




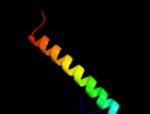
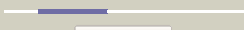

















Phyre2

| | |
|---------------|-----------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD2254c (-) _2528530_2528985 |
| Date | Mon Aug 5 13:25:39 BST 2019 |
| Unique Job ID | 79e3d7085eaac3cd |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|---|
| 1 | c5kvA_ |  Alignment |  | 98.2 | 17 | PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome c-type biogenesis protein ccda; PDBTitle: solution nmr structure of the membrane electron transporter ccda |
| 2 | c2n4xA_ |  Alignment |  | 93.0 | 12 | PDB header: membrane protein Chain: A: PDB Molecule: cytochrome c-type biogenesis protein (ccda); PDBTitle: structure of the transmembrane electron transporter ccda |
| 3 | c1afoB_ |  Alignment |  | 16.9 | 18 | PDB header: integral membrane protein Chain: B: PDB Molecule: glycophorin a; PDBTitle: dimeric transmembrane domain of human glycophorin a, nmr,2 20 structures |
| 4 | c4kt0F_ |  Alignment |  | 11.5 | 18 | PDB header: electron transport Chain: F: PDB Molecule: photosystem i subunit iii; PDBTitle: crystal structure of a virus like photosystem i from the2 cyanobacterium synechocystis pcc 6803 |
| 5 | d1jb0F_ |  Alignment |  | 10.9 | 18 | Fold: Single transmembrane helix Superfamily: Subunit III of photosystem I reaction centre, PsaF Family: Subunit III of photosystem I reaction centre, PsaF |
| 6 | c6fosF_ |  Alignment |  | 10.6 | 15 | PDB header: photosynthesis Chain: F: PDB Molecule: photosystem i reaction center subunit ii; PDBTitle: cyanidioschyzon merolae photosystem i |
| 7 | d1j0ta_ |  Alignment |  | 7.8 | 46 | Fold: Crustacean CHH/MIH/GIH neurohormone Superfamily: Crustacean CHH/MIH/GIH neurohormone Family: Crustacean CHH/MIH/GIH neurohormone |
| 8 | c1j0ta_ |  Alignment |  | 7.8 | 46 | PDB header: hormone/growth factor Chain: A: PDB Molecule: molt-inhibiting hormone; PDBTitle: the solution structure of molt-inhibiting hormone from the2 kuruma prawn |
| 9 | c2jp3A_ |  Alignment |  | 7.8 | 13 | PDB header: transcription Chain: A: PDB Molecule: fyxd domain-containing ion transport regulator 4; PDBTitle: solution structure of the human fxyd4 (chif) protein in sds2 micelles |
| 10 | c6igzF_ |  Alignment |  | 7.7 | 15 | PDB header: plant protein Chain: F: PDB Molecule: psaf; PDBTitle: structure of psi-lhci |
| 11 | c6cfwF_ |  Alignment |  | 7.2 | 10 | PDB header: membrane protein Chain: F: PDB Molecule: monovalent cation/h+ antiporter subunit b; PDBTitle: cryoem structure of a respiratory membrane-bound hydrogenase |

| | | | | | | |
|----|-------------------------|-----------|--------------|-----|----|---|
| 12 | c6ijjF_ | Alignment | | 7.0 | 16 | PDB header: membrane protein Chain: F; PDB Molecule: psaf; PDBTitle: photosystem i of chlamydomonas reinhardtii |
| 13 | c5n6mA_ | Alignment | | 6.9 | 11 | PDB header: membrane protein Chain: A; PDB Molecule: apolipoprotein n-acyltransferase; PDBTitle: structure of the membrane integral lipoprotein n-acyltransferase lnt2 from p. aeruginosa |
| 14 | c2mkvA_ | Alignment | | 6.8 | 14 | PDB header: transport protein Chain: A; PDB Molecule: sodium/potassium-transporting atpase subunit gamma; PDBTitle: structure of the na,k-atpase regulatory protein fxyd2b in micelles |
| 15 | c5xtdm_ | Alignment | | 6.7 | 12 | PDB header: oxidoreductase/electron transport Chain: M; PDB Molecule: nadh-ubiquinone oxidoreductase 75 kda subunit, PDBTitle: cryo-em structure of human respiratory complex i |
| 16 | c2jo1A_ | Alignment | | 6.5 | 13 | PDB header: hydrolase regulator Chain: A; PDB Molecule: phospholemman; PDBTitle: structure of the na,k-atpase regulatory protein fxyd1 in2 micelles |
| 17 | c5ireA_ | Alignment | | 5.9 | 13 | PDB header: virus Chain: A; PDB Molecule: e protein; PDBTitle: the cryo-em structure of zika virus |
| 18 | c5wsnC_ | Alignment | | 5.7 | 13 | PDB header: virus Chain: C; PDB Molecule: e protein; PDBTitle: structure of japanese encephalitis virus |
| 19 | c3n23E_ | Alignment | | 5.7 | 15 | PDB header: hydrolase Chain: E; PDB Molecule: na+/k+ atpase gamma subunit transcript variant a; PDBTitle: crystal structure of the high affinity complex between ouabain and the2 e2p form of the sodium-potassium pump |
| 20 | c1p58C_ | Alignment | | 5.6 | 13 | PDB header: virus Chain: C; PDB Molecule: major envelope protein e; PDBTitle: complex organization of dengue virus membrane proteins as revealed by2 9.5 angstrom cryo-em reconstruction |
| 21 | c4b03A_ | Alignment | not modelled | 5.5 | 20 | PDB header: virus Chain: A; PDB Molecule: dengue virus 1 e protein; PDBTitle: 6a electron cryomicroscopy structure of immature dengue virus serotype2 1 |
| 22 | c3s32A_ | Alignment | not modelled | 5.4 | 13 | PDB header: transcription Chain: A; PDB Molecule: set1/ash2 histone methyltransferase complex subunit ash2; PDBTitle: crystal structure of ash2l n-terminal domain |
| 23 | c2mfrA_ | Alignment | not modelled | 5.4 | 12 | PDB header: transferase Chain: A; PDB Molecule: insulin receptor; PDBTitle: solution structure of the transmembrane domain of the insulin receptor2 in micelles |
| 24 | c5o6vC_ | Alignment | not modelled | 5.3 | 13 | PDB header: virus Chain: C; PDB Molecule: envelope protein; PDBTitle: the cryo-em structure of tick-borne encephalitis virus complexed with2 fab fragment of neutralizing antibody 19/1786 |
| 25 | c2o01F_ | Alignment | not modelled | 5.3 | 18 | PDB header: photosynthesis Chain: F; PDB Molecule: photosystem i reaction center subunit iii, chloroplast; PDBTitle: the structure of a plant photosystem i supercomplex at 3.4 angstrom2 resolution |