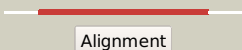

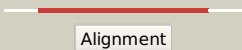

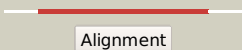







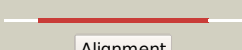















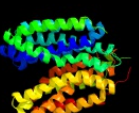




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2456c (-)_2756946_2758202
Date	Wed Aug 7 12:50:08 BST 2019
Unique Job ID	f9fd70b3f76cc0de

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6e9oA_	 Alignment		100.0	14	PDB header: membrane protein Chain: A: PDB Molecule: d-galactonate transport; PDBTitle: e. coli d-galactonate:proton symporter mutant e133q in the outward2 substrate-bound form
2	c3wdoA_	 Alignment		100.0	17	PDB header: transport protein Chain: A: PDB Molecule: mfs transporter; PDBTitle: structure of e. coli yajr transporter
3	c4ldsB_	 Alignment		100.0	14	PDB header: transport protein, membrane protein Chain: B: PDB Molecule: bicyclomycin resistance protein tcb; PDBTitle: the inward-facing structure of the glucose transporter from2 staphylococcus epidermidis
4	c4j05A_	 Alignment		100.0	13	PDB header: transport protein Chain: A: PDB Molecule: phosphate transporter; PDBTitle: crystal structure of a eukaryotic phosphate transporter
5	d1pv7a_	 Alignment		100.0	12	Fold: MFS general substrate transporter Superfamily: MFS general substrate transporter Family: LacY-like proton/sugar symporter
6	c1pv7B_	 Alignment		100.0	12	PDB header: transport protein Chain: B: PDB Molecule: lactose permease; PDBTitle: crystal structure of lactose permease with tdg
7	d1pw4a_	 Alignment		100.0	11	Fold: MFS general substrate transporter Superfamily: MFS general substrate transporter Family: Glycerol-3-phosphate transporter
8	c6h7dA_	 Alignment		100.0	12	PDB header: membrane protein Chain: A: PDB Molecule: sugar transport protein 10; PDBTitle: crystal structure of a. thaliana sugar transport protein 10 in complex2 with glucose in the outward occluded state
9	c6gs7A_	 Alignment		100.0	14	PDB header: membrane protein Chain: A: PDB Molecule: dipeptide and tripeptide permease a; PDBTitle: crystal structure of peptide transporter dtpa-nanobody in glycine2 buffer
10	c4ikyA_	 Alignment		100.0	14	PDB header: transport protein Chain: A: PDB Molecule: di-tripeptide abc transporter (permease); PDBTitle: crystal structure of peptide transporter pot (e310q mutant) in complex2 with sulfate
11	c6exsA_	 Alignment		100.0	13	PDB header: membrane protein Chain: A: PDB Molecule: peptide abc transporter permease; PDBTitle: crystal structure of a pot family transporter in complex with2 thioalcohol conjugated peptide.

12	c4zp0A_	Alignment		100.0	10	PDB header: transport protein Chain: A: PDB Molecule: multidrug transporter mdfa; PDBTitle: crystal structure of e. coli multidrug transporter mdfa in complex2 with deoxycholate
13	c4cl5B_	Alignment		100.0	12	PDB header: transport protein Chain: B: PDB Molecule: nitrate transporter 1.1; PDBTitle: crystal structure of the nitrate transporter nrt1.1 from2 arabidopsis thaliana in complex with nitrate.
14	c4w6vA_	Alignment		100.0	13	PDB header: transport protein Chain: A: PDB Molecule: di-/tripeptide transporter; PDBTitle: crystal structure of a peptide transporter from yersinia2 enterocolitica at 3 a resolution
15	c3o7pA_	Alignment		100.0	13	PDB header: transport protein Chain: A: PDB Molecule: l-fucose-proton symporter; PDBTitle: crystal structure of the e.coli fucose:proton symporter, fucp (n162a)
16	c4apsB_	Alignment		100.0	17	PDB header: transport protein Chain: B: PDB Molecule: di- or tripeptide h+ symporter; PDBTitle: crystal structure of a pot family peptide transporter in an inward2 open conformation.
17	c5c65A_	Alignment		100.0	11	PDB header: transport protein Chain: A: PDB Molecule: solute carrier family 2, facilitated glucose transporter PDBTitle: structure of the human glucose transporter glut3 / slc2a3
18	c6g9xB_	Alignment		100.0	15	PDB header: membrane protein Chain: B: PDB Molecule: major facilitator superfamily mfs_1; PDBTitle: crystal structure of a mfs transporter at 2.54 angstrom resolution
19	c6ei3A_	Alignment		100.0	15	PDB header: membrane protein Chain: A: PDB Molecule: proton-dependent oligopeptide transporter family protein; PDBTitle: crystal structure of auto inhibited pot family peptide transporter
20	c4ybgB_	Alignment		100.0	11	PDB header: transport protein/immune system Chain: B: PDB Molecule: solute carrier family 2, facilitated glucose transporter PDBTitle: rat glut5 with fv in the outward-open form
21	c4lepB_	Alignment	not modelled	100.0	13	PDB header: membrane protein, transport protein Chain: B: PDB Molecule: proton:oligopeptide symporter pot family; PDBTitle: structural insights into substrate recognition in proton dependent2 oligopeptide transporters
22	c4q65A_	Alignment	not modelled	100.0	13	PDB header: transport protein Chain: A: PDB Molecule: dipeptide permease d; PDBTitle: structure of the e. coli peptide transporter ybgh
23	c2gfpA_	Alignment	not modelled	100.0	12	PDB header: membrane protein Chain: A: PDB Molecule: multidrug resistance protein d; PDBTitle: structure of the multidrug transporter emrd from2 escherichia coli
24	c4pypA_	Alignment	not modelled	100.0	9	PDB header: transport protein Chain: A: PDB Molecule: solute carrier family 2, facilitated glucose transporter PDBTitle: crystal structure of the human glucose transporter glut1
25	c2xutC_	Alignment	not modelled	100.0	9	PDB header: transport protein Chain: C: PDB Molecule: proton/peptide symporter family protein; PDBTitle: crystal structure of a proton dependent oligopeptide (pot) family2 transporter.
26	c5aynA_	Alignment	not modelled	100.0	11	PDB header: transport protein Chain: A: PDB Molecule: solute carrier family 39 (iron-regulated transporter); PDBTitle: crystal structure of a bacterial homologue of iron transporter2 ferroportin in outward-facing state
27	c4gbzA_	Alignment	not modelled	100.0	12	PDB header: transport protein Chain: A: PDB Molecule: d-xylose-proton symporter; PDBTitle: the structure of the mfs (major facilitator superfamily) proton:xylose2 symporter xyle bound to d-glucose
28	c4iu8A_	Alignment	not modelled	100.0	11	PDB header: transport protein Chain: A: PDB Molecule: nitrite extrusion protein 2; PDBTitle: crystal structure of a membrane transporter (selenomethionine2 derivative)

29	c4iu9A_	Alignment	not modelled	100.0	11	PDB header: transport protein Chain: A: PDB Molecule: nitrite extrusion protein 2; PDBTitle: crystal structure of a membrane transporter
30	c5aymA_	Alignment	not modelled	100.0	11	PDB header: transport protein Chain: A: PDB Molecule: solute carrier family 39 (iron-regulated transporter); PDBTitle: crystal structure of a bacterial homologue of iron transporter2 ferroportin in outward-facing state with soaked iron
31	c4m64D_	Alignment	not modelled	99.9	10	PDB header: transport protein Chain: D: PDB Molecule: melibiose carrier protein; PDBTitle: 3d crystal structure of na+/melibiose symporter of salmonella2 typhimurium
32	c6ob7A_	Alignment	not modelled	99.7	9	PDB header: transport protein Chain: A: PDB Molecule: equilibrative nucleoside transporter 1; PDBTitle: human equilibrative nucleoside transporter-1, dilazep bound
33	c5xjIA_	Alignment	not modelled	75.3	9	PDB header: transport protein Chain: A: PDB Molecule: multi drug efflux transporter; PDBTitle: crystal structure of a mate family protein
34	c5y50A_	Alignment	not modelled	65.0	8	PDB header: membrane protein Chain: A: PDB Molecule: protein detoxification 14; PDBTitle: crystal structure of eukaryotic mate transporter atdtx14
35	c3mkuB_	Alignment	not modelled	52.2	12	PDB header: transport protein Chain: B: PDB Molecule: multi antimicrobial extrusion protein (na(+))/drug PDBTitle: structure of a cation-bound multidrug and toxin compound extrusion2 (mate) transporter
36	c3vvpA_	Alignment	not modelled	28.3	9	PDB header: transport protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of mate in complex with br-nrf
37	c3tijA_	Alignment	not modelled	19.6	17	PDB header: membrane protein Chain: A: PDB Molecule: snupc family protein; PDBTitle: crystal structure of a concentrative nucleoside transporter from2 vibrio cholerae
38	c5l2bC_	Alignment	not modelled	15.8	15	PDB header: transport protein Chain: C: PDB Molecule: nucleoside permease; PDBTitle: structure of cntnw n149s, e332a in an outward-facing state
39	c4n7wA_	Alignment	not modelled	14.0	13	PDB header: transport protein Chain: A: PDB Molecule: transporter, sodium/bile acid symporter family; PDBTitle: crystal structure of the sodium bile acid symporter from yersinia2 frederiksenii
40	c3hd6A_	Alignment	not modelled	12.8	14	PDB header: membrane protein, transport protein Chain: A: PDB Molecule: ammonium transporter rh type c; PDBTitle: crystal structure of the human rhesus glycoprotein rhcg
41	c3kpaB_	Alignment	not modelled	9.0	30	PDB header: ligase Chain: B: PDB Molecule: probable ubiquitin fold modifier conjugating enzyme; PDBTitle: ubiquitin fold modifier conjugating enzyme from leishmania major2 (probable)
42	c6fv6A_	Alignment	not modelled	8.7	9	PDB header: membrane protein Chain: A: PDB Molecule: aq128; PDBTitle: monomer structure of the mate family multidrug resistance transporter2 aq_128 from aquifex aeolicus in the outward-facing state
43	c3lk2T_	Alignment	not modelled	8.6	33	PDB header: protein binding Chain: T: PDB Molecule: leucine-rich repeat-containing protein 16a; PDBTitle: crystal structure of capz bound to the uncapping motif from carmil
44	c2nuuF_	Alignment	not modelled	8.2	12	PDB header: transport protein/signaling protein Chain: F: PDB Molecule: ammonia channel; PDBTitle: regulating the escherichia coli ammonia channel: the crystal structure2 of the amtb-glnk complex
45	c2kncA_	Alignment	not modelled	7.7	12	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iib; PDBTitle: platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
46	c5a1sB_	Alignment	not modelled	7.3	17	PDB header: transport protein Chain: B: PDB Molecule: citrate-sodium symporter; PDBTitle: crystal structure of the sodium-dependent citrate symporter secits2 form salmonella enterica.
47	c3qngD_	Alignment	not modelled	7.1	15	PDB header: membrane protein, transport protein Chain: D: PDB Molecule: pts system, cellobiose-specific iic component; PDBTitle: crystal structure of the transporter chbc, the iic component from the2 n,n'-diacetylchitobiose-specific phosphotransferase system
48	c6cc4A_	Alignment	not modelled	7.1	11	PDB header: transport protein Chain: A: PDB Molecule: soluble cytochrome b562, lipid ii flippase murj chimera; PDBTitle: structure of murj from escherichia coli
49	c2g9pA_	Alignment	not modelled	7.0	21	PDB header: antimicrobial protein Chain: A: PDB Molecule: antimicrobial peptide latarcin 2a; PDBTitle: nmr structure of a novel antimicrobial peptide, latarcin 2a,2 from spider (lachesana tarabaevi) venom
50	d2in1a1	Alignment	not modelled	6.6	30	Fold: UBC-like Superfamily: UBC-like Family: UFCl-like
51	c6ijjK_	Alignment	not modelled	6.4	5	PDB header: membrane protein Chain: K: PDB Molecule: psak; PDBTitle: photosystem i of chlamydomonas reinhardtii
52	c4k1cA_	Alignment	not modelled	6.2	11	PDB header: membrane protein/metal transport Chain: A: PDB Molecule: vacuolar calcium ion transporter; PDBTitle: vcx1 calcium/proton exchanger
53	c3is1A_	Alignment	not modelled	6.0	16	PDB header: hydrolase regulator Chain: A: PDB Molecule: phospholemman;

53	c4jv1b_	Alignment	not modelled	6.0	10	PDBTitle: structure of the na,k-atpase regulatory protein fxyd1 in2 micelles
54	c5aexl_	Alignment	not modelled	5.5	9	PDB header: membrane protein Chain: j: PDB Molecule: ammonium transporter mep2; PDBTitle: crystal structure of saccharomyces cerevisiae mep2