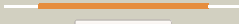

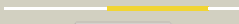





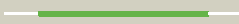



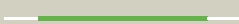
















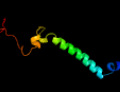
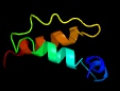


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0128 (-) _155665_156444
Date	Tue Jul 23 14:50:17 BST 2019
Unique Job ID	9f99bda4f4163968

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3wdoA_</a>	 Alignment		81.7	13	<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="#">c5edlA_</a>	 Alignment		75.9	15	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative hmp/thiamine permease protein ykoe; <b>PDBTitle:</b> crystal structure of an s-component of ecf transporter
3	<a href="#">c4w6vA_</a>	 Alignment		73.0	15	<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
4	<a href="#">c5aynA_</a>	 Alignment		58.4	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
5	<a href="#">d1pv7a_</a>	 Alignment		52.8	11	<b>Fold:</b> MFS general substrate transporter <b>Superfamily:</b> MFS general substrate transporter <b>Family:</b> LacY-like proton/sugar symporter
6	<a href="#">c1pv7B_</a>	 Alignment		52.8	11	<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
7	<a href="#">c5aymA_</a>	 Alignment		51.4	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
8	<a href="#">c1ldaA_</a>	 Alignment		51.1	17	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> glycerol uptake facilitator protein; <b>PDBTitle:</b> crystal structure of the e. coli glycerol facilitator (glpf) without2 substrate glycerol
9	<a href="#">d1fx8a_</a>	 Alignment		51.1	17	<b>Fold:</b> Aquaporin-like <b>Superfamily:</b> Aquaporin-like <b>Family:</b> Aquaporin-like
10	<a href="#">c4zp0A_</a>	 Alignment		47.4	10	<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="#">c6h7dA_</a>	 Alignment		44.0	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

12	<a href="#">d1bcce2</a>	Alignment		43.9	23	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> ISP transmembrane anchor <b>Family:</b> ISP transmembrane anchor
13	<a href="#">c6e9oA_</a>	Alignment		39.3	7	<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
14	<a href="#">c4xjnM_</a>	Alignment		39.2	19	<b>PDB header:</b> viral protein/rna <b>Chain:</b> M: <b>PDB Molecule:</b> nucleocapsid; <b>PDBTitle:</b> structure of the parainfluenza virus 5 nucleocapsid-rna complex: an2 insight into paramyxovirus polymerase activity
15	<a href="#">c4ldsB_</a>	Alignment		35.3	13	<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
16	<a href="#">c5tsaA_</a>	Alignment		32.7	14	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> membrane protein; <b>PDBTitle:</b> crystal structure of the zrt-/irt-like protein from bordetella2 bronchiseptica with bound zn2+
17	<a href="#">c3c02A_</a>	Alignment		29.6	12	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> aquaglyceroporin; <b>PDBTitle:</b> x-ray structure of the aquaglyceroporin from plasmodium falciparum
18	<a href="#">c2f2bA_</a>	Alignment		29.4	11	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> aquaporin aqpm; <b>PDBTitle:</b> crystal structure of integral membrane protein aquaporin aqpm at 1.68a2 resolution
19	<a href="#">c5v2sA_</a>	Alignment		27.4	17	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> envelope glycoprotein b; <b>PDBTitle:</b> crystal structure of glycoprotein b from herpes simplex virus type i
20	<a href="#">c4uftB_</a>	Alignment		27.3	23	<b>PDB header:</b> rna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> nucleoprotein; <b>PDBTitle:</b> structure of the helical measles virus nucleocapsid
21	<a href="#">c5c65A_</a>	Alignment	not modelled	26.9	14	<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
22	<a href="#">c4co6A_</a>	Alignment	not modelled	26.1	24	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> nucleoprotein; <b>PDBTitle:</b> crystal structure of the nipah virus rna free2 nucleoprotein-phosphoprotein complex
23	<a href="#">c5e4vA_</a>	Alignment	not modelled	26.0	19	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> nucleoprotein,phosphoprotein; <b>PDBTitle:</b> crystal structure of measles n0-p complex
24	<a href="#">c4pypA_</a>	Alignment	not modelled	24.0	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> crystal structure of the human glucose transporter glut1
25	<a href="#">c2b5fD_</a>	Alignment	not modelled	23.6	11	<b>PDB header:</b> transport protein,membrane protein <b>Chain:</b> D: <b>PDB Molecule:</b> aquaporin; <b>PDBTitle:</b> crystal structure of the spinach aquaporin sopip2;1 in an2 open conformation to 3.9 resolution
26	<a href="#">d1ppje2</a>	Alignment	not modelled	22.8	21	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> ISP transmembrane anchor <b>Family:</b> ISP transmembrane anchor
27	<a href="#">d1e12a_</a>	Alignment	not modelled	21.8	8	<b>Fold:</b> Family A G protein-coupled receptor-like <b>Superfamily:</b> Family A G protein-coupled receptor-like <b>Family:</b> Bacteriorhodopsin-like
28	<a href="#">c2jagA_</a>	Alignment	not modelled	17.5	8	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> halorhodopsin; <b>PDBTitle:</b> I1-intermediate of halorhodopsin t203v
						<b>PDB header:</b> membrane protein

29	<a href="#">c2gfpA</a>	Alignment	not modelled	17.4	11	<b>Chain:</b> A; <b>PDB Molecule:</b> multidrug resistance protein d; <b>PDBTitle:</b> structure of the multidrug transporter emrd from2 escherichia coli
30	<a href="#">c3hfxA</a>	Alignment	not modelled	17.1	17	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> l-carnitine/gamma-butyrobetaine antiporter; <b>PDBTitle:</b> crystal structure of carnitine transporter
31	<a href="#">c6af0C</a>	Alignment	not modelled	16.2	50	<b>PDB header:</b> transcription <b>Chain:</b> C; <b>PDB Molecule:</b> cdc73 protein; <b>PDBTitle:</b> structure of ctr9, paf1 and cdc73 ternary complex from myceliophthora2 thermophila
32	<a href="#">c5i32A</a>	Alignment	not modelled	15.7	12	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> aquaporin tip2-1; <b>PDBTitle:</b> ammonia permeable aquaporin attp2;1
33	<a href="#">d1h6ia</a>	Alignment	not modelled	14.9	11	<b>Fold:</b> Aquaporin-like <b>Superfamily:</b> Aquaporin-like <b>Family:</b> Aquaporin-like
34	<a href="#">c5jngA</a>	Alignment	not modelled	13.1	9	<b>PDB header:</b> transferase/antibiotic <b>Chain:</b> A; <b>PDB Molecule:</b> phospho-n-acetylmuramoyl-pentapeptide-transferase; <b>PDBTitle:</b> mray tunicamycin complex
35	<a href="#">c2yvxD</a>	Alignment	not modelled	12.9	5	<b>PDB header:</b> transport protein <b>Chain:</b> D; <b>PDB Molecule:</b> mg2+ transporter mgte; <b>PDBTitle:</b> crystal structure of magnesium transporter mgte
36	<a href="#">c1ciiA</a>	Alignment	not modelled	11.6	15	<b>PDB header:</b> transmembrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> colicin ia; <b>PDBTitle:</b> colicin ia
37	<a href="#">d1fvia1</a>	Alignment	not modelled	11.5	29	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> DNA ligase/mRNA capping enzyme postcatalytic domain
38	<a href="#">d1ycga1</a>	Alignment	not modelled	11.0	16	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Flavodoxin-related
39	<a href="#">d1c1ia1</a>	Alignment	not modelled	11.0	15	<b>Fold:</b> Toxins' membrane translocation domains <b>Superfamily:</b> Colicin <b>Family:</b> Colicin
40	<a href="#">c5d7tC</a>	Alignment	not modelled	10.8	17	<b>PDB header:</b> transport protein <b>Chain:</b> C; <b>PDB Molecule:</b> s-component for folate; <b>PDBTitle:</b> folate ecf transporter: apo state
41	<a href="#">c2qxvB</a>	Alignment	not modelled	10.3	50	<b>PDB header:</b> gene regulation <b>Chain:</b> B; <b>PDB Molecule:</b> enhancer of zeste homolog 2; <b>PDBTitle:</b> structural basis of ezh2 recognition by eed
42	<a href="#">c3gd8A</a>	Alignment	not modelled	10.1	12	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> aquaporin-4; <b>PDBTitle:</b> crystal structure of human aquaporin 4 at 1.8 and its mechanism of2 conductance
43	<a href="#">c6g2jY</a>	Alignment	not modelled	9.7	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> Y; <b>PDB Molecule:</b> mcg5603; <b>PDBTitle:</b> mouse mitochondrial complex i in the active state
44	<a href="#">c5ldwY</a>	Alignment	not modelled	9.2	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> Y; <b>PDB Molecule:</b> nadh dehydrogenase [ubiquinone] 1 alpha subcomplex subunit <b>PDBTitle:</b> structure of mammalian respiratory complex i, class1
45	<a href="#">c4ainB</a>	Alignment	not modelled	8.9	12	<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.
46	<a href="#">c4ikyA</a>	Alignment	not modelled	8.9	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
47	<a href="#">c6gtrD</a>	Alignment	not modelled	8.8	41	<b>PDB header:</b> transcription <b>Chain:</b> D; <b>PDB Molecule:</b> duf1778 domain-containing protein; <b>PDBTitle:</b> structure of the atat y144f mutant toxin bound to the c-terminus of2 the antitoxin atar and acetyl-coa
48	<a href="#">d1mowa1</a>	Alignment	not modelled	8.8	55	<b>Fold:</b> Homing endonuclease-like <b>Superfamily:</b> Homing endonucleases <b>Family:</b> Group I mobile intron endonuclease
49	<a href="#">d1m6ya1</a>	Alignment	not modelled	8.6	21	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> Putative methyltransferase TM0872, insert domain <b>Family:</b> Putative methyltransferase TM0872, insert domain
50	<a href="#">c2x2oA</a>	Alignment	not modelled	8.5	35	<b>PDB header:</b> flavoprotein <b>Chain:</b> A; <b>PDB Molecule:</b> nrdr protein; <b>PDBTitle:</b> the flavoprotein nrdr from bacillus cereus with the initially oxidized2 fmn cofactor in an intermediate radiation reduced state
51	<a href="#">c5zghK</a>	Alignment	not modelled	8.4	31	<b>PDB header:</b> photosynthesis <b>Chain:</b> K; <b>PDB Molecule:</b> psak; <b>PDBTitle:</b> cryo-em structure of the red algal psi-lhcr
52	<a href="#">d1rh1a2</a>	Alignment	not modelled	8.2	16	<b>Fold:</b> Toxins' membrane translocation domains <b>Superfamily:</b> Colicin <b>Family:</b> Colicin
53	<a href="#">d1af5a</a>	Alignment	not modelled	8.1	40	<b>Fold:</b> Homing endonuclease-like <b>Superfamily:</b> Homing endonucleases <b>Family:</b> Group I mobile intron endonuclease
54	<a href="#">d1t9ia</a>	Alignment	not modelled	8.1	36	<b>Fold:</b> Homing endonuclease-like <b>Superfamily:</b> Homing endonucleases <b>Family:</b> Group I mobile intron endonuclease
55	<a href="#">d1wg8a1</a>	Alignment	not modelled	8.0	36	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> Putative methyltransferase TM0872, insert domain <b>Family:</b> Putative methyltransferase TM0872, insert domain
						<b>Fold:</b> Homing endonuclease-like

56	<a href="#">d1m5xa_</a>	Alignment	not modelled	7.7	40	<b>Superfamily:</b> Homing endonucleases <b>Family:</b> Group I mobile intron endonuclease
57	<a href="#">c2b6pA_</a>	Alignment	not modelled	7.5	13	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> lens fiber major intrinsic protein; <b>PDBTitle:</b> x-ray structure of lens aquaporin-0 (aqp0) (lens mip) in an open pore2 state
58	<a href="#">c5kkpA_</a>	Alignment	not modelled	7.4	15	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> pseudouridylate synthase 7; <b>PDBTitle:</b> crystal structure of human pseudouridylate synthase 7
59	<a href="#">c4apsB_</a>	Alignment	not modelled	7.4	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.
60	<a href="#">d2a5la1</a>	Alignment	not modelled	7.4	5	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> WrbA-like
61	<a href="#">c5a72B_</a>	Alignment	not modelled	6.9	50	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> B; <b>PDB Molecule:</b> dna endonuclease i-cvui; <b>PDBTitle:</b> crystal structure of the homing endonuclease i-cvui in complex2 with its target (sro1.3) in the presence of 2 mm ca
62	<a href="#">d2arka1</a>	Alignment	not modelled	6.9	21	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> WrbA-like
63	<a href="#">d1vmea1</a>	Alignment	not modelled	6.6	5	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Flavodoxin-related
64	<a href="#">c6irtA_</a>	Alignment	not modelled	6.5	17	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> 4f2 cell-surface antigen heavy chain; <b>PDBTitle:</b> human lat1-4f2hc complex bound with bch
65	<a href="#">d1bhpa_</a>	Alignment	not modelled	6.1	32	<b>Fold:</b> Crambin-like <b>Superfamily:</b> Crambin-like <b>Family:</b> Crambin-like
66	<a href="#">c4ybgB_</a>	Alignment	not modelled	5.9	13	<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
67	<a href="#">c2i88A_</a>	Alignment	not modelled	5.9	16	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> colicin-e1; <b>PDBTitle:</b> crystal structure of the channel-forming domain of colicin e1
68	<a href="#">c3fniA_</a>	Alignment	not modelled	5.8	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> putative diflavin flavoprotein a 3; <b>PDBTitle:</b> crystal structure of a diflavin flavoprotein a3 (all3895) from nostoc2 sp., northeast structural genomics consortium target nsr431a
69	<a href="#">c2jpa_</a>	Alignment	not modelled	5.8	54	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A; <b>PDB Molecule:</b> bacteriocin lactococcin-g subunit alpha; <b>PDBTitle:</b> lactococcin g-a in dpc
70	<a href="#">c2ghjD_</a>	Alignment	not modelled	5.5	26	<b>PDB header:</b> structural protein <b>Chain:</b> D; <b>PDB Molecule:</b> 50s ribosomal protein l20; <b>PDBTitle:</b> crystal structure of folded and partially unfolded forms of aquifex2 aeolicus ribosomal protein l20
71	<a href="#">c3tkaA_</a>	Alignment	not modelled	5.3	36	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> ribosomal rna small subunit methyltransferase h; <b>PDBTitle:</b> crystal structure and solution saxs of methyltransferase rsmh from2 e.coli
72	<a href="#">d2fug71</a>	Alignment	not modelled	5.3	38	<b>Fold:</b> N domain of copper amine oxidase-like <b>Superfamily:</b> Frataxin/Nqo15-like <b>Family:</b> Nqo15-like