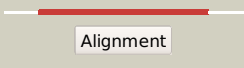
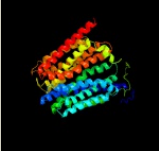
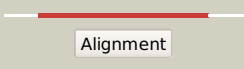

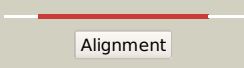

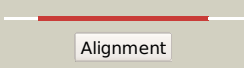

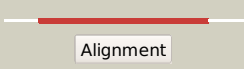
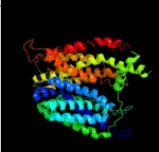
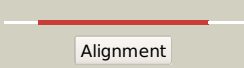

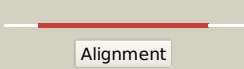
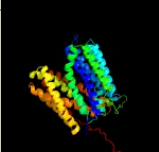
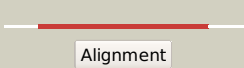
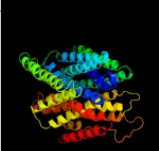
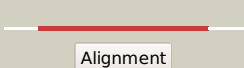

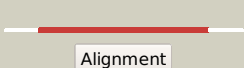

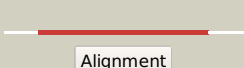



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0783c_(emrB)_876821_878443
Date	Fri Jul 26 01:50:36 BST 2019
Unique Job ID	512db821a77285d7

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1pw4a_	 Alignment		100.0	12	Fold: MFS general substrate transporter Superfamily: MFS general substrate transporter Family: Glycerol-3-phosphate transporter
2	c6e9oA_	 Alignment		100.0	15	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
3	c4zp0A_	 Alignment		100.0	17	PDB header: transport protein Chain: A: PDB Molecule: multidrug transporter mdfa; PDBTitle: crystal structure of e. coli multidrug transporter mdfa in complex2 with deoxycholate
4	c4ldsB_	 Alignment		100.0	16	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
5	c4cl5B_	 Alignment		100.0	11	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.
6	c6gs7A_	 Alignment		100.0	10	PDB header: membrane protein Chain: A: PDB Molecule: dipeptide and tripeptide permease a; PDBTitle: crystal structure of peptide transporter dtpa-nanobody in glycine2 buffer
7	c3wdoA_	 Alignment		100.0	17	PDB header: transport protein Chain: A: PDB Molecule: mfs transporter; PDBTitle: structure of e. coli yajr transporter
8	c4apsB_	 Alignment		100.0	14	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.
9	c4ikyA_	 Alignment		100.0	13	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
10	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
11	c6exsA_	 Alignment		100.0	15	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	c2gfpA_	Alignment		100.0	21	PDB header: membrane protein Chain: A: PDB Molecule: multidrug resistance protein d; PDBTitle: structure of the multidrug transporter emrd from2 escherichia coli
13	c6h7dA_	Alignment		100.0	13	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
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	c5c65A_	Alignment		100.0	13	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	c6ei3A_	Alignment		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
17	c4gbzA_	Alignment		100.0	11	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
18	c4j05A_	Alignment		100.0	16	PDB header: transport protein Chain: A: PDB Molecule: phosphate transporter; PDBTitle: crystal structure of a eukaryotic phosphate transporter
19	c3o7pA_	Alignment		100.0	15	PDB header: transport protein Chain: A: PDB Molecule: l-fucose-proton symporter; PDBTitle: crystal structure of the e.coli fucose:proton symporter, fucp (n162a)
20	c2xutC_	Alignment		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.
21	c4ppyA_	Alignment	not modelled	100.0	11	PDB header: transport protein Chain: A: PDB Molecule: solute carrier family 2, facilitated glucose transporter PDBTitle: crystal structure of the human glucose transporter glut1
22	c4ybyqB_	Alignment	not modelled	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
23	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
24	c4iu8A_	Alignment	not modelled	100.0	14	PDB header: transport protein Chain: A: PDB Molecule: nitrite extrusion protein 2; PDBTitle: crystal structure of a membrane transporter (selenomethionine2 derivative)
25	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
26	c4iu9A_	Alignment	not modelled	100.0	12	PDB header: transport protein Chain: A: PDB Molecule: nitrite extrusion protein 2; PDBTitle: crystal structure of a membrane transporter
27	d1pv7a_	Alignment	not modelled	100.0	12	Fold: MFS general substrate transporter Superfamily: MFS general substrate transporter Family: LacY-like proton/sugar symporter
28	c1pv7B_	Alignment	not modelled	100.0	12	PDB header: transport protein Chain: B: PDB Molecule: lactose permease; PDBTitle: crystal structure of lactose permease with tdg
						PDB header: transport protein

29	c5aynA_	Alignment	not modelled	100.0	14	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
30	c5aymA_	Alignment	not modelled	100.0	15	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	9	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	11	PDB header: transport protein Chain: A; PDB Molecule: equilibrative nucleoside transporter 1; PDBTitle: human equilibrative nucleoside transporter-1, dilazep bound
33	c4kppA_	Alignment	not modelled	65.1	8	PDB header: membrane protein Chain: A; PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of h+/ca2+ exchanger cax
34	c2w2eA_	Alignment	not modelled	64.0	11	PDB header: membrane protein Chain: A; PDB Molecule: aquaporin pip2-7 7; PDBTitle: 1.15 angstrom crystal structure of p.pastoris aquaporin, aqy1, in a2 closed conformation at ph 3.5
35	c3b9yA_	Alignment	not modelled	36.1	11	PDB header: transport protein Chain: A; PDB Molecule: ammonium transporter family rh-like protein; PDBTitle: crystal structure of the nitrosomonas europaea rh protein
36	c2g9pA_	Alignment	not modelled	21.4	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
37	c6adqP_	Alignment	not modelled	15.5	8	PDB header: electron transport Chain: P; PDB Molecule: prokaryotic respiratory supercomplex associate factor 1 PDBTitle: respiratory complex ciii2civ2sod2 from mycobacterium smegmatis
38	c5xpdA_	Alignment	not modelled	13.3	10	PDB header: transport protein Chain: A; PDB Molecule: sugar transporter; PDBTitle: sugar transporter of atsweet13 in inward-facing state with a substrate2 analog
39	d1xmea1	Alignment	not modelled	7.8	15	Fold: Cytochrome c oxidase subunit I-like Superfamily: Cytochrome c oxidase subunit I-like Family: Cytochrome c oxidase subunit I-like
40	c2jraB_	Alignment	not modelled	7.3	13	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: protein rpa2121; PDBTitle: a novel domain-swapped solution nmr structure of protein rpa2121 from2 rhodospseudomonas palustris. northeast structural genomics target rpt6
41	c3v5uA_	Alignment	not modelled	6.9	9	PDB header: metal transport Chain: A; PDB Molecule: uncharacterized membrane protein mj0091; PDBTitle: structure of sodium/calcium exchanger from methanocaldococcus2 jannaschii dsm 2661
42	c3eh4A_	Alignment	not modelled	6.9	15	PDB header: oxidoreductase Chain: A; PDB Molecule: cytochrome c oxidase subunit 1; PDBTitle: structure of the reduced form of cytochrome ba3 oxidase from thermus2 thermophilus
43	c2jpwA_	Alignment	not modelled	6.7	21	PDB header: contractile protein Chain: A; PDB Molecule: troponin i, cardiac muscle; PDBTitle: solution structure of the bisphosphorylated cardiac2 specific n-extension of cardiac troponin i
44	c5y50A_	Alignment	not modelled	6.6	8	PDB header: membrane protein Chain: A; PDB Molecule: protein detoxification 14; PDBTitle: crystal structure of eukaryotic mate transporter atdtx14
45	d3proc1	Alignment	not modelled	6.6	12	Fold: Alpha-lytic protease prodomain-like Superfamily: Alpha-lytic protease prodomain Family: Alpha-lytic protease prodomain
46	c4dveA_	Alignment	not modelled	6.3	15	PDB header: transport protein Chain: A; PDB Molecule: biotin transporter bioy; PDBTitle: crystal structure at 2.1 a of the s-component for biotin from an ecf-2 type abc transporter