Phyre2

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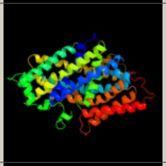
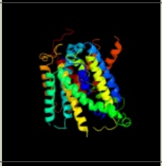
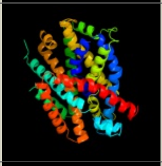
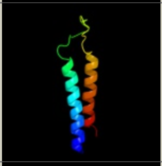
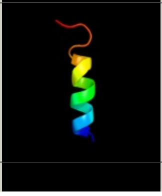
| Description | P16256 |
| Date | Thu Jan 5 11:35:02 GMT 2012 |
| Unique Job ID | 2a093629c09581a7 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c2xq2A_ | Alignment |  | 100.0 | 18 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**sodium/glucose cotransporter;<br>**PDBTitle:** structure of the k294a mutant of vsglt |
| 2 | c3dh4A_ | Alignment |  | 100.0 | 16 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**sodium/glucose cotransporter;<br>**PDBTitle:** crystal structure of sodium/sugar symporter with bound galactose from2 vibrio parahaemolyticus |
| 3 | c3giaA_ | Alignment |  | 99.8 | 12 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**uncharacterized protein mj0609;<br>**PDBTitle:** crystal structure of apct transporter |
| 4 | c2jlnA_ | Alignment |  | 99.7 | 13 | **PDB header:**membrane protein<br>**Chain:** A: **PDB Molecule:**mhp1;<br>**PDBTitle:** structure of mhp1, a nucleobase-cation-symport-1 family2 transporter |
| 5 | c3lrcC_ | Alignment |  | 99.4 | 11 | **PDB header:**transport protein<br>**Chain:** C: **PDB Molecule:**arginine/agmatine antiporter;<br>**PDBTitle:** structure of e. coli adic (p1) |
| 6 | c2w8aC_ | Alignment |  | 99.2 | 11 | **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 |
| 7 | c3hfxA_ | Alignment |  | 98.8 | 14 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**l-carnitine/gamma-butyrobetaine antiporter;<br>**PDBTitle:** crystal structure of carnitine transporter |
| 8 | d2a65a1 | Alignment |  | 96.4 | 12 | **Fold:**SNF-like<br>**Superfamily:**SNF-like<br>**Family:**SNF-like |
| 9 | c3mk7F_ | Alignment |  | 15.3 | 8 | **PDB header:**oxidoreductase<br>**Chain:** F: **PDB Molecule:**cytochrome c oxidase, cbb3-type, subunit p;<br>**PDBTitle:** the structure of cbb3 cytochrome oxidase |
| 10 | c2k9yB_ | Alignment |  | 7.1 | 32 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**ephrin type-a receptor 2;<br>**PDBTitle:** epha2 dimeric structure in the lipidic bicelle at ph 5.0 |
| 11 | c2k9yA_ | Alignment |  | 7.1 | 32 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**ephrin type-a receptor 2;<br>**PDBTitle:** epha2 dimeric structure in the lipidic bicelle at ph 5.0 |

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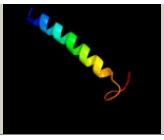
| 12 | d1eysh2 | Alignment |  | 6.8 | 23 | **Fold:**Single transmembrane helix<br>**Superfamily:**Photosystem II reaction centre subunit H, transmembrane region<br>**Family:**Photosystem II reaction centre subunit H, transmembrane region |

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|---|---|---|---|---|---|---|
| 13 | d1j4na_ | Alignment |  | 5.8 | 12 | **Fold:**Aquaporin-like<br>**Superfamily:**Aquaporin-like<br>**Family:**Aquaporin-like |