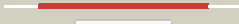



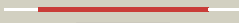



















# Phyre2

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Description	RVBD0849 (-) _946059_947318
Date	Fri Jul 26 01:50:43 BST 2019
Unique Job ID	7130035357425176

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3wdoA_</a>	 Alignment		100.0	15	<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
2	<a href="#">c6e9oA_</a>	 Alignment		100.0	11	<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
3	<a href="#">d1pv7a_</a>	 Alignment		100.0	10	<b>Fold:</b> MFS general substrate transporter <b>Superfamily:</b> MFS general substrate transporter <b>Family:</b> LacY-like proton/sugar symporter
4	<a href="#">c6exsA_</a>	 Alignment		100.0	13	<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.
5	<a href="#">c1pv7B_</a>	 Alignment		100.0	10	<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
6	<a href="#">c6gs7A_</a>	 Alignment		100.0	15	<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
7	<a href="#">c4ikyA_</a>	 Alignment		100.0	18	<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
8	<a href="#">c4apsB_</a>	 Alignment		100.0	17	<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.
9	<a href="#">c4cl5B_</a>	 Alignment		100.0	13	<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.
10	<a href="#">c4zp0A_</a>	 Alignment		100.0	13	<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
11	<a href="#">d1pw4a_</a>	 Alignment		100.0	10	<b>Fold:</b> MFS general substrate transporter <b>Superfamily:</b> MFS general substrate transporter <b>Family:</b> Glycerol-3-phosphate transporter

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="#">c6ei3A_</a>	Alignment		100.0	20	<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
14	<a href="#">c4ldsB_</a>	Alignment		100.0	15	<b>PDB header:</b> transport protein, membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> bicyclomycin resistance protein tcb; <b>PDBTitle:</b> the inward-facing structure of the glucose transporter from2 staphylococcus epidermidis
15	<a href="#">c6g9xB_</a>	Alignment		100.0	15	<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
16	<a href="#">c2gfpA_</a>	Alignment		100.0	17	<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
17	<a href="#">c5aynA_</a>	Alignment		100.0	11	<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
18	<a href="#">c4q65A_</a>	Alignment		100.0	17	<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
19	<a href="#">c4j05A_</a>	Alignment		100.0	10	<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
20	<a href="#">c4iu8A_</a>	Alignment		100.0	10	<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)
21	<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
22	<a href="#">c5aymA_</a>	Alignment	not modelled	100.0	11	<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
23	<a href="#">c2xutC_</a>	Alignment	not modelled	100.0	16	<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.
24	<a href="#">c3o7pA_</a>	Alignment	not modelled	100.0	13	<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)
25	<a href="#">c4iu9A_</a>	Alignment	not modelled	100.0	13	<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
26	<a href="#">c6h7dA_</a>	Alignment	not modelled	100.0	12	<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
27	<a href="#">c4ybgB_</a>	Alignment	not modelled	100.0	11	<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="#">c5c65A_</a>	Alignment	not modelled	100.0	12	<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

29	<a href="#">c4m64D_</a>	Alignment	not modelled	100.0	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
30	<a href="#">c4pypA_</a>	Alignment	not modelled	100.0	10	<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
31	<a href="#">c4gbzA_</a>	Alignment	not modelled	99.9	10	<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
32	<a href="#">c6ob7A_</a>	Alignment	not modelled	99.7	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	78.2	9	<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	74.4	11	<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="#">c4z3pA_</a>	Alignment	not modelled	47.1	10	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> putative drug/sodium antiporter; <b>PDBTitle:</b> mate transporter clbm in complex with rb+
36	<a href="#">c4lz9A_</a>	Alignment	not modelled	41.2	9	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> bh2163 protein; <b>PDBTitle:</b> structure of mate multidrug transporter dinf-bh in complex with r6g
37	<a href="#">c6nbxG_</a>	Alignment	not modelled	28.3	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G; <b>PDB Molecule:</b> nadh-quinone oxidoreductase subunit j; <b>PDBTitle:</b> t.elongatus ndh (data-set 2)
38	<a href="#">c3vvpA_</a>	Alignment	not modelled	12.4	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
39	<a href="#">c2g9pA_</a>	Alignment	not modelled	10.6	36	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A; <b>PDB Molecule:</b> antimicrobial peptide laticin 2a; <b>PDBTitle:</b> nmr structure of a novel antimicrobial peptide, laticin 2a,2 from spider (lachesana tarabaevi) venom
40	<a href="#">c2jp3A_</a>	Alignment	not modelled	8.3	16	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> fxyd domain-containing ion transport regulator 4; <b>PDBTitle:</b> solution structure of the human fxyd4 (chif) protein in sds2 micelles
41	<a href="#">c2m7gA_</a>	Alignment	not modelled	7.8	13	<b>PDB header:</b> cell adhesion, structural protein, elect <b>Chain:</b> A; <b>PDB Molecule:</b> geopilin domain 1 protein; <b>PDBTitle:</b> structure of the type iva major pilin from the electrically conductive2 bacterial nanowires of geobacter sulfurreducens
42	<a href="#">c6oh2A_</a>	Alignment	not modelled	6.8	10	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> cmp-sialic acid transporter; <b>PDBTitle:</b> x-ray crystal structure of the mouse cmp-sialic acid transporter in2 complex with cmp, by lipidic cubic phase
43	<a href="#">c2d1kC_</a>	Alignment	not modelled	5.9	22	<b>PDB header:</b> structural protein <b>Chain:</b> C; <b>PDB Molecule:</b> metastasis suppressor protein 1; <b>PDBTitle:</b> ternary complex of the wh2 domain of mim with actin-dnase i
44	<a href="#">c3ug9A_</a>	Alignment	not modelled	5.7	14	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> archaeal-type opsin 1, archaeal-type opsin 2; <b>PDBTitle:</b> crystal structure of the closed state of channelrhodopsin