# Phyre$^2$

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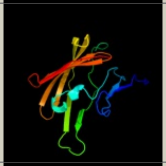
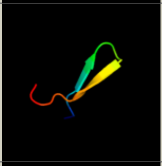
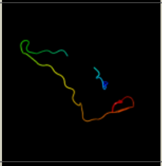
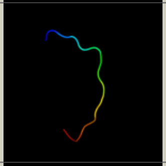
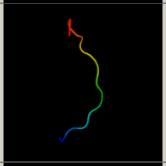
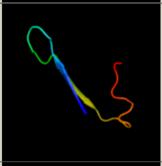
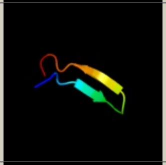
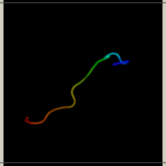
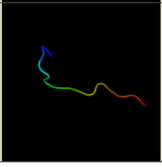
| Description | P32687 |
| Date | Thu Jan 5 11:50:11 GMT 2012 |
| Unique Job ID | 4bc62ba7c66e389a |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | d2in5a1 | Alignment |  | 100.0 | 41 | **Fold:**YmcC-like<br>**Superfamily:**YmcC-like<br>**Family:**YmcC-like |
| 2 | d2byoa1 | Alignment |  | 49.7 | 17 | **Fold:**LolA-like prokaryotic lipoproteins and lipoprotein localization factors<br>**Superfamily:**Prokaryotic lipoproteins and lipoprotein localization factors<br>**Family:**LppX-like |
| 3 | c3fzxA_ | Alignment |  | 31.8 | 16 | **PDB header:**lipid binding protein<br>**Chain:** A: **PDB Molecule:**putative exported protein;<br>**PDBTitle:** crystal structure of a putative exported protein with ymcc-like fold2 (bf2203) from bacteroides fragilis nctc 9343 at 2.22 a resolution |
| 4 | c3jslA_ | Alignment |  | 21.7 | 26 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**dna ligase;<br>**PDBTitle:** crystal structure of the adenylation domain of nad+-2 dependent dna ligase from staphylococcus aureus |
| 5 | c2x6vB_ | Alignment |  | 17.6 | 15 | **PDB header:**transcription/dna<br>**Chain:** B: **PDB Molecule:**t-box transcription factor tbx5;<br>**PDBTitle:** crystal structure of human tbx5 in the dna-bound and dna-2 free form |
| 6 | c3iz5P_ | Alignment |  | 17.2 | 25 | **PDB header:**ribosome<br>**Chain:** P: **PDB Molecule:**60s ribosomal protein l15 (l15e);<br>**PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome |
| 7 | d1ffki_ | Alignment |  | 12.9 | 25 | **Fold:**Ribosomal proteins S24e, L23 and L15e<br>**Superfamily:**Ribosomal proteins S24e, L23 and L15e<br>**Family:**L15e |
| 8 | d1bmlc3 | Alignment |  | 12.5 | 20 | **Fold:**beta-Grasp (ubiquitin-like)<br>**Superfamily:**Staphylokinase/streptokinase<br>**Family:**Staphylokinase/streptokinase |
| 9 | d1v9pa3 | Alignment |  | 12.3 | 32 | **Fold:**ATP-grasp<br>**Superfamily:**DNA ligase/mRNA capping enzyme, catalytic domain<br>**Family:**Adenylation domain of NAD+-dependent DNA ligase |
| 10 | d1vqom1 | Alignment |  | 10.7 | 25 | **Fold:**Ribosomal proteins S24e, L23 and L15e<br>**Superfamily:**Ribosomal proteins S24e, L23 and L15e<br>**Family:**L15e |
| 11 | c4a1cL_ | Alignment |  | 10.2 | 31 | **PDB header:**ribosome<br>**Chain:** L: **PDB Molecule:**ribosomal protein l15;<br>**PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 4. |

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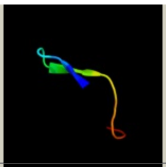
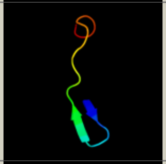
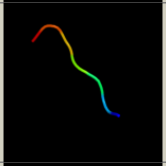
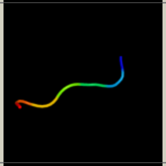
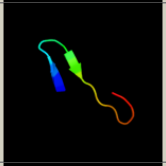
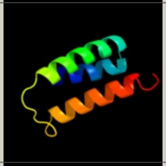
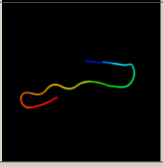
|---|---|---|---|---|---|---|
| 12 | c2we7A_ | Alignment |  | 10.2 | 24 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**xanthine dehydrogenase;<br>**PDBTitle:** crystal structure of mycobacterium tuberculosis rv0376c2 homologue from mycobacterium smegmatis |
| 13 | d1a0ia1 | Alignment |  | 9.8 | 25 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**DNA ligase/mRNA capping enzyme postcatalytic domain |
| 14 | c2k6tA_ | Alignment |  | 9.7 | 29 | **PDB header:**hormone<br>**Chain:** A: **PDB Molecule:**insulin-like 3 a chain;<br>**PDBTitle:** solution structure of the relaxin-like factor |
| 15 | c2h8bA_ | Alignment |  | 9.7 | 29 | **PDB header:**hormone/growth factor<br>**Chain:** A: **PDB Molecule:**insulin-like 3;<br>**PDBTitle:** solution structure of insl3 |
| 16 | d1jj2l_ | Alignment |  | 9.5 | 25 | **Fold:**Ribosomal proteins S24e, L23 and L15e<br>**Superfamily:**Ribosomal proteins S24e, L23 and L15e<br>**Family:**L15e |
| 17 | c2k6uA_ | Alignment |  | 9.3 | 29 | **PDB header:**hormone<br>**Chain:** A: **PDB Molecule:**insulin-like 3 a chain;<br>**PDBTitle:** the solution structure of a conformationally restricted2 fully active derivative of the human relaxin-like factor3 (rlf) |
| 18 | c1c9lA_ | Alignment |  | 9.2 | 31 | **PDB header:**endocytosis/exocytosis<br>**Chain:** A: **PDB Molecule:**clathrin;<br>**PDBTitle:** peptide-in-groove interactions link target proteins to the2 b-propeller of clathrin |
| 19 | d3bqoa1 | Alignment |  | 9.1 | 14 | **Fold:**Telomeric repeat binding factor (TRF) dimerisation domain<br>**Superfamily:**Telomeric repeat binding factor (TRF) dimerisation domain<br>**Family:**Telomeric repeat binding factor (TRF) dimerisation domain |
| 20 | d1utca2 | Alignment |  | 7.9 | 31 | **Fold:**7-bladed beta-propeller<br>**Superfamily:**Clathrin heavy-chain terminal domain<br>**Family:**Clathrin heavy-chain terminal domain |
| 21 | d2blna1 | Alignment | not modelled | 7.9 | 3 | **Fold:**FMT C-terminal domain-like<br>**Superfamily:**FMT C-terminal domain-like<br>**Family:**Post formyltransferase domain |
| 22 | d1dgsa3 | Alignment | not modelled | 7.5 | 21 | **Fold:**ATP-grasp<br>**Superfamily:**DNA ligase/mRNA capping enzyme, catalytic domain<br>**Family:**Adenylation domain of NAD+-dependent DNA ligase |
| 23 | d1p5dx2 | Alignment | not modelled | 7.0 | 29 | **Fold:**Phosphoglucomutase, first 3 domains<br>**Superfamily:**Phosphoglucomutase, first 3 domains<br>**Family:**Phosphoglucomutase, first 3 domains |
| 24 | c3bu8B_ | Alignment | not modelled | 6.8 | 5 | **PDB header:**dna binding protein<br>**Chain:** B: **PDB Molecule:**telomeric repeat-binding factor 2;<br>**PDBTitle:** crystal structure of trf2 trfh domain and tin2 peptide2 complex |
| 25 | d1ogmx1 | Alignment | not modelled | 6.7 | 11 | **Fold:**Dextranase, N-terminal domain<br>**Superfamily:**Dextranase, N-terminal domain<br>**Family:**Dextranase, N-terminal domain |
| 26 | d1h6fa_ | Alignment | not modelled | 6.5 | 27 | **Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f<br>**Superfamily:**p53-like transcription factors<br>**Family:**T-box |
| 27 | d2cupa3 | Alignment | not modelled | 6.5 | 40 | **Fold:**Glucocorticoid receptor-like (DNA-binding domain)<br>**Superfamily:**Glucocorticoid receptor-like (DNA-binding domain)<br>**Family:**LIM domain |
| 28 | c3o44G_ | Alignment | not modelled | 6.4 | 12 | **PDB header:**toxin<br>**Chain:** G: **PDB Molecule:**hemolysin;<br>**PDBTitle:** crystal structure of the vibrio cholerae cytolysin (hlya) heptameric2 pore |
|  |  |  |  |  |  | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**atp-binding cassette sub-family b |

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| 29 | c3nhaA_ | Alignment | not modelled | 6.2 | 23 | member 6, mitochondrial;<br>**PDBTitle:** nucleotide binding domain of human abcb6 (adp mg bound structure) |
| 30 | c3mlqE_ | Alignment | not modelled | 6.2 | 19 | **PDB header:**transferase/transcription<br>**Chain:** E: **PDB Molecule:**transcription-repair coupling factor;<br>**PDBTitle:** crystal structure of the thermus thermophilus transcription-repair2 coupling factor rna polymerase interacting domain with the thermus3 aquaticus rna polymerase beta1 domain |
| 31 | c3f6zB_ | Alignment | not modelled | 6.0 | 20 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**putative uncharacterized protein;<br>**PDBTitle:** crystal structure of pseudomonas aeruginosa mlic in complex2 with hen egg white lysozyme |
| 32 | c2jkbA_ | Alignment | not modelled | 6.0 | 18 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**sialidase b;<br>**PDBTitle:** crystal structure of streptococcus pneumoniae nanb in2 complex with 2,7-anhydro-neu5ac |
| 33 | c1eb0A_ | Alignment | not modelled | 5.9 | 8 | **PDB header:**chaperone<br>**Chain:** A: **PDB Molecule:**urease accessory protein uree;<br>**PDBTitle:** crystal structure of bacillus pasteurii uree at 1.85 a,2 phased by siras. type i crystal form. |
| 34 | d1b04a_ | Alignment | not modelled | 5.8 | 26 | **Fold:**ATP-grasp<br>**Superfamily:**DNA ligase/mRNA capping enzyme, catalytic domain<br>**Family:**Adenylation domain of NAD+-dependent DNA ligase |
| 35 | d4tsva_ | Alignment | not modelled | 5.8 | 26 | **Fold:**TNF-like<br>**Superfamily:**TNF-like<br>**Family:**TNF-like |
| 36 | c1bpoA_ | Alignment | not modelled | 5.6 | 31 | **PDB header:**membrane protein<br>**Chain:** A: **PDB Molecule:**protein (clathrin);<br>**PDBTitle:** clathrin heavy-chain terminal domain and linker |
| 37 | d2dlqa1 | Alignment | not modelled | 5.6 | 25 | **Fold:**beta-beta-alpha zinc fingers<br>**Superfamily:**beta-beta-alpha zinc fingers<br>**Family:**Classic zinc finger, C2H2 |
| 38 | d1bhia_ | Alignment | not modelled | 5.5 | 14 | **Fold:**beta-beta-alpha zinc fingers<br>**Superfamily:**beta-beta-alpha zinc fingers<br>**Family:**Classic zinc finger, C2H2 |
| 39 | d1oh0a_ | Alignment | not modelled | 5.4 | 13 | **Fold:**Cystatin-like<br>**Superfamily:**NTF2-like<br>**Family:**Ketosteroid isomerase-like |