# Phyre2

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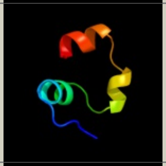
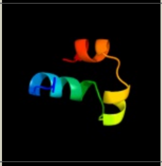
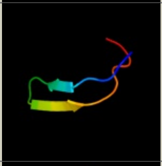
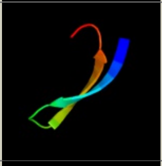
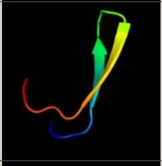
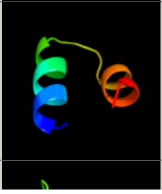
|---|---|
| Email | l.a.kelley@imperial.ac.uk |
| Description | P77243 |
| Date | Thu Jan 5 12:26:44 GMT 2012 |
| Unique Job ID | c8b48861b9a1b681 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | d1szqa_ | Alignment |  | 100.0 | 97 | **Fold:**2-methylcitrate dehydratase PrpD<br>**Superfamily:**2-methylcitrate dehydratase PrpD<br>**Family:**2-methylcitrate dehydratase PrpD |
| 2 | c2hp0A_ | Alignment |  | 100.0 | 16 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**ids-epimerase;<br>**PDBTitle:** crystal structure of iminodisuccinate epimerase |
| 3 | d2a1ja1 | Alignment |  | 33.6 | 9 | **Fold:**SAM domain-like<br>**Superfamily:**RuvA domain 2-like<br>**Family:**Hef domain-like |
| 4 | d2aq0a1 | Alignment |  | 31.8 | 9 | **Fold:**SAM domain-like<br>**Superfamily:**RuvA domain 2-like<br>**Family:**Hef domain-like |
| 5 | d1vqza1 | Alignment |  | 24.8 | 10 | **Fold:**SufE/NifU<br>**Superfamily:**SufE/NifU<br>**Family:**SP1160 C-terminal domain-like |
| 6 | c3cw1D_ | Alignment |  | 19.5 | 19 | **PDB header:**splicing<br>**Chain:** D: **PDB Molecule:**small nuclear ribonucleoprotein sm d3;<br>**PDBTitle:** crystal structure of human spliceosomal u1 snrnp |
| 7 | c1b34A_ | Alignment |  | 17.8 | 19 | **PDB header:**rna binding protein<br>**Chain:** A: **PDB Molecule:**protein (small nuclear ribonucleoprotein sm d1);<br>**PDBTitle:** crystal structure of the d1d2 sub-complex from the human snrnp core2 domain |
| 8 | d1b34a_ | Alignment |  | 17.8 | 19 | **Fold:**Sm-like fold<br>**Superfamily:**Sm-like ribonucleoproteins<br>**Family:**Sm motif of small nuclear ribonucleoproteins, SNRNP |
| 9 | d1i8fa_ | Alignment |  | 16.9 | 8 | **Fold:**Sm-like fold<br>**Superfamily:**Sm-like ribonucleoproteins<br>**Family:**Sm motif of small nuclear ribonucleoproteins, SNRNP |
| 10 | c3cw15_ | Alignment |  | 15.9 | 9 | **PDB header:**splicing<br>**Chain:** 5: **PDB Molecule:**small nuclear ribonucleoprotein g;<br>**PDB Fragment:**residues 1-215; **PDBTitle:** crystal structure of human spliceosomal u1 snrnp |
| 11 | d2jfga3 | Alignment |  | 15.9 | 27 | **Fold:**Ribokinase-like<br>**Superfamily:**MurD-like peptide ligases, catalytic domain<br>**Family:**MurCDEF |

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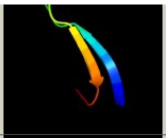
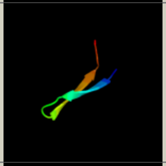
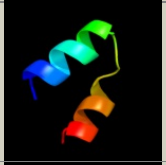
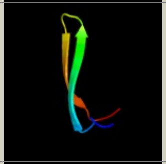
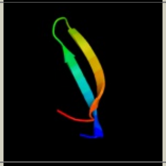
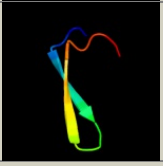
|---|---|---|---|---|---|---|
| 12 | c2fwkB_ | Alignment |  | 15.9 | 19 | **PDB header:**dna binding protein<br>**Chain:** B: **PDB Molecule:**u6 snrna-associated sm-like protein lsm5;<br>**PDBTitle:** crystal structure of cryptosporidium parvum u6 snrna-associated sm-2 like protein lsm5 |
| 13 | d1d3ba_ | Alignment |  | 15.1 | 19 | **Fold:**Sm-like fold<br>**Superfamily:**Sm-like ribonucleoproteins<br>**Family:**Sm motif of small nuclear ribonucleoproteins, SNRNP |
| 14 | d1j6ua3 | Alignment |  | 15.1 | 17 | **Fold:**Ribokinase-like<br>**Superfamily:**MurD-like peptide ligases, catalytic domain<br>**Family:**MurCDEF |
| 15 | c3swnT_ | Alignment |  | 15.0 | 8 | **PDB header:**rna binding protein<br>**Chain:** T: **PDB Molecule:**u6 snrna-associated sm-like protein lsm6;<br>**PDBTitle:** structure of the lsm657 complex: an assembly intermediate of the lsm12 7 and lsm2 8 rings |
| 16 | c3bw1A_ | Alignment |  | 15.0 | 4 | **PDB header:**rna binding protein<br>**Chain:** A: **PDB Molecule:**u6 snrna-associated sm-like protein lsm3;<br>**PDBTitle:** crystal structure of homomeric yeast lsm3 exhibiting novel octameric2 ring organisation |
| 17 | c3pgwQ_ | Alignment |  | 14.5 | 18 | **PDB header:**splicing/dna/rna<br>**Chain:** Q: **PDB Molecule:**sm b;<br>**PDBTitle:** crystal structure of human u1 snrnp |
| 18 | d1i4k1_ | Alignment |  | 14.4 | 14 | **Fold:**Sm-like fold<br>**Superfamily:**Sm-like ribonucleoproteins<br>**Family:**Sm motif of small nuclear ribonucleoproteins, SNRNP |
| 19 | d1mgqa_ | Alignment |  | 13.1 | 9 | **Fold:**Sm-like fold<br>**Superfamily:**Sm-like ribonucleoproteins<br>**Family:**Sm motif of small nuclear ribonucleoproteins, SNRNP |
| 20 | c3cw1A_ | Alignment |  | 13.1 | 18 | **PDB header:**splicing<br>**Chain:** A: **PDB Molecule:**small nuclear ribonucleoprotein-associated proteins b and<br>**PDBTitle:** crystal structure of human spliceosomal u1 snrnp |
| 21 | c3pgwB_ | Alignment | not modelled | 12.5 | 18 | **PDB header:**splicing/dna/rna<br>**Chain:** B: **PDB Molecule:**sm b;<br>**PDBTitle:** crystal structure of human u1 snrnp |
| 22 | d1pzna1 | Alignment | not modelled | 12.5 | 6 | **Fold:**SAM domain-like<br>**Superfamily:**Rad51 N-terminal domain-like<br>**Family:**DNA repair protein Rad51, N-terminal domain |
| 23 | d1e6va2 | Alignment | not modelled | 12.4 | 23 | **Fold:**Ferredoxin-like<br>**Superfamily:**Methyl-coenzyme M reductase subunits<br>**Family:**Methyl-coenzyme M reductase alpha and beta chain N-terminal domain |
| 24 | d1jbma_ | Alignment | not modelled | 12.2 | 8 | **Fold:**Sm-like fold<br>**Superfamily:**Sm-like ribonucleoproteins<br>**Family:**Sm motif of small nuclear ribonucleoproteins, SNRNP |
| 25 | c3swnA_ | Alignment | not modelled | 12.0 | 10 | **PDB header:**rna binding protein<br>**Chain:** A: **PDB Molecule:**u6 snrna-associated sm-like protein lsm5;<br>**PDBTitle:** structure of the lsm657 complex: an assembly intermediate of the lsm12 7 and lsm2 8 rings |
| 26 | d2fwka1 | Alignment | not modelled | 12.0 | 23 | **Fold:**Sm-like fold<br>**Superfamily:**Sm-like ribonucleoproteins<br>**Family:**Sm motif of small nuclear ribonucleoproteins, SNRNP |
| 27 | d1h641_ | Alignment | not modelled | 11.7 | 16 | **Fold:**Sm-like fold<br>**Superfamily:**Sm-like ribonucleoproteins<br>**Family:**Sm motif of small nuclear ribonucleoproteins, SNRNP |
| 28 | d1d3bb_ | Alignment | not modelled | 11.5 | 18 | **Fold:**Sm-like fold<br>**Superfamily:**Sm-like ribonucleoproteins<br>**Family:**Sm motif of small nuclear ribonucleoproteins, SNRNP |
| 29 | c3cw1Z_ | Alignment | not modelled | 11.3 | 10 | **PDB header:**splicing<br>**Chain:** Z: **PDB Molecule:**small nuclear ribonucleoprotein f; |

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|---|---|---|---|---|---|---|
| | | | | | | **PDBTitle:** crystal structure of human spliceosomal u1 snrnp |
| 30 | d1kfta_ | Alignment | not modelled | 11.3 | 16 | **Fold:**SAM domain-like<br>**Superfamily:**RuvA domain 2-like<br>**Family:**Excinuclease UvrC C-terminal domain |
| 31 | c1kftA_ | Alignment | not modelled | 11.3 | 16 | **PDB header:**dna binding protein<br>**Chain:** A: **PDB Molecule:**excinuclease abc subunit c;<br>**PDBTitle:** solution structure of the c-terminal domain of uvrc from e-2 coli |
| 32 | d2bgwa1 | Alignment | not modelled | 10.7 | 22 | **Fold:**SAM domain-like<br>**Superfamily:**RuvA domain 2-like<br>**Family:**Hef domain-like |
| 33 | d1m5q1_ | Alignment | not modelled | 10.7 | 10 | **Fold:**Sm-like fold<br>**Superfamily:**Sm-like ribonucleoproteins<br>**Family:**Sm motif of small nuclear ribonucleoproteins, SNRNP |
| 34 | d1th7a1 | Alignment | not modelled | 10.6 | 9 | **Fold:**Sm-like fold<br>**Superfamily:**Sm-like ribonucleoproteins<br>**Family:**Sm motif of small nuclear ribonucleoproteins, SNRNP |
| 35 | d2i1qa1 | Alignment | not modelled | 10.4 | 16 | **Fold:**SAM domain-like<br>**Superfamily:**Rad51 N-terminal domain-like<br>**Family:**DNA repair protein Rad51, N-terminal domain |
| 36 | c3swnC_ | Alignment | not modelled | 10.3 | 18 | **PDB header:**rna binding protein<br>**Chain:** C: **PDB Molecule:**u6 snrna-associated sm-like protein lsm7;<br>**PDBTitle:** structure of the lsm657 complex: an assembly intermediate of the lsm12 7 and lsm2 8 rings |
| 37 | d1d3bl_ | Alignment | not modelled | 10.2 | 18 | **Fold:**Sm-like fold<br>**Superfamily:**Sm-like ribonucleoproteins<br>**Family:**Sm motif of small nuclear ribonucleoproteins, SNRNP |
| 38 | d1kn0a_ | Alignment | not modelled | 10.0 | 21 | **Fold:**dsRBD-like<br>**Superfamily:**dsRNA-binding domain-like<br>**Family:**The homologous-pairing domain of Rad52 recombinase |
| 39 | c3iacA_ | Alignment | not modelled | 9.7 | 6 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**glucuronate isomerase;<br>**PDBTitle:** 2.2 angstrom crystal structure of glucuronate isomerase from2 salmonella typhimurium. |
| 40 | d1gg4a4 | Alignment | not modelled | 8.8 | 18 | **Fold:**Ribokinase-like<br>**Superfamily:**MurD-like peptide ligases, catalytic domain<br>**Family:**MurCDEF |
| 41 | d1bjna_ | Alignment | not modelled | 8.6 | 13 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**GABA-aminotransferase-like |
| 42 | d2a1jb1 | Alignment | not modelled | 8.1 | 9 | **Fold:**SAM domain-like<br>**Superfamily:**RuvA domain 2-like<br>**Family:**Hef domain-like |
| 43 | d1e8ca3 | Alignment | not modelled | 8.1 | 14 | **Fold:**Ribokinase-like<br>**Superfamily:**MurD-like peptide ligases, catalytic domain<br>**Family:**MurCDEF |
| 44 | c1y7wB_ | Alignment | not modelled | 8.1 | 8 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**halotolerant alpha-type carbonic anhydrase (dca ii);<br>**PDBTitle:** crystal structure of a halotolerant carbonic anhydrase from dunaliella2 salina |
| 45 | c2e12B_ | Alignment | not modelled | 8.0 | 25 | **PDB header:**translation<br>**Chain:** B: **PDB Molecule:**hypothetical protein xcc3642;<br>**PDBTitle:** the crystal structure of xc5848 from xanthomonas campestris2 adopting a novel variant of sm-like motif |
| 46 | d1dw0a_ | Alignment | not modelled | 7.9 | 13 | **Fold:**Cytochrome c<br>**Superfamily:**Cytochrome c<br>**Family:**monodomain cytochrome c |
| 47 | d1o5za2 | Alignment | not modelled | 7.5 | 19 | **Fold:**Ribokinase-like<br>**Superfamily:**MurD-like peptide ligases, catalytic domain<br>**Family:**Folylpolyglutamate synthetase |
| 48 | c1b34B_ | Alignment | not modelled | 7.5 | 5 | **PDB header:**rna binding protein<br>**Chain:** B: **PDB Molecule:**protein (small nuclear ribonucleoprotein sm d2);<br>**PDBTitle:** crystal structure of the d1d2 sub-complex from the human snrnp core2 domain |
| 49 | d1b34b_ | Alignment | not modelled | 7.5 | 5 | **Fold:**Sm-like fold<br>**Superfamily:**Sm-like ribonucleoproteins<br>**Family:**Sm motif of small nuclear ribonucleoproteins, SNRNP |
| 50 | c3k8rA_ | Alignment | not modelled | 7.4 | 10 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** crystal structure of protein of unknown function (yp_427503.1) from2 rhodospirillum rubrum atcc 11170 at 2.75 a resolution |
| 51 | d1vlfm2 | Alignment | not modelled | 7.1 | 7 | **Fold:**Formate dehydrogenase/DMSO reductase, domains 1-3<br>**Superfamily:**Formate dehydrogenase/DMSO reductase, domains 1-3<br>**Family:**Formate dehydrogenase/DMSO reductase, domains 1-3 |
| 52 | c2k1vB_ | Alignment | not modelled | 6.8 | 25 | **PDB header:**hormone<br>**Chain:** B: **PDB Molecule:**relaxin-3;<br>**PDBTitle:** r3/i5 relaxin chimera |
| 53 | c1h2iG_ | Alignment | not modelled | 6.7 | 21 | **PDB header:**dna-binding protein<br>**Chain:** G: **PDB Molecule:**dna repair protein rad52 homolog;<br>**PDBTitle:** human rad52 protein, n-terminal domain |
| 54 | c2dfwA_ | Alignment | not modelled | 6.6 | 14 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**salt-tolerant glutaminase;<br>**PDBTitle:** crystal structure of a major fragment of the salt-tolerant2 glutaminase from micrococcus luteus k-3 |
| 55 | d1vp7b_ | Alignment | not modelled | 6.5 | 11 | **Fold:**Spectrin repeat-like<br>**Superfamily:**XseB-like |

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| | | | | | | **Family:**XseB-like |
| 56 | d1p3da3 | Alignment | not modelled | 6.5 | 30 | **Fold:**Ribokinase-like<br>**Superfamily:**MurD-like peptide ligases, catalytic domain<br>**Family:**MurCDEF |
| 57 | d2f02a1 | Alignment | not modelled | 6.3 | 10 | **Fold:**Ribokinase-like<br>**Superfamily:**Ribokinase-like<br>**Family:**Ribokinase-like |
| 58 | c1vqzA_ | Alignment | not modelled | 6.1 | 9 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**lipoate-protein ligase, putative;<br>**PDBTitle:** crystal structure of a putative lipoate-protein ligase a (sp_1160)2 from streptococcus pneumoniae tigr4 at 1.99 a resolution |
| 59 | d1x2ia1 | Alignment | not modelled | 6.0 | 12 | **Fold:**SAM domain-like<br>**Superfamily:**RuvA domain 2-like<br>**Family:**Hef domain-like |
| 60 | d1sg5a1 | Alignment | not modelled | 6.0 | 28 | **Fold:**Rof/RNase P subunit-like<br>**Superfamily:**Rof/RNase P subunit-like<br>**Family:**Rof-like |
| 61 | c1xhoB_ | Alignment | not modelled | 5.9 | 17 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**chorismate mutase;<br>**PDBTitle:** chorismate mutase from clostridium thermocellum cth-682 |
| 62 | d1xhoa_ | Alignment | not modelled | 5.9 | 17 | **Fold:**Bacillus chorismate mutase-like<br>**Superfamily:**YjgF-like<br>**Family:**Chorismate mutase |
| 63 | d1vp7a_ | Alignment | not modelled | 5.8 | 11 | **Fold:**Spectrin repeat-like<br>**Superfamily:**XseB-like<br>**Family:**XseB-like |
| 64 | d1gu2a_ | Alignment | not modelled | 5.8 | 21 | **Fold:**Cytochrome c<br>**Superfamily:**Cytochrome c<br>**Family:**monodomain cytochrome c |
| 65 | d1ju3a2 | Alignment | not modelled | 5.8 | 19 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**PepX catalytic domain-like |
| 66 | c3eagA_ | Alignment | not modelled | 5.4 | 14 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**udp-n-acetylmuramate:l-alanyl-gamma-d-glutamyl-meso-<br>**PDBTitle:** the crystal structure of udp-n-acetylmuramate:l-alanyl-gamma-d-2 glutamyl-meso-diaminopimelate ligase (mpl) from neisseria3 meningitides |
| 67 | d1fnja_ | Alignment | not modelled | 5.1 | 10 | **Fold:**Bacillus chorismate mutase-like<br>**Superfamily:**YjgF-like<br>**Family:**Chorismate mutase |