# Phyre$^2$

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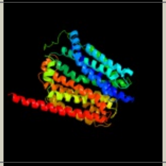
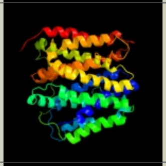
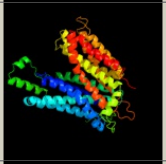
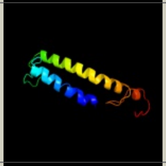
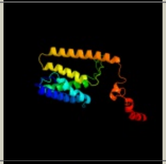
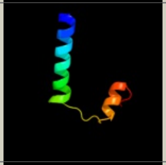
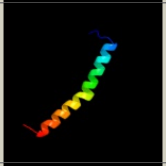
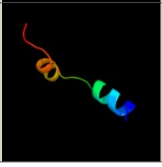
| Description | P02921 |
| Date | Thu Jan 5 10:57:37 GMT 2012 |
| Unique Job ID | f1ebd18e6787ca4f |

## Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | d1pv7a_ | Alignment |  | 100.0 | 12 | **Fold:**MFS general substrate transporter<br>**Superfamily:**MFS general substrate transporter<br>**Family:**LacY-like proton/sugar symporter |
| 2 | d1pw4a_ | Alignment |  | 100.0 | 12 | **Fold:**MFS general substrate transporter<br>**Superfamily:**MFS general substrate transporter<br>**Family:**Glycerol-3-phosphate transporter |
| 3 | c2gfpA_ | Alignment |  | 99.9 | 12 | **PDB header:**membrane protein<br>**Chain:** A: **PDB Molecule:**multidrug resistance protein d;<br>**PDBTitle:** structure of the multidrug transporter emrd from2 escherichia coli |
| 4 | c3o7pA_ | Alignment |  | 99.9 | 12 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**l-fucose-proton symporter;<br>**PDBTitle:** crystal structure of the e.coli fucose:proton symporter, fucp (n162a) |
| 5 | c2xutC_ | Alignment |  | 99.8 | 12 | **PDB header:**transport protein<br>**Chain:** C: **PDB Molecule:**proton/peptide symporter family protein;<br>**PDBTitle:** crystal structure of a proton dependent oligopeptide (pot)2 family transporter. |
| 6 | c3qnqD_ | Alignment |  | 85.4 | 13 | **PDB header:**membrane protein, transport protein<br>**Chain:** D: **PDB Molecule:**pts system, cellobiose-specific iic component;<br>**PDBTitle:** crystal structure of the transporter chbc, the iic component from the2 n,n'-diacetylchitobiose-specific phosphotransferase system |
| 7 | c3hd6A_ | Alignment |  | 49.9 | 10 | **PDB header:**membrane protein, transport protein<br>**Chain:** A: **PDB Molecule:**ammonium transporter rh type c;<br>**PDBTitle:** crystal structure of the human rhesus glycoprotein rhcg |
| 8 | c3b9yA_ | Alignment |  | 39.8 | 12 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**ammonium transporter family rh-like protein;<br>**PDBTitle:** crystal structure of the nitrosomonas europaea rh protein |
| 9 | c3d9sB_ | Alignment |  | 19.0 | 20 | **PDB header:**membrane protein<br>**Chain:** B: **PDB Molecule:**aquaporin-5;<br>**PDBTitle:** human aquaporin 5 (aqp5) - high resolution x-ray structure |
| 10 | d1grja1 | Alignment |  | 16.3 | 13 | **Fold:**Long alpha-hairpin<br>**Superfamily:**GreA transcript cleavage protein, N-terminal domain<br>**Family:**GreA transcript cleavage protein, N-terminal domain |
| 11 | c2f9jP_ | Alignment |  | 15.6 | 24 | **PDB header:**rna binding protein<br>**Chain:** P: **PDB Molecule:**splicing factor 3b subunit 1;<br>**PDBTitle:** 3.0 angstrom resolution structure of a y22m mutant of the spliceosomal2 protein p14 bound to a region of sf3b155 |

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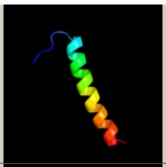
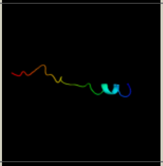
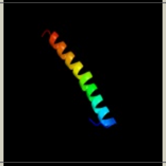
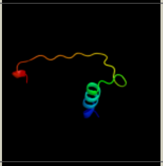
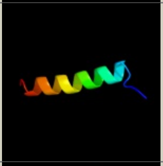
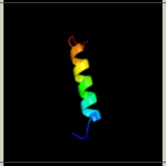
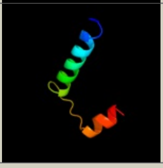
| 12 | d2ia9a1 | Alignment |  | 14.4 | 21 | **Fold:**SpoVG-like<br>**Superfamily:**SpoVG-like<br>**Family:**SpoVG-like |
| 13 | c2xzmV_ | Alignment |  | 8.7 | 17 | **PDB header:**ribosome<br>**Chain:** V: **PDB Molecule:**rps17e;<br>**PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1 |
| 14 | d1u69a_ | Alignment |  | 8.2 | 27 | **Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Family:**3-demethylubiquinone-9 3-methyltransferase |
| 15 | d2f23a1 | Alignment |  | 8.1 | 19 | **Fold:**Long alpha-hairpin<br>**Superfamily:**GreA transcript cleavage protein, N-terminal domain<br>**Family:**GreA transcript cleavage protein, N-terminal domain |
| 16 | c3e56A_ | Alignment |  | 7.3 | 21 | **PDB header:**unknown function<br>**Chain:** A: **PDB Molecule:**putative uncharacterized protein;<br>**PDBTitle:** the 2.0 angstrom resolution crystal structure of npr1517, a putative2 heterocyst differentiation inhibitor from nostoc punctiforme |
| 17 | c2yggA_ | Alignment |  | 6.7 | 21 | **PDB header:**metal binding protein/transport protein<br>**Chain:** A: **PDB Molecule:**sodium/hydrogen exchanger 1;<br>**PDBTitle:** complex of cambr and cam |
| 18 | c3qx3B_ | Alignment |  | 6.3 | 20 | **PDB header:**isomerase/dna/isomerase inhibitor<br>**Chain:** B: **PDB Molecule:**dna topoisomerase 2-beta;<br>**PDBTitle:** human topoisomerase iibeta in complex with dna and etoposide |
| 19 | c1q0wA_ | Alignment |  | 6.1 | 23 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**vacuolar protein sorting-associated protein<br>**PDBTitle:** solution structure of vps27 amino-terminal uim-ubiquitin2 complex |
| 20 | d1ymga1 | Alignment |  | 6.0 | 11 | **Fold:**Aquaporin-like<br>**Superfamily:**Aquaporin-like<br>**Family:**Aquaporin-like |
| 21 | c1ymgA_ | Alignment | not modelled | 6.0 | 11 | **PDB header:**membrane protein<br>**Chain:** A: **PDB Molecule:**lens fiber major intrinsic protein;<br>**PDBTitle:** the channel architecture of aquaporin o at 2.2 angstrom resolution |
| 22 | c3bpqC_ | Alignment | not modelled | 5.9 | 13 | **PDB header:**toxin<br>**Chain:** C: **PDB Molecule:**antitoxin relb3;<br>**PDBTitle:** crystal structure of relb-rele antitoxin-toxin complex from2 methanococcus jannaschii |
| 23 | c1xaoA_ | Alignment | not modelled | 5.9 | 18 | **PDB header:**chaperone<br>**Chain:** A: **PDB Molecule:**mitochondrial protein import protein mas5;<br>**PDBTitle:** hsp40-ydj1 dimerization domain |
| 24 | c1qysA_ | Alignment | not modelled | 5.9 | 16 | **PDB header:**de novo protein<br>**Chain:** A: **PDB Molecule:**top7;<br>**PDBTitle:** crystal structure of top7: a computationally designed2 protein with a novel fold |
| 25 | c1v9xA_ | Alignment | not modelled | 5.8 | 8 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**poly (adp-ribose) polymerase;<br>**PDBTitle:** solution structure of the first zn-finger domain of2 poly(adp-ribose) polymerase-1 |
| 26 | c1ji6A_ | Alignment | not modelled | 5.8 | 8 | **PDB header:**toxin<br>**Chain:** A: **PDB Molecule:**pesticidial crystal protein cry3bb;<br>**PDBTitle:** crystal structure of the insecticidal bacterial del2 endotoxin cry3bb1 bacillus thuringiensis |
| 27 | c1zi7C_ | Alignment | not modelled | 5.7 | 14 | **PDB header:**lipid binding protein<br>**Chain:** C: **PDB Molecule:**kes1 protein;<br>**PDBTitle:** structure of truncated yeast oxysterol binding protein osh4 |
| 28 | c1zvuA_ | Alignment | not modelled | 5.6 | 13 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**topoisomerase iv subunit a;<br>**PDBTitle:** structure of the full-length e. coli parc subunit |
| | | | | | | **PDB header:**transferase |

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| 29 | c1zxaB_ | Alignment | not modelled | 5.5 | 10 | **Chain:** B: **PDB Molecule:**cgmp-dependent protein kinase 1, alpha isozyme;<br>**PDBTitle:** solution structure of the coiled-coil domain of cgmp-2 dependent protein kinase ia |
| 30 | c3i05B_ | Alignment | not modelled | 5.5 | 20 | **PDB header:**ligase<br>**Chain:** B: **PDB Molecule:**tryptophanyl-trna synthetase;<br>**PDBTitle:** tryptophanyl-trna synthetase from trypanosoma brucei |
| 31 | c1bjtA_ | Alignment | not modelled | 5.5 | 13 | **PDB header:**topoisomerase<br>**Chain:** A: **PDB Molecule:**topoisomerase ii;<br>**PDBTitle:** topoisomerase ii residues 409-1201 |
| 32 | d1bjta_ | Alignment | not modelled | 5.5 | 13 | **Fold:**Type II DNA topoisomerase<br>**Superfamily:**Type II DNA topoisomerase<br>**Family:**Type II DNA topoisomerase |
| 33 | d1zhxa1 | Alignment | not modelled | 5.4 | 14 | **Fold:**Oxysterol-binding protein-like<br>**Superfamily:**Oxysterol-binding protein-like<br>**Family:**Oxysterol-binding protein |
| 34 | c3kk1B_ | Alignment | not modelled | 5.4 | 6 | **PDB header:**transferase/dna<br>**Chain:** B: **PDB Molecule:**reverse transcriptase p51 subunit;<br>**PDBTitle:** hiv-1 reverse transcriptase-dna complex with nuceotide inhibitor gs-2 9148-diphosphate bound in nucleotide site |
| 35 | d1uw0a_ | Alignment | not modelled | 5.3 | 15 | **Fold:**Glucocorticoid receptor-like (DNA-binding domain)<br>**Superfamily:**Glucocorticoid receptor-like (DNA-binding domain)<br>**Family:**PARP-type zinc finger |
| 36 | c2qjkM_ | Alignment | not modelled | 5.3 | 13 | **PDB header:**electron transport<br>**Chain:** M: **PDB Molecule:**cytochrome b;<br>**PDBTitle:** crystal structure analysis of mutant rhodobacter2 sphaeroides bc1 with stigmatellin and antimycin |
| 37 | c2wl2B_ | Alignment | not modelled | 5.3 | 17 | **PDB header:**isomerase<br>**Chain:** B: **PDB Molecule:**dna gyrase subunit a;<br>**PDBTitle:** crystal structure of n-terminal domain of gyra with the2 antibiotic simocyclinone d8 |
| 38 | d2zd1b1 | Alignment | not modelled | 5.2 | 6 | **Fold:**DNA/RNA polymerases<br>**Superfamily:**DNA/RNA polymerases<br>**Family:**Reverse transcriptase |
| 39 | d2cqea1 | Alignment | not modelled | 5.1 | 14 | **Fold:**CCCH zinc finger<br>**Superfamily:**CCCH zinc finger<br>**Family:**CCCH zinc finger |
| 40 | c1rthA_ | Alignment | not modelled | 5.1 | 6 | **PDB header:**nucleotidyltransferase<br>**Chain:** A: **PDB Molecule:**hiv-1 reverse transcriptase;<br>**PDBTitle:** high resolution structures of hiv-1 rt from four rt-2 inhibitor complexes |
| 41 | d1hara_ | Alignment | not modelled | 5.0 | 6 | **Fold:**DNA/RNA polymerases<br>**Superfamily:**DNA/RNA polymerases<br>**Family:**Reverse transcriptase |