Phyre2

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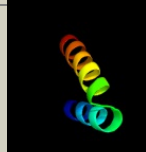
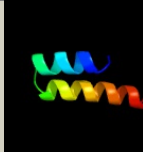
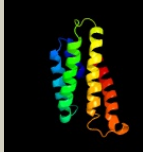
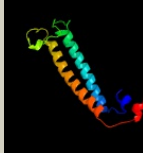
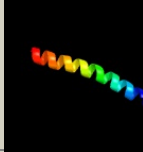
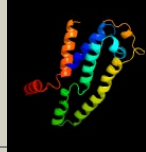
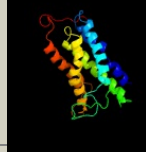
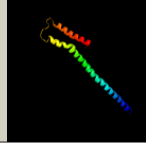
| Email | mdejesus@rockefeller.edu |
| Description | RVBD1491c_(-)_1681214_1681972 |
| Date | Fri Aug 2 13:30:07 BST 2019 |
| Unique Job ID | 15b0ef99d9d3a5a4 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c5d7tC_ | Alignment |  | 90.1 | 25 | **PDB header:**transport protein<br>**Chain:** C: **PDB Molecule:**s-component for folate;<br>**PDBTitle:** folate ecf transporter: apo state |
| 2 | c4huqS_ | Alignment |  | 86.6 | 15 | **PDB header:**hydrolase<br>**Chain:** S: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** crystal structure of a transporter |
| 3 | c4z7fD_ | Alignment |  | 84.5 | 10 | **PDB header:**transport protein<br>**Chain:** D: **PDB Molecule:**folate ecf transporter;<br>**PDBTitle:** crystal structure of folt bound with folic acid |
| 4 | c3p5nA_ | Alignment |  | 64.1 | 25 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**riboflavin uptake protein;<br>**PDBTitle:** structure and mechanism of the s component of a bacterial ecf2 transporter |
| 5 | c4hzuS_ | Alignment |  | 61.1 | 11 | **PDB header:**hydrolase, transport protein<br>**Chain:** S: **PDB Molecule:**predicted membrane protein;<br>**PDBTitle:** structure of a bacterial energy-coupling factor transporter |
| 6 | d1xmea1 | Alignment |  | 59.4 | 17 | **Fold:**Cytochrome c oxidase subunit I-like<br>**Superfamily:**Cytochrome c oxidase subunit I-like<br>**Family:**Cytochrome c oxidase subunit I-like |
| 7 | c2jp3A_ | Alignment |  | 35.3 | 18 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**fxyd domain-containing ion transport regulator 4;<br>**PDBTitle:** solution structure of the human fxyd4 (chif) protein in sds2 micelles |
| 8 | c6c14A_ | Alignment |  | 30.8 | 14 | **PDB header:**membrane protein, metal transport<br>**Chain:** A: **PDB Molecule:**protocadherin-15;<br>**PDBTitle:** cryoem structure of mouse pcdh15-1ec-lhfpl5 complex |
| 9 | c6humB_ | Alignment |  | 17.7 | 12 | **PDB header:**proton transport<br>**Chain:** B: **PDB Molecule:**nad(p)h-quinone oxidoreductase subunit 2;<br>**PDBTitle:** structure of the photosynthetic complex i from thermosynechococcus2 elongatus |
| 10 | c2b2hA_ | Alignment |  | 16.6 | 12 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**ammonium transporter;<br>**PDBTitle:** ammonium transporter amt-1 from a. fulgidus (as) |
| 11 | c5n9yB_ | Alignment |  | 11.9 | 13 | **PDB header:**membrane protein<br>**Chain:** B: **PDB Molecule:**zinc transport protein zntb;<br>**PDBTitle:** the full-length structure of zntb |

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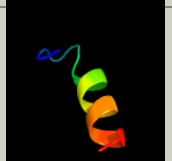
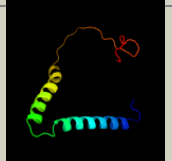
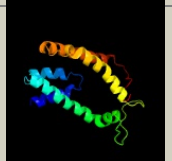
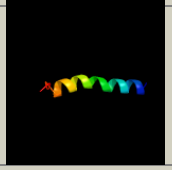
| 12 | c3rkoM_ | Alignment |  | 11.7 | 11 | **PDB header:**oxidoreductase<br>**Chain:** M: **PDB Molecule:**nadh-quinone oxidoreductase subunit m;<br>**PDBTitle:** crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution |
| 13 | c1ciiA_ | Alignment |  | 8.9 | 14 | **PDB header:**transmembrane protein<br>**Chain:** A: **PDB Molecule:**colicin ia;<br>**PDBTitle:** colicin ia |
| 14 | c5edlA_ | Alignment |  | 8.7 | 18 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**putative hmp/thiamine permease protein ykoe;<br>**PDBTitle:** crystal structure of an s-component of ecf transporter |
| 15 | c4j8cA_ | Alignment |  | 8.4 | 29 | **PDB header:**chaperone<br>**Chain:** A: **PDB Molecule:**hsc70-interacting protein;<br>**PDBTitle:** crystal structure of the dimerization domain of hsc70-interacting2 protein |
| 16 | c4j8cB_ | Alignment |  | 8.4 | 29 | **PDB header:**chaperone<br>**Chain:** B: **PDB Molecule:**hsc70-interacting protein;<br>**PDBTitle:** crystal structure of the dimerization domain of hsc70-interacting2 protein |
| 17 | c4djiA_ | Alignment |  | 8.1 | 10 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**probable glutamate/gamma-aminobutyrate antiporter;<br>**PDBTitle:** structure of glutamate-gaba antiporter gadc |
| 18 | d1ciia1 | Alignment |  | 6.8 | 19 | **Fold:**Toxins' membrane translocation domains<br>**Superfamily:**Colicin<br>**Family:**Colicin |
| 19 | c5oonA_ | Alignment |  | 6.5 | 18 | **PDB header:**membrane protein<br>**Chain:** A: **PDB Molecule:**undecaprenyl-diphosphatase;<br>**PDBTitle:** structure of undecaprenyl-pyrophosphate phosphatase, baca |
| 20 | c2na6B_ | Alignment |  | 6.2 | 28 | **PDB header:**apoptosis<br>**Chain:** B: **PDB Molecule:**tumor necrosis factor receptor superfamily member 6;<br>**PDBTitle:** transmembrane domain of mouse fas/cd95 death receptor |
| 21 | c2na6C_ | Alignment | not modelled | 6.2 | 28 | **PDB header:**apoptosis<br>**Chain:** C: **PDB Molecule:**tumor necrosis factor receptor superfamily member 6;<br>**PDBTitle:** transmembrane domain of mouse fas/cd95 death receptor |
| 22 | c2na6A_ | Alignment | not modelled | 6.2 | 28 | **PDB header:**apoptosis<br>**Chain:** A: **PDB Molecule:**tumor necrosis factor receptor superfamily member 6;<br>**PDBTitle:** transmembrane domain of mouse fas/cd95 death receptor |
| 23 | c1zrtD_ | Alignment | not modelled | 6.1 | 10 | **PDB header:**oxidoreductase/metal transport<br>**Chain:** D: **PDB Molecule:**cytochrome c1;<br>**PDBTitle:** rhodobacter capsulatus cytochrome bc1 complex with2 stigmatellin bound |
| 24 | d1pw4a_ | Alignment | not modelled | 5.9 | 22 | **Fold:**MFS general substrate transporter<br>**Superfamily:**MFS general substrate transporter<br>**Family:**Glycerol-3-phosphate transporter |
| 25 | c4ev6E_ | Alignment | not modelled | 5.9 | 10 | **PDB header:**metal transport<br>**Chain:** E: **PDB Molecule:**magnesium transport protein cora;<br>**PDBTitle:** the complete structure of cora magnesium transporter from2 methanocaldococcus jannaschii |
| 26 | d1kpla_ | Alignment | not modelled | 5.8 | 24 | **Fold:**Clc chloride channel<br>**Superfamily:**Clc chloride channel<br>**Family:**Clc chloride channel |