

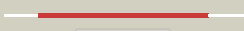








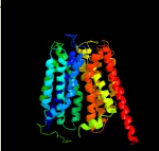





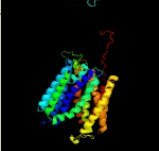

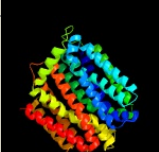

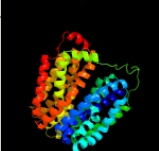


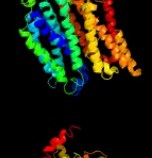
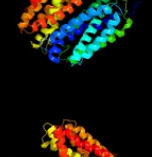

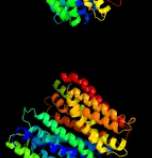
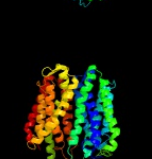

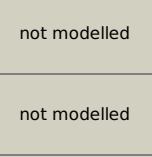


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD1902c_(nanT)_2149013_2150281
 Date Fri Aug 2 13:30:52 BST 2019
 Unique Job ID 50ef6b0a723ff18e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	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
2	c5c65A_	 Alignment		100.0	15	PDB header: transport protein Chain: A: PDB Molecule: solute carrier family 2, facilitated glucose transporter PDBTitle: structure of the human glucose transporter glut3 / slc2a3
3	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
4	c4j05A_	 Alignment		100.0	14	PDB header: transport protein Chain: A: PDB Molecule: phosphate transporter; PDBTitle: crystal structure of a eukaryotic phosphate transporter
5	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
6	d1pw4a_	 Alignment		100.0	14	Fold: MFS general substrate transporter Superfamily: MFS general substrate transporter Family: Glycerol-3-phosphate transporter
7	c4ldsB_	 Alignment		100.0	16	PDB header: transport protein, membrane protein Chain: B: PDB Molecule: bicyclomycin resistance protein tcab; PDBTitle: the inward-facing structure of the glucose transporter from2 staphylococcus epidermidis
8	c4gbzA_	 Alignment		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
9	c3wdoA_	 Alignment		100.0	13	PDB header: transport protein Chain: A: PDB Molecule: mfs transporter; PDBTitle: structure of e. coli yajr transporter
10	c4zp0A_	 Alignment		100.0	16	PDB header: transport protein Chain: A: PDB Molecule: multidrug transporter mdfa; PDBTitle: crystal structure of e. coli multidrug transporter mdfa in complex2 with deoxycholate
11	d1pv7a_	 Alignment		100.0	11	Fold: MFS general substrate transporter Superfamily: MFS general substrate transporter Family: LacY-like proton/sugar symporter

12	c1pv7B_	Alignment		100.0	11	PDB header: transport protein Chain: B: PDB Molecule: lactose permease; PDBTitle: crystal structure of lactose permease with tdg
13	c6g9xB_	Alignment		100.0	14	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
14	c4pypA_	Alignment		100.0	17	PDB header: transport protein Chain: A: PDB Molecule: solute carrier family 2, facilitated glucose transporter PDBTitle: crystal structure of the human glucose transporter glut1
15	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.
16	c3o7pA_	Alignment		100.0	11	PDB header: transport protein Chain: A: PDB Molecule: l-fucose-proton symporter; PDBTitle: crystal structure of the e.coli fucose:proton symporter, fucp (n162a)
17	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
18	c4w6vA_	Alignment		100.0	14	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
19	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.
20	c6gs7A_	Alignment		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
21	c4apsB_	Alignment	not modelled	100.0	13	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.
22	c4iu8A_	Alignment	not modelled	100.0	10	PDB header: transport protein Chain: A: PDB Molecule: nitrite extrusion protein 2; PDBTitle: crystal structure of a membrane transporter (selenomethionine2 derivative)
23	c2gfpA_	Alignment	not modelled	100.0	17	PDB header: membrane protein Chain: A: PDB Molecule: multidrug resistance protein d; PDBTitle: structure of the multidrug transporter emrd from2 escherichia coli
24	c4iu9A_	Alignment	not modelled	99.9	11	PDB header: transport protein Chain: A: PDB Molecule: nitrite extrusion protein 2; PDBTitle: crystal structure of a membrane transporter
25	c6ei3A_	Alignment	not modelled	99.9	14	PDB header: membrane protein Chain: A: PDB Molecule: proton-dependent oligopeptide transporter family protein; PDBTitle: crystal structure of auto inhibited pot family peptide transporter
26	c4lepB_	Alignment	not modelled	99.9	11	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
27	c4q65A_	Alignment	not modelled	99.9	13	PDB header: transport protein Chain: A: PDB Molecule: dipeptide permease d; PDBTitle: structure of the e. coli peptide transporter ybgh
28	c5aynA_	Alignment	not modelled	99.9	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 PDB header: transport protein Chain: C: PDB Molecule: proton/peptide symporter family protein; PDBTitle: crystal structure of a proton dependent oligopeptide (pot) family2 transporter.
29	c2xutC_	Alignment	not modelled	99.9	9	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
30	c5aymA_	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
31	c4m64D_	Alignment	not modelled	99.8	9	PDB header: transport protein Chain: A: PDB Molecule: equilibrative nucleoside transporter 1; PDBTitle: human equilibrative nucleoside transporter-1, dilazep bound
32	c6ob7A_	Alignment	not modelled	99.6	11	PDB header: transport protein Chain: A: PDB Molecule: multi drug efflux transporter; PDBTitle: crystal structure of a mate family protein
33	c5xjA_	Alignment	not modelled	66.2	7	PDB header: membrane protein Chain: A: PDB Molecule: protein detoxification 14; PDBTitle: crystal structure of eukaryotic mate transporter atdtx14
34	c5y50A_	Alignment	not modelled	59.9	9	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
35	c3qngD_	Alignment	not modelled	36.9	9	PDB header: protein transport Chain: B: PDB Molecule: peroxisomal biogenesis factor 14; PDBTitle: crystal structure of the conserved n-terminal domain of the2 peroxisomal matrix-protein-import receptor, pex14p
36	c3ff5B_	Alignment	not modelled	34.4	19	PDB header: signaling protein Chain: B: PDB Molecule: peroxin 14; PDBTitle: crystal structure of the conserved n-terminal domain of2 pex14 from trypanosoma brucei
37	c5aonB_	Alignment	not modelled	31.9	19	PDB header: membrane protein Chain: B: PDB Molecule: aminobenzoyl-glutamate transporter; PDBTitle: structure and function of neisseria gonorrhoeae mtrf illuminates a2 class of antimetabolite efflux pumps
38	c4r1iB_	Alignment	not modelled	31.7	11	PDB header: transport protein Chain: A: PDB Molecule: ammonium transporter family rh-like protein; PDBTitle: crystal structure of the nitrosomonas europaea rh protein
39	c3b9yA_	Alignment	not modelled	31.7	12	PDB header: membrane protein Chain: A: PDB Molecule: peroxin 14; PDBTitle: targeting the pex14-pex5 interaction by small molecules provides novel2 therapeutic routes to treat trypanosomiasis.
40	c5l87A_	Alignment	not modelled	25.5	15	PDB header: oxidoreductase Chain: G: PDB Molecule: nadh-ubiquinone oxidoreductase 75 kda subunit, PDBTitle: structure of mammalian respiratory complex i, class1
41	c5ldwg_	Alignment	not modelled	23.6	18	PDB header: membrane protein Chain: A: PDB Molecule: ammonium transporter; PDBTitle: sensor amt protein
42	c6eu6A_	Alignment	not modelled	23.3	5	PDB header: protein transport Chain: A: PDB Molecule: peroxisomal membrane anchor protein pex14; PDBTitle: structure of pex14 in complex with pex19
43	c2w85A_	Alignment	not modelled	20.4	19	PDB header: transport protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of mate in complex with br-nrf
44	c3vvpA_	Alignment	not modelled	19.8	9	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
45	c3mkuB_	Alignment	not modelled	18.0	8	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
46	c2g9pA_	Alignment	not modelled	17.6	36	PDB header: transport protein Chain: A: PDB Molecule: probable glutamate/gamma-aminobutyrate antiporter; PDBTitle: structure of glutamate-gaba antiporter gadc
47	c4djiA_	Alignment	not modelled	16.0	17	Fold: Cytochrome c Superfamily: Cytochrome c Family: Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
48	d1pbya1	Alignment	not modelled	15.7	10	PDB header: transport protein Chain: A: PDB Molecule: sodium/glucose cotransporter; PDBTitle: crystal structure of sodium/sugar symporter with bound galactose from2 vibrio parahaemolyticus
49	c3dh4A_	Alignment	not modelled	15.5	9	PDB header: protein transport/inhibitor Chain: C: PDB Molecule: bimax1 peptide; PDBTitle: mouse importin alpha: bimax1 peptide complex
50	c3ukwC_	Alignment	not modelled	15.5	21	PDB header: protein transport Chain: A: PDB Molecule: nuclear envelope pore membrane protein pom 121; PDBTitle: structure of mouse importin a1 bound to pom121nls
51	c4yi0A_	Alignment	not modelled	13.8	10	Fold: Cytochrome c Superfamily: Cytochrome c Family: Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
52	d1jmx1	Alignment	not modelled	13.2	8	PDB header: membrane protein, transport protein Chain: A: PDB Molecule: ammonium transporter rh type c; PDBTitle: crystal structure of the human rhesus glycoprotein rhcg
53	c3hd6A_	Alignment	not modelled	11.4	7	

54	c6humB_	Alignment	not modelled	9.4	10	PDB header: proton transport Chain: B: PDB Molecule: nad(p)h-quinone oxidoreductase subunit 2; PDBTitle: structure of the photosynthetic complex i from thermosynechococcus2 elongatus
55	d1u7ga_	Alignment	not modelled	8.7	15	Fold: Ammonium transporter Superfamily: Ammonium transporter Family: Ammonium transporter
56	c2ndjA_	Alignment	not modelled	8.3	18	PDB header: membrane protein Chain: A: PDB Molecule: potassium voltage-gated channel subfamily e member 3; PDBTitle: structural basis for kcne3 and estrogen modulation of the kcnq12 channel
57	c5aexJ_	Alignment	not modelled	7.8	13	PDB header: membrane protein Chain: J: PDB Molecule: ammonium transporter mep2; PDBTitle: crystal structure of saccharomyces cerevisiae mep2
58	c4lz9A_	Alignment	not modelled	7.7	11	PDB header: transport protein Chain: A: PDB Molecule: bh2163 protein; PDBTitle: structure of mate multidrug transporter dinf-bh in complex with r6g
59	c5nvaA_	Alignment	not modelled	7.5	7	PDB header: membrane protein Chain: A: PDB Molecule: putative sodium:solute symporter; PDBTitle: substrate-bound outward-open state of a na+-coupled sialic acid2 symporter reveals a novel na+-site
60	c2bbjB_	Alignment	not modelled	7.4	7	PDB header: metal transport/membrane protein Chain: B: PDB Molecule: divalent cation transport-related protein; PDBTitle: crystal structure of the cora mg2+ transporter
61	c5i20E_	Alignment	not modelled	6.9	11	PDB header: membrane protein Chain: E: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of protein
62	c3rgbG_	Alignment	not modelled	6.7	12	PDB header: oxidoreductase Chain: G: PDB Molecule: methane monooxygenase subunit c2; PDBTitle: crystal structure of particulate methane monooxygenase from2 methylococcus capsulatus (bath)
63	c3chxG_	Alignment	not modelled	6.5	12	PDB header: membrane protein Chain: G: PDB Molecule: pmoc; PDBTitle: crystal structure of methylosinus trichosporium ob3b particulate2 methane monooxygenase (pmmo)
64	c6oh2A_	Alignment	not modelled	6.4	7	PDB header: transport protein Chain: A: PDB Molecule: cmp-sialic acid transporter; PDBTitle: x-ray crystal structure of the mouse cmp-sialic acid transporter in2 complex with cmp, by lipidic cubic phase
65	c1yewC_	Alignment	not modelled	6.3	12	PDB header: oxidoreductase, membrane protein Chain: C: PDB Molecule: particulate methane monooxygenase subunit c2; PDBTitle: crystal structure of particulate methane monooxygenase
66	c2bcxB_	Alignment	not modelled	6.2	38	PDB header: calcium binding protein Chain: B: PDB Molecule: ryanodine receptor 1; PDBTitle: crystal structure of calmodulin in complex with a ryanodine receptor2 peptide
67	c5y79A_	Alignment	not modelled	6.2	7	PDB header: transport protein Chain: A: PDB Molecule: putative hexose phosphate translocator; PDBTitle: crystal structure of the triose-phosphate/phosphate translocator in2 complex with 3-phosphoglycerate
68	c2kncA_	Alignment	not modelled	6.0	13	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iiB; PDBTitle: platelet integrin alfaIIB-beta3 transmembrane-cytoplasmic2 heterocomplex
69	c3v5uA_	Alignment	not modelled	5.7	13	PDB header: metal transport Chain: A: PDB Molecule: uncharacterized membrane protein mj0091; PDBTitle: structure of sodium/calcium exchanger from methanocaldococcus2 jannaschii dsm 2661
70	c3lvge_	Alignment	not modelled	5.6	14	PDB header: structural protein Chain: E: PDB Molecule: clathrin light chain b; PDBTitle: crystal structure of a clathrin heavy chain and clathrin light chain2 complex
71	c2b6pA_	Alignment	not modelled	5.6	10	PDB header: membrane protein Chain: A: PDB Molecule: lens fiber major intrinsic protein; PDBTitle: x-ray structure of lens aquaporin-0 (aqp0) (lens mip) in an open pore2 state
72	c3rfrK_	Alignment	not modelled	5.5	12	PDB header: oxidoreductase Chain: K: PDB Molecule: pmoc; PDBTitle: crystal structure of particulate methane monooxygenase (pmmo) from2 methylocystis sp. strain m
73	d3cx5c2	Alignment	not modelled	5.5	5	Fold: Heme-binding four-helical bundle Superfamily: Transmembrane di-heme cytochromes Family: Cytochrome b of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
74	c5b16B_	Alignment	not modelled	5.5	13	PDB header: hydrolase Chain: B: PDB Molecule: microprocessor complex subunit dgcr8; PDBTitle: x-ray structure of drosha in complex with the c-terminal tail of2 dgcr8.
75	c4qtnB_	Alignment	not modelled	5.3	6	PDB header: transport protein Chain: B: PDB Molecule: nicotinamide riboside transporter pnuc; PDBTitle: crystal structure of the vitamin b3 transporter pnuc
76	c3twgB_	Alignment	not modelled	5.2	22	PDB header: unknown function Chain: B: PDB Molecule: alpha4f3af3d; PDBTitle: crystal structure of the de novo designed fluorinated peptide2 alpha4f3af3d
77	c5sv0C_	Alignment	not modelled	5.2	9	PDB header: transport protein Chain: C: PDB Molecule: biopolymer transport protein exbb; PDBTitle: structure of the exbb/exbd complex from e. coli at ph 7.0
78	c4z3pA_	Alignment	not modelled	5.1	8	PDB header: transport protein Chain: A: PDB Molecule: putative drug/sodium antiporter; PDBTitle: mate transporter clbm in complex with rb+