# Phyre$^2$

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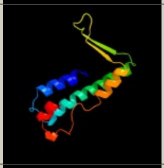
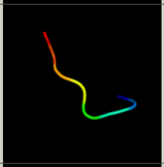
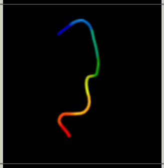
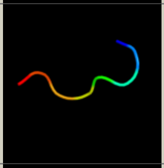
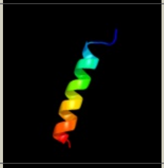
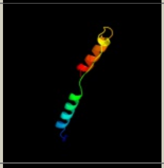
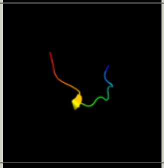
| Description | Q96FX8 |
| Date | Fri May 25 09:35:23 BST 2012 |
| Unique Job ID | e3d5bae4829733c1 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c3b8eB_ | Alignment |  | 21.2 | 13 | **PDB header:**hydrolase/transport protein<br>**Chain:** B: **PDB Molecule:**sodium/potassium-transporting atpase subunit<br>**PDBTitle:** crystal structure of the sodium-potassium pump |
| 2 | c3rkoL_ | Alignment |  | 19.7 | 17 | **PDB header:**oxidoreductase<br>**Chain:** L: **PDB Molecule:**nadh-quinone oxidoreductase subunit l;<br>**PDBTitle:** crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution |
| 3 | c2pm5B_ | Alignment |  | 12.3 | 38 | **PDB header:**antimicrobial protein<br>**Chain:** B: **PDB Molecule:**neutrophil defensin 1 (hnp-1) (hp-1) (hp1) (defensin, alpha<br>**PDBTitle:** human alpha-defensin 1 derivative (hnp1) |
| 4 | c2pm5A_ | Alignment |  | 12.3 | 38 | **PDB header:**antimicrobial protein<br>**Chain:** A: **PDB Molecule:**neutrophil defensin 1 (hnp-1) (hp-1) (hp1) (defensin, alpha<br>**PDBTitle:** human alpha-defensin 1 derivative (hnp1) |
| 5 | c2pm1A_ | Alignment |  | 12.3 | 38 | **PDB header:**antimicrobial protein<br>**Chain:** A: **PDB Molecule:**neutrophil defensin 1 (hnp-1) (hp-1) (hp1)<br>**PDBTitle:** derivative of human alpha-defensin 1 (hnp1) |
| 6 | c2wwaC_ | Alignment |  | 10.9 | 28 | **PDB header:**ribosome<br>**Chain:** C: **PDB Molecule:**protein transport protein seb2;<br>**PDBTitle:** cryo-em structure of idle yeast ssh1 complex bound to the2 yeast 80s ribosome |
| 7 | c3jrtA_ | Alignment |  | 10.0 | 18 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**integron cassette protein vpc_cass2;<br>**PDBTitle:** structure from the mobile metagenome of v. paracholerae:2 integron cassette protein vpc_cass2 |
| 8 | c3hieA_ | Alignment |  | 9.4 | 31 | **PDB header:**exocytosis<br>**Chain:** A: **PDB Molecule:**exocyst complex component sec3;<br>**PDBTitle:** structure of the membrane-binding domain of the sec3 subunit2 of the exocyst complex |
| 9 | c1mctI_ | Alignment |  | 9.0 | 13 | **PDB header:**complex(proteinase/inhibitor)<br>**Chain:** I: **PDB Molecule:**trypsin inhibitor a;<br>**PDBTitle:** the refined 1.6 angstroms resolution crystal structure of2 the complex formed between porcine beta-trypsin and mcti-a,3 a trypsin inhibitor of squash family |
| 10 | d1mcti_ | Alignment |  | 9.0 | 13 | **Fold:**Knottins (small inhibitors, toxins, lectins)<br>**Superfamily:**Plant inhibitors of proteinases and amylases<br>**Family:**Plant inhibitors of proteinases and amylases |
| 11 | c2w8aC_ | Alignment |  | 7.1 | 14 | **PDB header:**membrane protein<br>**Chain:** C: **PDB Molecule:**glycine betaine transporter betp;<br>**PDBTitle:** crystal structure of the sodium-coupled glycine betaine2 symporter betp from corynebacterium glutamicum with bound3 substrate |

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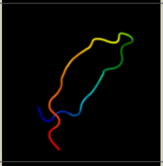
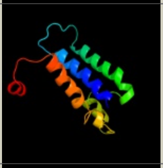
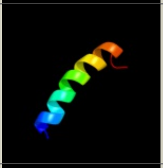
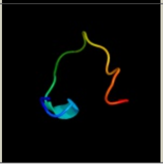
| 12 | c3a58A_ | Alignment |  | 6.8 | 29 | **PDB header:**protein transport/exocytosis<br>**Chain:** A: **PDB Molecule:**exocyst complex component sec3;<br>**PDBTitle:** crystal structure of sec3p - rho1p complex from2 saccharomyces cerevisiae |
| 13 | d1dtxa_ | Alignment |  | 6.2 | 14 | **Fold:**BPTI-like<br>**Superfamily:**BPTI-like<br>**Family:**Small Kunitz-type inhibitors & BPTI-like toxins |
| 14 | d1j4na_ | Alignment |  | 6.2 | 11 | **Fold:**Aquaporin-like<br>**Superfamily:**Aquaporin-like<br>**Family:**Aquaporin-like |
| 15 | d1f2si_ | Alignment |  | 5.6 | 13 | **Fold:**Knottins (small inhibitors, toxins, lectins)<br>**Superfamily:**Plant inhibitors of proteinases and amylases<br>**Family:**Plant inhibitors of proteinases and amylases |
| 16 | c1f2sI_ | Alignment |  | 5.6 | 13 | **PDB header:**hydrolase/hydrolase inhibitor<br>**Chain:** I: **PDB Molecule:**trypsin inhibitor a;<br>**PDBTitle:** crystal structure of the complex formed between bovine beta-2 trypsin and mcti-a, a trypsin inhibitor of squash family3 at 1.8 a resolution |
| 17 | c2oyyF_ | Alignment |  | 5.2 | 27 | **PDB header:**unknown function<br>**Chain:** F: **PDB Molecule:**hexameric cytochrome;<br>**PDBTitle:** hthp: a hexameric tyrosine-coordinated heme protein |
| 18 | d1itua_ | Alignment |  | 5.1 | 37 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Metallo-dependent hydrolases<br>**Family:**Renal dipeptidase |

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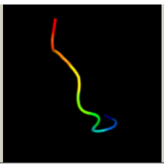
| 19 | c2ctuA_ | Alignment |  | 5.1 | 33 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**zinc finger protein 483;<br>**PDBTitle:** solution structure of zinc finger domain from human zn2 finger protein 483 |