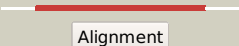



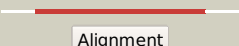





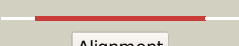











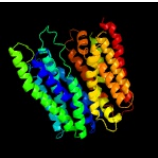


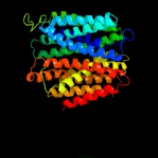
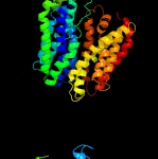
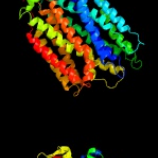
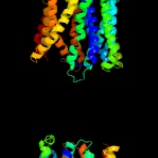
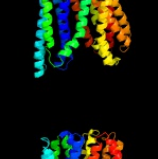
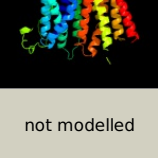


# Phyre2

Email [mdejesus@rockefeller.edu](mailto:mdejesus@rockefeller.edu)  
 Description RVBD1737c\_(narK2)\_1964190\_1965377  
 Date Fri Aug 2 13:30:34 BST 2019  
 Unique Job ID 2cdb87e82f28e437

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6e9oA_</a>	 Alignment		100.0	16	<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
2	<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
3	<a href="#">c4zp0A_</a>	 Alignment		100.0	14	<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
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="#">c6g9xB_</a>	 Alignment		100.0	16	<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
6	<a href="#">c2gfpA_</a>	 Alignment		100.0	11	<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
7	<a href="#">d1pv7a_</a>	 Alignment		100.0	12	<b>Fold:</b> MFS general substrate transporter <b>Superfamily:</b> MFS general substrate transporter <b>Family:</b> LacY-like proton/sugar symporter
8	<a href="#">c1pv7B_</a>	 Alignment		100.0	12	<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
9	<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
10	<a href="#">c4cl5B_</a>	 Alignment		100.0	16	<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.
11	<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

12	<a href="#">c4w6vA</a>	Alignment		100.0	16	<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
13	<a href="#">c4iu8A</a>	Alignment		100.0	15	<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)
14	<a href="#">c3o7pA</a>	Alignment		100.0	16	<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)
15	<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.
16	<a href="#">c4ikyA</a>	Alignment		100.0	13	<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
17	<a href="#">c4j05A</a>	Alignment		100.0	13	<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
18	<a href="#">c6exsA</a>	Alignment		100.0	11	<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.
19	<a href="#">c5aynA</a>	Alignment		100.0	10	<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
20	<a href="#">c4q65A</a>	Alignment		100.0	15	<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
21	<a href="#">c4iu9A</a>	Alignment	not modelled	100.0	16	<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
22	<a href="#">c6h7dA</a>	Alignment	not modelled	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
23	<a href="#">c5c65A</a>	Alignment	not modelled	100.0	13	<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
24	<a href="#">c6ei3A</a>	Alignment	not modelled	100.0	12	<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
25	<a href="#">c4lepB</a>	Alignment	not modelled	100.0	12	<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
26	<a href="#">c4pypA</a>	Alignment	not modelled	100.0	15	<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
27	<a href="#">c4yqbB</a>	Alignment	not modelled	100.0	15	<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
28	<a href="#">c2xutC</a>	Alignment	not modelled	100.0	13	<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.

29	<a href="#">c4gbzA_</a>	Alignment	not modelled	100.0	12	<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="#">c5aymA_</a>	Alignment	not modelled	100.0	9	<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
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	99.8	9	<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="#">c5xjA_</a>	Alignment	not modelled	93.9	10	<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
34	<a href="#">c5y50A_</a>	Alignment	not modelled	86.0	9	<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
35	<a href="#">c5kk2E_</a>	Alignment	not modelled	71.2	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
36	<a href="#">c3b9yA_</a>	Alignment	not modelled	36.7	11	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> ammonium transporter family rh-like protein; <b>PDBTitle:</b> crystal structure of the nitrosomonas europaea rh protein
37	<a href="#">c3vvpA_</a>	Alignment	not modelled	25.5	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
38	<a href="#">c4n7wA_</a>	Alignment	not modelled	23.5	12	<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
39	<a href="#">c6idrA_</a>	Alignment	not modelled	16.1	11	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> mate family efflux transporter; <b>PDBTitle:</b> crystal structure of vibrio cholerae mate transporter vcmn in the bent2 form
40	<a href="#">c2g9pA_</a>	Alignment	not modelled	12.7	36	<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
41	<a href="#">c6eu6A_</a>	Alignment	not modelled	9.8	11	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> ammonium transporter; <b>PDBTitle:</b> sensor amt protein
42	<a href="#">c5aexB_</a>	Alignment	not modelled	7.9	11	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> ammonium transporter mep2; <b>PDBTitle:</b> crystal structure of saccharomyces cerevisiae mep2
43	<a href="#">c6qkcJ_</a>	Alignment	not modelled	7.4	15	<b>PDB header:</b> membrane protein <b>Chain:</b> J: <b>PDB Molecule:</b> voltage-dependent calcium channel gamma-8 subunit; <b>PDBTitle:</b> glua1/2 in complex with auxiliary subunit gamma-8
44	<a href="#">c3qnqD_</a>	Alignment	not modelled	7.2	10	<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
45	<a href="#">c3mkuB_</a>	Alignment	not modelled	7.1	11	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> multi antimicrobial extrusion protein (na+ )/drug <b>PDBTitle:</b> structure of a cation-bound multidrug and toxin compound extrusion2 (mate) transporter
46	<a href="#">c4ainB_</a>	Alignment	not modelled	7.0	10	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> glycine betaine transporter betp; <b>PDBTitle:</b> crystal structure of betp with asymmetric protomers.
47	<a href="#">c1w8xP_</a>	Alignment	not modelled	6.0	26	<b>PDB header:</b> virus <b>Chain:</b> P: <b>PDB Molecule:</b> protein p16; <b>PDBTitle:</b> structural analysis of prd1