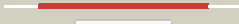











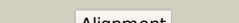



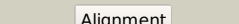







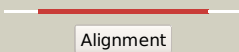
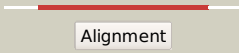
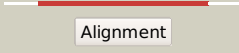
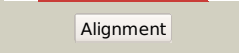
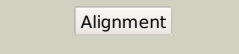
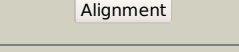
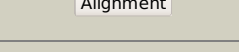
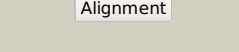
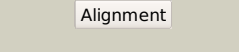
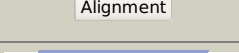
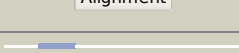
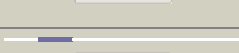
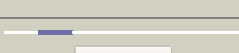

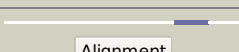


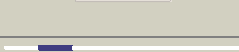
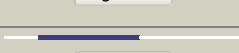
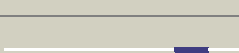
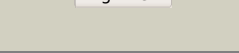
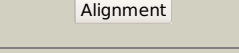
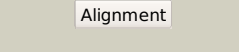
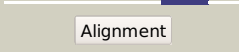
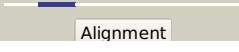
# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1258c_(-)_1406087_1407346
Date	Wed Jul 31 22:05:35 BST 2019
Unique Job ID	c07dc4fdc03d142f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3wdoA_</a>	 Alignment		100.0	12	<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
2	<a href="#">d1pv7a_</a>	 Alignment		100.0	11	<b>Fold:</b> MFS general substrate transporter <b>Superfamily:</b> MFS general substrate transporter <b>Family:</b> LacY-like proton/sugar symporter
3	<a href="#">c1pv7B_</a>	 Alignment		100.0	11	<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
4	<a href="#">d1pw4a_</a>	 Alignment		100.0	13	<b>Fold:</b> MFS general substrate transporter <b>Superfamily:</b> MFS general substrate transporter <b>Family:</b> Glycerol-3-phosphate transporter
5	<a href="#">c6e9oA_</a>	 Alignment		100.0	13	<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
6	<a href="#">c5aynA_</a>	 Alignment		100.0	12	<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
7	<a href="#">c4j05A_</a>	 Alignment		100.0	11	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> phosphate transporter; <b>PDBTitle:</b> crystal structure of a eukaryotic phosphate transporter
8	<a href="#">c5aymA_</a>	 Alignment		100.0	12	<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
9	<a href="#">c4zp0A_</a>	 Alignment		100.0	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> multidrug transporter mdfa; <b>PDBTitle:</b> crystal structure of e. coli multidrug transporter mdfa in complex2 with deoxycholate
10	<a href="#">c6gs7A_</a>	 Alignment		100.0	16	<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
11	<a href="#">c4ikyA_</a>	 Alignment		100.0	14	<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

12	<a href="#">c4ldsB_</a>	Alignment		100.0	13	<b>PDB header:</b> transport protein, membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> bicyclomycin resistance protein tcab; <b>PDBTitle:</b> the inward-facing structure of the glucose transporter from2 staphylococcus epidermidis
13	<a href="#">c4w6vA_</a>	Alignment		100.0	13	<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
14	<a href="#">c4cl5B_</a>	Alignment		100.0	14	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> nitrate transporter 1.1; <b>PDBTitle:</b> crystal structure of the nitrate transporter nrt1.1 from2 arabidopsis thaliana in complex with nitrate.
15	<a href="#">c6exsA_</a>	Alignment		100.0	9	<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.
16	<a href="#">c6g9xB_</a>	Alignment		100.0	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
17	<a href="#">c4apsB_</a>	Alignment		100.0	12	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> di- or tripeptide h+ symporter; <b>PDBTitle:</b> crystal structure of a pot family peptide transporter in an inward2 open conformation.
18	<a href="#">c5c65A_</a>	Alignment		100.0	12	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> solute carrier family 2, facilitated glucose transporter <b>PDBTitle:</b> structure of the human glucose transporter glut3 / slc2a3
19	<a href="#">c2gfpA_</a>	Alignment		100.0	13	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> multidrug resistance protein d; <b>PDBTitle:</b> structure of the multidrug transporter emrd from2 escherichia coli
20	<a href="#">c6h7dA_</a>	Alignment		100.0	11	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> sugar transport protein 10; <b>PDBTitle:</b> crystal structure of a. thaliana sugar transport protein 10 in complex2 with glucose in the outward occluded state
21	<a href="#">c3o7pA_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> l-fucose-proton symporter; <b>PDBTitle:</b> crystal structure of the e.coli fucose:proton symporter, fucp (n162a)
22	<a href="#">c4q65A_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> dipeptide permease d; <b>PDBTitle:</b> structure of the e. coli peptide transporter ybgh
23	<a href="#">c4ybqB_</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> transport protein/immune system <b>Chain:</b> B: <b>PDB Molecule:</b> solute carrier family 2, facilitated glucose transporter <b>PDBTitle:</b> rat glut5 with fv in the outward-open form
24	<a href="#">c4iu8A_</a>	Alignment	not modelled	99.9	9	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> nitrite extrusion protein 2; <b>PDBTitle:</b> crystal structure of a membrane transporter (selenomethionine2 derivative)
25	<a href="#">c6ei3A_</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> proton-dependent oligopeptide transporter family protein; <b>PDBTitle:</b> crystal structure of auto inhibited pot family peptide transporter
26	<a href="#">c4lepB_</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> membrane protein, transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> proton:oligopeptide symporter pot family; <b>PDBTitle:</b> structural insights into substrate recognition in proton dependent2 oligopeptide transporters
27	<a href="#">c4iu9A_</a>	Alignment	not modelled	99.9	11	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> nitrite extrusion protein 2; <b>PDBTitle:</b> crystal structure of a membrane transporter
28	<a href="#">c4ppyA_</a>	Alignment	not modelled	99.9	11	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> solute carrier family 2, facilitated glucose transporter <b>PDBTitle:</b> crystal structure of the human glucose transporter glut1

29	<a href="#">c4gbzA</a>	 Alignment	not modelled	99.9	10	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> d-xylose-proton symporter; <b>PDBTitle:</b> the structure of the mfs (major facilitator superfamily) proton:xylose2 symporter xyle bound to d-glucose
30	<a href="#">c2xutC</a>	 Alignment	not modelled	99.9	12	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> proton/peptide symporter family protein; <b>PDBTitle:</b> crystal structure of a proton dependent oligopeptide (pot) family2 transporter.
31	<a href="#">c4m64D</a>	 Alignment	not modelled	99.9	11	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> melibiose carrier protein; <b>PDBTitle:</b> 3d crystal structure of na+/melibiose symporter of salmonella2 typhimurium
32	<a href="#">c6ob7A</a>	 Alignment	not modelled	99.7	10	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> equilibrative nucleoside transporter 1; <b>PDBTitle:</b> human equilibrative nucleoside transporter-1, dilazep bound
33	<a href="#">c3vvpA</a>	 Alignment	not modelled	66.8	10	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of mate in complex with br-nrf
34	<a href="#">c5xijA</a>	 Alignment	not modelled	53.8	8	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> multi drug efflux transporter; <b>PDBTitle:</b> crystal structure of a mate family protein
35	<a href="#">c3fewX</a>	 Alignment	not modelled	40.1	22	<b>PDB header:</b> immune system <b>Chain:</b> X: <b>PDB Molecule:</b> colicin s4; <b>PDBTitle:</b> structure and function of colicin s4, a colicin with a duplicated2 receptor binding domain
36	<a href="#">c2jp3A</a>	 Alignment	not modelled	35.5	11	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> fxyd domain-containing ion transport regulator 4; <b>PDBTitle:</b> solution structure of the human fxyd4 (chif) protein in sds2 micelles
37	<a href="#">c6hwhX</a>	 Alignment	not modelled	33.0	18	<b>PDB header:</b> electron transport <b>Chain:</b> X: <b>PDB Molecule:</b> cytochrome c oxidase polypeptide 4; <b>PDBTitle:</b> structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
38	<a href="#">d1rh1a2</a>	 Alignment	not modelled	31.7	15	<b>Fold:</b> Toxins' membrane translocation domains <b>Superfamily:</b> Colicin <b>Family:</b> Colicin
39	<a href="#">c5y50A</a>	 Alignment	not modelled	27.2	10	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein detoxification 14; <b>PDBTitle:</b> crystal structure of eukaryotic mate transporter atdtx14
40	<a href="#">c1rh1A</a>	 Alignment	not modelled	21.7	14	<b>PDB header:</b> antibiotic <b>Chain:</b> A: <b>PDB Molecule:</b> colicin b; <b>PDBTitle:</b> crystal structure of the cytotoxic bacterial protein2 colicin b at 2.5 a resolution
41	<a href="#">d1cola</a>	 Alignment	not modelled	17.1	17	<b>Fold:</b> Toxins' membrane translocation domains <b>Superfamily:</b> Colicin <b>Family:</b> Colicin
42	<a href="#">c2g9pA</a>	 Alignment	not modelled	15.9	29	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> antimicrobial peptide latarcin 2a; <b>PDBTitle:</b> nmr structure of a novel antimicrobial peptide, latarcin 2a,2 from spider (lachesana tarabaevi) venom
43	<a href="#">c6i1rA</a>	 Alignment	not modelled	13.0	6	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> cmp-sialic acid transporter 1; <b>PDBTitle:</b> crystal structure of cmp bound cst in an outward facing conformation
44	<a href="#">c2jo1A</a>	 Alignment	not modelled	11.3	13	<b>PDB header:</b> hydrolase regulator <b>Chain:</b> A: <b>PDB Molecule:</b> phospholemman; <b>PDBTitle:</b> structure of the na,k-atpase regulatory protein fxyd1 in2 micelles
45	<a href="#">c4n7wA</a>	 Alignment	not modelled	9.4	9	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> transporter, sodium/bile acid symporter family; <b>PDBTitle:</b> crystal structure of the sodium bile acid symporter from yersinia2 frederiksenii
46	<a href="#">c2mkvA</a>	 Alignment	not modelled	8.4	16	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> sodium/potassium-transporting atpase subunit gamma; <b>PDBTitle:</b> structure of the na,k-atpase regulatory protein fxyd2b in micelles
47	<a href="#">c6o7ua</a>	 Alignment	not modelled	8.3	16	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> <b>PDBTitle:</b> saccharomyces cerevisiae v-atpase stv1-vo
48	<a href="#">c3hd6A</a>	 Alignment	not modelled	7.7	11	<b>PDB header:</b> membrane protein, transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> ammonium transporter rh type c; <b>PDBTitle:</b> crystal structure of the human rhesus glycoprotein rhcg
49	<a href="#">c3qnqD</a>	 Alignment	not modelled	7.4	13	<b>PDB header:</b> membrane protein, transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> pts system, cellobiose-specific iic component; <b>PDBTitle:</b> crystal structure of the transporter chbc, the iic component from the2 n,n'-diacetylchitobiose-specific phosphotransferase system
50	<a href="#">c2kncA</a>	 Alignment	not modelled	7.0	12	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> integrin alpha-iib; <b>PDBTitle:</b> platelet integrin alfa-iib-beta3 transmembrane-cytoplasmic2 heterocomplex
51	<a href="#">c2w8aC</a>	 Alignment	not modelled	6.1	10	<b>PDB header:</b> membrane protein <b>Chain:</b> C: <b>PDB Molecule:</b> glycine betaine transporter betp; <b>PDBTitle:</b> crystal structure of the sodium-coupled glycine betaine2 symporter betp from corynebacterium glutamicum with bound3 substrate
52	<a href="#">c5kk2E</a>	 Alignment	not modelled	6.0	12	<b>PDB header:</b> membrane protein, transport protein, sig <b>Chain:</b> E: <b>PDB Molecule:</b> voltage-dependent calcium channel gamma-2 subunit; <b>PDBTitle:</b> architecture of fully occupied glua2 ampa receptor - tarp complex2 elucidated by single particle cryo-electron microscopy
53	<a href="#">c1a87A</a>	 Alignment	not modelled	5.9	12	<b>PDB header:</b> bacteriocin <b>Chain:</b> A: <b>PDB Molecule:</b> colicin n;

					<b>PDBTitle:</b> colicin n
54	<a href="#">d1a87a_</a>	Alignment	not modelled	5.9	12
					<b>Fold:</b> Toxins' membrane translocation domains <b>Superfamily:</b> Colicin <b>Family:</b> Colicin
55	<a href="#">c6nbxG_</a>	Alignment	not modelled	5.3	9
					<b>PDB header:</b> oxidoreductase <b>Chain:</b> G; <b>PDB Molecule:</b> nadh-quinone oxidoreductase subunit j; <b>PDBTitle:</b> t.elongatus ndh (data-set 2)