
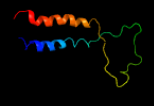

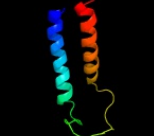



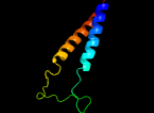
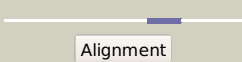
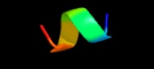
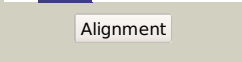

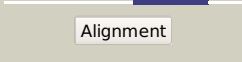
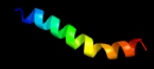
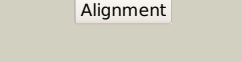

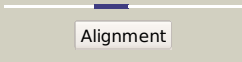
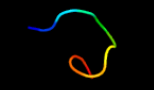
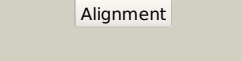

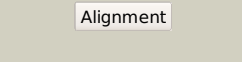

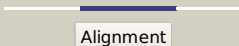
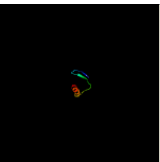




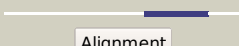

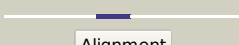
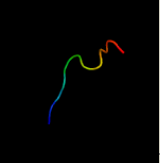




Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD1440_(secG)_1617843_1618076
 Date Wed Jul 31 22:05:55 BST 2019
 Unique Job ID 686e21245ee32b84

Detailed template information

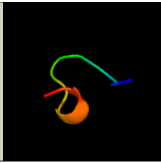
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2akiA_	 Alignment		98.2	21	PDB header: protein transport Chain: A: PDB Molecule: protein-export membrane protein secg; PDBTitle: normal mode-based flexible fitted coordinates of a translocating2 secyeg protein-conducting channel into the cryo-em map of a secyeg-3 nascent chain-70s ribosome complex from e. coli
2	c3dinE_	 Alignment		97.9	22	PDB header: membrane protein, protein transport Chain: E: PDB Molecule: preprotein translocase subunit secg; PDBTitle: crystal structure of the protein-translocation complex formed by the2 secy channel and the seca atpase
3	c3dl8F_	 Alignment		97.5	28	PDB header: protein transport Chain: F: PDB Molecule: protein-export membrane protein secg; PDBTitle: structure of the complex of aquifex aeolicus secyeg and bacillus2 subtilis seca
4	c5awwG_	 Alignment		87.8	20	PDB header: protein transport/immune system Chain: G: PDB Molecule: putative preprotein translocase, secg subunit; PDBTitle: precise resting state of thermus thermophilus secyeg
5	c5uz5G_	 Alignment		11.7	71	PDB header: nuclear protein/rna Chain: G: PDB Molecule: 56 kda u1 small nuclear ribonucleoprotein component; PDBTitle: s. cerevisiae u1 snrnp
6	c2mxbA_	 Alignment		8.5	40	PDB header: membrane protein Chain: A: PDB Molecule: erythropoietin receptor; PDBTitle: structure of the transmembrane domain of the mouse erythropoietin2 receptor
7	d1v54I_	 Alignment		8.1	14	Fold: Single transmembrane helix Superfamily: Mitochondrial cytochrome c oxidase subunit VIIC (aka VIIIA) Family: Mitochondrial cytochrome c oxidase subunit VIIC (aka VIIIA)
8	c3iprC_	 Alignment		7.4	8	PDB header: transferase Chain: C: PDB Molecule: pts system, iia component; PDBTitle: crystal structure of the enterococcus faecalis gluconate2 specific eiia phosphotransferase system component
9	d1pdoa_	 Alignment		7.1	27	Fold: PTS system fructose IIA component-like Superfamily: PTS system fructose IIA component-like Family: EIIA-man component-like
10	c4tkzA_	 Alignment		6.9	36	PDB header: transferase Chain: A: PDB Molecule: putative uncharacterized protein gbs1890; PDBTitle: crystal structure of phosphotransferase system component eiia from2 streptococcus agalactiae
11	c3hl6B_	 Alignment		6.9	24	PDB header: unknown function Chain: B: PDB Molecule: pathogenicity island protein; PDBTitle: staphylococcus aureus pathogenicity island 3 orf9 protein

12	c2zvfG_	 Alignment		6.5	25	PDB header: ligase Chain: G: PDB Molecule: alanyl-trna synthetase; PDBTitle: crystal structure of archaeoglobus fulgidus alanyl-trna2 synthetase c-terminal dimerization domain
13	c6fmgC_	 Alignment		6.4	25	PDB header: transferase Chain: C: PDB Molecule: pts system mannose-specific transporter subunit iiaB; PDBTitle: structure of the mannose transporter iia domain from streptococcus pneumoniae
14	c2lp1A_	 Alignment		6.3	23	PDB header: membrane protein Chain: A: PDB Molecule: c99; PDBTitle: the solution nmr structure of the transmembrane c-terminal domain of2 the amyloid precursor protein (c99)
15	c1spfA_	 Alignment		6.1	38	PDB header: lipoprotein(surface film) Chain: A: PDB Molecule: pulmonary surfactant-associated polypeptide c; PDBTitle: the nmr structure of the pulmonary surfactant-associated2 polypeptide sp-c in an apolar solvent contains a valyl-3 rich alpha-helix
16	c3lpzA_	 Alignment		6.0	42	PDB header: protein transport Chain: A: PDB Molecule: get4 (yor164c homolog); PDBTitle: crystal structure of c. therm. get4
17	c3lfhF_	 Alignment		6.0	33	PDB header: transferase Chain: F: PDB Molecule: phosphotransferase system, mannose/fructose-specific PDBTitle: crystal structure of manxa from thermoanaerobacter tengcongensis

18

[c5t3uA_](#)

Alignment



5.6

36

PDB header:transport protein
Chain: A: **PDB Molecule:**pts system, iia component;
PDBTitle: crystal structure of the pts iia protein associated with the fucose2 utilization operon from streptococcus pneumoniae