 9.0 | 13 | **PDB header:**ribosome<br>**Chain:** I: **PDB Molecule:**ribosomal protein s9;<br>**PDBTitle:** homology model for the spinach chloroplast 30s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome. |
| 23 | c1rl2A_ | Alignment | not modelled | 8.7 | 26 | **PDB header:**ribosomal protein<br>**Chain:** A: **PDB Molecule:**protein (ribosomal protein l2);<br>**PDBTitle:** ribosomal protein l2 rna-binding domain from bacillus2 stearothermophilus |
| 24 | d1ttaa_ | Alignment | not modelled | 8.6 | 12 | **Fold:**Prealbumin-like<br>**Superfamily:**Transthyretin (synonym: prealbumin)<br>**Family:**Transthyretin (synonym: prealbumin) |
| 25 | d1viga_ | Alignment | not modelled | 8.4 | 11 | **Fold:**Eukaryotic type KH-domain (KH-domain type I)<br>**Superfamily:**Eukaryotic type KH-domain (KH-domain type I)<br>**Family:**Eukaryotic type KH-domain (KH-domain type I) |
| 26 | c1tuaA_ | Alignment | not modelled | 8.3 | 18 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**hypothetical protein ape0754;<br>**PDBTitle:** 1.5 a crystal structure of a protein of unknown function2 ape0754 from aeropyrum pernix |
| 27 | c3s2xB_ | Alignment | not modelled | 8.2 | 7 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**acetyl-coa synthase subunit alpha;<br>**PDBTitle:** structure of acetyl-coenzyme a synthase alpha subunit c-terminal2 domain |
| 28 | c2eq9C_ | Alignment | not modelled | 7.7 | 35 | **PDB header:**oxidoreductase<br>**Chain:** C: **PDB Molecule:**pyruvate dehydrogenase complex, dihydrolipoamide<br>**PDBTitle:** crystal structure of lipoamide dehydrogenase from |

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| | | | | | | thermus thermophilus2 hb8 with psbdb |
| 29 | d1wvna1 | Alignment | not modelled | 7.4 | 24 | **Fold:**Eukaryotic type KH-domain (KH-domain type I)<br>**Superfamily:**Eukaryotic type KH-domain (KH-domain type I)<br>**Family:**Eukaryotic type KH-domain (KH-domain type I) |
| 30 | c2xzml_ | Alignment | not modelled | 7.3 | 14 | **PDB header:**ribosome<br>**Chain:** I: **PDB Molecule:**rps16e;<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 1 |
| 31 | c2eq7C_ | Alignment | not modelled | 7.0 | 18 | **PDB header:**oxidoreductase<br>**Chain:** C: **PDB Molecule:**2-oxoglutarate dehydrogenase e2 component;<br>**PDBTitle:** crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdo |
| 32 | d2ctfa1 | Alignment | not modelled | 6.9 | 12 | **Fold:**Eukaryotic type KH-domain (KH-domain type I)<br>**Superfamily:**Eukaryotic type KH-domain (KH-domain type I)<br>**Family:**Eukaryotic type KH-domain (KH-domain type I) |
| 33 | c1psbD_ | Alignment | not modelled | 6.6 | 40 | **PDB header:**metal binding protein<br>**Chain:** D: **PDB Molecule:**ndr ser/thr kinase-like protein;<br>**PDBTitle:** solution structure of calcium loaded s100b complexed to a2 peptide from n-terminal regulatory domain of ndr kinase. |
| 34 | d2ctea1 | Alignment | not modelled | 6.5 | 11 | **Fold:**Eukaryotic type KH-domain (KH-domain type I)<br>**Superfamily:**Eukaryotic type KH-domain (KH-domain type I)<br>**Family:**Eukaryotic type KH-domain (KH-domain type I) |
| 35 | c3oqhB_ | Alignment | not modelled | 6.5 | 7 | **PDB header:**ligase<br>**Chain:** B: **PDB Molecule:**putative uncharacterized protein yvmc;<br>**PDBTitle:** crystal structure of b. licheniformis cdps yvmc-blic |
| 36 | c2b66D_ | Alignment | not modelled | 6.2 | 33 | **PDB header:**ribosome<br>**Chain:** D: **PDB Molecule:**50s ribosomal protein l2;<br>**PDBTitle:** 50s ribosomal subunit from a crystal structure of release factor rf1,2 trnas and mrna bound to the ribosome. this file contains the 50s3 subunit from a crystal structure of release factor rf1, trnas and4 mrna bound to the ribosome and is described in remark 400 |
| 37 | d1x4na1 | Alignment | not modelled | 6.1 | 17 | **Fold:**Eukaryotic type KH-domain (KH-domain type I)<br>**Superfamily:**Eukaryotic type KH-domain (KH-domain type I)<br>**Family:**Eukaryotic type KH-domain (KH-domain type I) |
| 38 | d1tfpa_ | Alignment | not modelled | 5.5 | 14 | **Fold:**Prealbumin-like<br>**Superfamily:**Transthyretin (synonym: prealbumin)<br>**Family:**Transthyretin (synonym: prealbumin) |
| 39 | c3io3A_ | Alignment | not modelled | 5.4 | 33 | **PDB header:**chaperone<br>**Chain:** A: **PDB Molecule:**deha2d07832p;<br>**PDBTitle:** get3 with adp from d. hansenii in closed form |
| 40 | d1rl2a1 | Alignment | not modelled | 5.4 | 26 | **Fold:**SH3-like barrel<br>**Superfamily:**Translation proteins SH3-like domain<br>**Family:**C-terminal domain of ribosomal protein L2 |
| 41 | d1hh2p3 | Alignment | not modelled | 5.3 | 57 | **Fold:**Alpha-lytic protease prodomain-like<br>**Superfamily:**Prokaryotic type KH domain (KH-domain type II)<br>**Family:**Prokaryotic type KH domain (KH-domain type II) |
| 42 | c1psbC_ | Alignment | not modelled | 5.2 | 40 | **PDB header:**metal binding protein<br>**Chain:** C: **PDB Molecule:**ndr ser/thr kinase-like protein;<br>**PDBTitle:** solution structure of calcium loaded s100b complexed to a2 peptide from n-terminal regulatory domain of ndr kinase. |
| 43 | c2ftcB_ | Alignment | not modelled | 5.1 | 22 | **PDB header:**ribosome<br>**Chain:** B: **PDB Molecule:**mitochondrial ribosomal protein l2;<br>**PDBTitle:** structural model for the large subunit of the mammalian mitochondrial2 ribosome |