
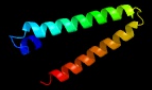
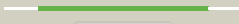
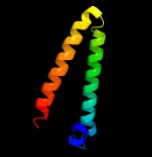
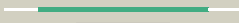
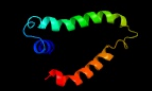




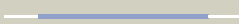








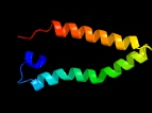

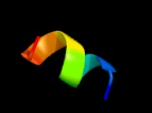


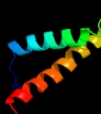

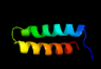

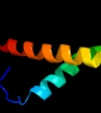
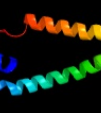



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0841 (-) _937596_937838
Date	Fri Jul 26 01:50:43 BST 2019
Unique Job ID	4442e023c30b64c1

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5aymA</a>	 Alignment		62.0	15	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> solute carrier family 39 (iron-regulated transporter); <b>PDBTitle:</b> crystal structure of a bacterial homologue of iron transporter2 ferroportin in outward-facing state with soaked iron
2	<a href="#">c5aynA</a>	 Alignment		59.0	15	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> solute carrier family 39 (iron-regulated transporter); <b>PDBTitle:</b> crystal structure of a bacterial homologue of iron transporter2 ferroportin in outward-facing state
3	<a href="#">c4ikyA</a>	 Alignment		49.0	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> di-tripeptide abc transporter (permease); <b>PDBTitle:</b> crystal structure of peptide transporter pot (e310q mutant) in complex2 with sulfate
4	<a href="#">c3wdoA</a>	 Alignment		46.0	14	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> mfs transporter; <b>PDBTitle:</b> structure of e. coli yajr transporter
5	<a href="#">c4w6vA</a>	 Alignment		33.6	16	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> di-tripeptide transporter; <b>PDBTitle:</b> crystal structure of a peptide transporter from yersinia2 enterocolitica at 3 a resolution
6	<a href="#">c6exsA</a>	 Alignment		23.2	13	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> peptide abc transporter permease; <b>PDBTitle:</b> crystal structure of a pot family transporter in complex with2 thioalcohol conjugated peptide.
7	<a href="#">c4o9tH</a>	 Alignment		18.7	43	<b>PDB header:</b> membrane protein <b>Chain:</b> H: <b>PDB Molecule:</b> nad(p) transhydrogenase subunit beta; <b>PDBTitle:</b> mechanism of transhydrogenase coupling proton translocation and2 hydride transfer
8	<a href="#">c6e9oA</a>	 Alignment		14.0	21	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> d-galactonate transport; <b>PDBTitle:</b> e. coli d-galactonate:proton symporter mutant e133q in the outward2 substrate-bound form
9	<a href="#">c6gs7A</a>	 Alignment		11.5	22	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> dipeptide and tripeptide permease a; <b>PDBTitle:</b> crystal structure of peptide transporter dtpa-nanobody in glycine2 buffer
10	<a href="#">c6g9xB</a>	 Alignment		11.4	13	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> major facilitator superfamily mfs_1; <b>PDBTitle:</b> crystal structure of a mfs transporter at 2.54 angstrom resolution
11	<a href="#">c2micB</a>	 Alignment		10.1	78	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> tumor necrosis factor receptor superfamily member 16; <b>PDBTitle:</b> nmr structure of p75 transmembrane domain in dpc micelles

12	<a href="#">c2micA_</a>	Alignment		10.1	78	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> tumor necrosis factor receptor superfamily member 16; <b>PDBTitle:</b> nmr structure of p75 transmembrane domain in dpc micelles
13	<a href="#">c1s6cB_</a>	Alignment		9.0	67	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> potassium voltage-gated channel subfamily d member 2; <b>PDBTitle:</b> crystal structure of the complex between kchip1 and kv4.2 n1-30
14	<a href="#">c5aezA_</a>	Alignment		8.9	15	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> mep2; <b>PDBTitle:</b> crystal structure of candida albicans mep2
15	<a href="#">c4o9uB_</a>	Alignment		8.0	45	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> nad(p) transhydrogenase subunit beta; <b>PDBTitle:</b> mechanism of transhydrogenase coupling proton translocation and2 hydride transfer
16	<a href="#">d1u7ga_</a>	Alignment		7.2	13	<b>Fold:</b> Ammonium transporter <b>Superfamily:</b> Ammonium transporter <b>Family:</b> Ammonium transporter
17	<a href="#">c4oleD_</a>	Alignment		7.0	40	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> next to brca1 gene 1 protein; <b>PDBTitle:</b> crystal structure of a neighbor of brca1 gene 1 (nbr1) from homo2 sapiens at 2.52 a resolution
18	<a href="#">c5aexJ_</a>	Alignment		6.9	15	<b>PDB header:</b> membrane protein <b>Chain:</b> J: <b>PDB Molecule:</b> ammonium transporter mep2; <b>PDBTitle:</b> crystal structure of saccharomyces cerevisiae mep2
19	<a href="#">c1pv7B_</a>	Alignment		6.8	13	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> lactose permease; <b>PDBTitle:</b> crystal structure of lactose permease with tdg
20	<a href="#">d1pv7a_</a>	Alignment		6.8	13	<b>Fold:</b> MFS general substrate transporter <b>Superfamily:</b> MFS general substrate transporter <b>Family:</b> LacY-like proton/sugar symporter
21	<a href="#">d1wvfa1</a>	Alignment	not modelled	5.2	50	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> FAD-linked oxidases, C-terminal domain <b>Family:</b> Vanillyl-alcohol oxidase-like
22	<a href="#">c3l32B_</a>	Alignment	not modelled	5.1	42	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoprotein; <b>PDBTitle:</b> structure of the dimerisation domain of the rabies virus2 phosphoprotein