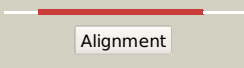

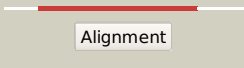

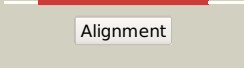

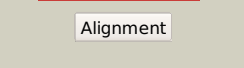

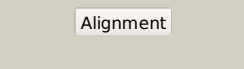

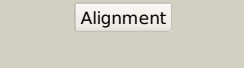

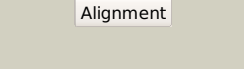

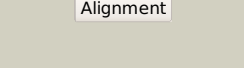

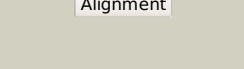

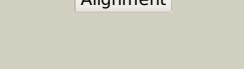

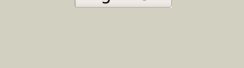

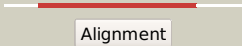

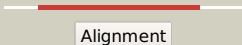

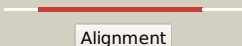



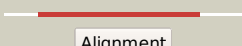

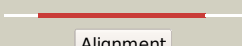

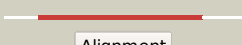






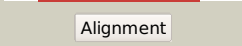


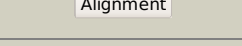
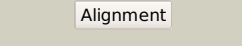
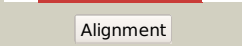
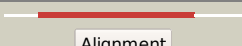


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2209 (-) _2473408_2474946
Date	Mon Aug 5 13:25:33 BST 2019
Unique Job ID	a6e70171f4d4ab8f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1pw4a_	 Alignment		100.0	10	Fold: MFS general substrate transporter Superfamily: MFS general substrate transporter Family: Glycerol-3-phosphate transporter
2	c4zp0A_	 Alignment		100.0	11	PDB header: transport protein Chain: A: PDB Molecule: multidrug transporter mdfa; PDBTitle: crystal structure of e. coli multidrug transporter mdfa in complex2 with deoxycholate
3	c3wdoA_	 Alignment		100.0	13	PDB header: transport protein Chain: A: PDB Molecule: mfs transporter; PDBTitle: structure of e. coli yajr transporter
4	c6e9oA_	 Alignment		100.0	13	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
5	c4ldsB_	 Alignment		100.0	13	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
6	c3o7pA_	 Alignment		100.0	10	PDB header: transport protein Chain: A: PDB Molecule: l-fucose-proton symporter; PDBTitle: crystal structure of the e.coli fucose:proton symporter, fucp (n162a)
7	c6g9xB_	 Alignment		100.0	9	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
8	c6h7dA_	 Alignment		100.0	14	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	c2gfpA_	 Alignment		100.0	14	PDB header: membrane protein Chain: A: PDB Molecule: multidrug resistance protein d; PDBTitle: structure of the multidrug transporter emrd from2 escherichia coli
10	c4j05A_	 Alignment		100.0	12	PDB header: transport protein Chain: A: PDB Molecule: phosphate transporter; PDBTitle: crystal structure of a eukaryotic phosphate transporter
11	c5aynA_	 Alignment		100.0	12	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

12	c4apsB_	 Alignment		100.0	9	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.
13	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
14	c4ybgB_	 Alignment		100.0	14	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
15	c5c65A_	 Alignment		100.0	14	PDB header: transport protein Chain: A: PDB Molecule: solute carrier family 2, facilitated glucose transporter PDBTitle: structure of the human glucose transporter glut3 / slc2a3
16	c6exsA_	 Alignment		100.0	11	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.
17	d1pv7a_	 Alignment		100.0	12	Fold: MFS general substrate transporter Superfamily: MFS general substrate transporter Family: LacY-like proton/sugar symporter
18	c4cl5B_	 Alignment		100.0	8	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.
19	c1pv7B_	 Alignment		100.0	12	PDB header: transport protein Chain: B: PDB Molecule: lactose permease; PDBTitle: crystal structure of lactose permease with tdg
20	c5aymA_	 Alignment		100.0	13	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
21	c6gs7A_	 Alignment	not modelled	100.0	12	PDB header: membrane protein Chain: A: PDB Molecule: dipeptide and tripeptide permease a; PDBTitle: crystal structure of peptide transporter dtpa-nanobody in glycine2 buffer
22	c4pypA_	 Alignment	not modelled	100.0	14	PDB header: transport protein Chain: A: PDB Molecule: solute carrier family 2, facilitated glucose transporter PDBTitle: crystal structure of the human glucose transporter glut1
23	c6ei3A_	 Alignment	not modelled	100.0	13	PDB header: membrane protein Chain: A: PDB Molecule: proton-dependent oligopeptide transporter family protein; PDBTitle: crystal structure of auto inhibited pot family peptide transporter
24	c4q65A_	 Alignment	not modelled	100.0	12	PDB header: transport protein Chain: A: PDB Molecule: dipeptide permease d; PDBTitle: structure of the e. coli peptide transporter ybgh
25	c4w6vA_	 Alignment	not modelled	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
26	c4gbzA_	 Alignment	not modelled	100.0	15	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
27	c2xutC_	 Alignment	not modelled	100.0	12	PDB header: transport protein Chain: C: PDB Molecule: proton/peptide symporter family protein; PDBTitle: crystal structure of a proton dependent oligopeptide (pot) family2 transporter.
28	c4lepB_	 Alignment	not modelled	99.9	12	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

29	c4iu9A_	Alignment	not modelled	99.9	12	PDB header: transport protein Chain: A: PDB Molecule: nitrite extrusion protein 2; PDBTitle: crystal structure of a membrane transporter
30	c4iu8A_	Alignment	not modelled	99.9	12	PDB header: transport protein Chain: A: PDB Molecule: nitrite extrusion protein 2; PDBTitle: crystal structure of a membrane transporter (selenomethionine2 derivative)
31	c4m64D_	Alignment	not modelled	99.8	7	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	99.8	10	PDB header: transport protein Chain: A: PDB Molecule: equilibrative nucleoside transporter 1; PDBTitle: human equilibrative nucleoside transporter-1, dilazep bound
33	c5bz3A_	Alignment	not modelled	30.5	14	PDB header: transport protein Chain: A: PDB Molecule: na(+)/h(+) antiporter; PDBTitle: crystal structure of sodium proton antiporter napa in outward-facing2 conformation.
34	c5gxwB_	Alignment	not modelled	13.3	33	PDB header: protein binding Chain: B: PDB Molecule: peptide from nuclear mitotic apparatus protein 1; PDBTitle: importin and numa complex
35	c4bwzA_	Alignment	not modelled	13.1	12	PDB header: transport protein Chain: A: PDB Molecule: na(+)/h(+) antiporter; PDBTitle: crystal structure of the sodium proton antiporter, napa
36	c2jmvA_	Alignment	not modelled	12.2	21	PDB header: antiviral protein Chain: A: PDB Molecule: scytovirin; PDBTitle: solution structure of scytovirin refined against residual2 dipolar couplings
37	c2g9pA_	Alignment	not modelled	10.1	14	PDB header: antimicrobial protein Chain: A: PDB Molecule: antimicrobial peptide laticin 2a; PDBTitle: nmr structure of a novel antimicrobial peptide, laticin 2a,2 from spider (lachesana tarabaevi) venom
38	d2eiaa2	Alignment	not modelled	9.4	36	Fold: Retrovirus capsid protein, N-terminal core domain Superfamily: Retrovirus capsid protein, N-terminal core domain Family: Retrovirus capsid protein, N-terminal core domain
39	c2kvtA_	Alignment	not modelled	9.0	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein yaia; PDBTitle: solution nmr structure of yaia from escherichia eoli. northeast2 structural genomics target er244
40	c3ukwC_	Alignment	not modelled	8.4	33	PDB header: protein transport/inhibitor Chain: C: PDB Molecule: bimax1 peptide; PDBTitle: mouse importin alpha: bimax1 peptide complex
41	c3lfmA_	Alignment	not modelled	8.1	32	PDB header: oxidoreductase Chain: A: PDB Molecule: protein fto; PDBTitle: crystal structure of the fat mass and obesity associated (fto) protein2 reveals basis for its substrate specificity
42	c6cc4A_	Alignment	not modelled	7.5	10	PDB header: transport protein Chain: A: PDB Molecule: soluble cytochrome b562, lipid ii flippase murj chimera; PDBTitle: structure of murj from escherichia coli
43	c5sxpG_	Alignment	not modelled	7.3	33	PDB header: signaling protein/ligase Chain: G: PDB Molecule: e3 ubiquitin-protein ligase itchy homolog; PDBTitle: structural basis for the interaction between itch prr and beta-pix
44	c3vvpA_	Alignment	not modelled	6.7	14	PDB header: transport protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of mate in complex with br-nrf
45	c5kzoA_	Alignment	not modelled	6.6	24	PDB header: transcription Chain: A: PDB Molecule: neurogenic locus notch homolog protein 1; PDBTitle: notch1 transmembrane and associated juxtamembrane segment
46	c5v2sA_	Alignment	not modelled	6.2	17	PDB header: viral protein Chain: A: PDB Molecule: envelope glycoprotein b; PDBTitle: crystal structure of glycoprotein b from herpes simplex virus type i
47	c1rb8J_	Alignment	not modelled	5.8	59	PDB header: virus/dna Chain: J: PDB Molecule: small core protein; PDBTitle: the phix174 dna binding protein j in two different capsid2 environments.