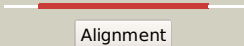

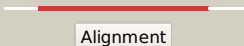

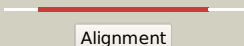
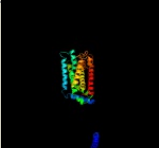






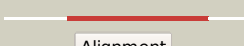




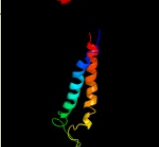

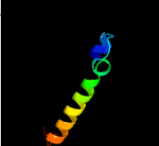

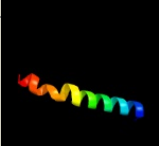
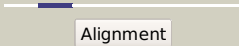


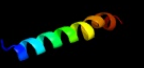

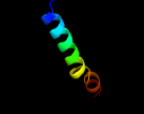
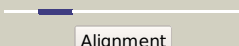

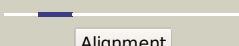
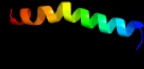
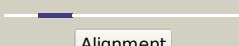

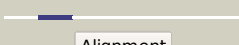


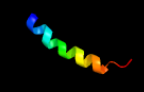

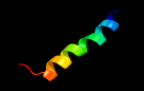
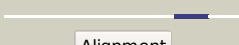
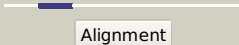
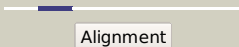


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3783_(rfbD)_4229436_4230278
Date	Fri Aug 9 18:20:49 BST 2019
Unique Job ID	048b30bb34d2b6f3

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6an7D_</a>	 Alignment		100.0	19	<b>PDB header:</b> transport protein <b>Chain:</b> D; <b>PDB Molecule:</b> transport permease protein; <b>PDBTitle:</b> crystal structure of o-antigen polysaccharide abc-transporter
2	<a href="#">c6an7C_</a>	 Alignment		100.0	19	<b>PDB header:</b> transport protein <b>Chain:</b> C; <b>PDB Molecule:</b> transport permease protein; <b>PDBTitle:</b> crystal structure of o-antigen polysaccharide abc-transporter
3	<a href="#">c5do7B_</a>	 Alignment		99.9	12	<b>PDB header:</b> transport protein <b>Chain:</b> B; <b>PDB Molecule:</b> atp-binding cassette sub-family g member 8; <b>PDBTitle:</b> crystal structure of the human sterol transporter abcg5/abcg8
4	<a href="#">c5do7A_</a>	 Alignment		99.8	8	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> atp-binding cassette sub-family g member 5; <b>PDBTitle:</b> crystal structure of the human sterol transporter abcg5/abcg8
5	<a href="#">c5njgB_</a>	 Alignment		99.8	10	<b>PDB header:</b> transport protein <b>Chain:</b> B; <b>PDB Molecule:</b> atp-binding cassette sub-family g member 2; <b>PDBTitle:</b> structure of an abc transporter: part of the structure that could be2 built de novo
6	<a href="#">c5nj3B_</a>	 Alignment		99.8	9	<b>PDB header:</b> transport protein <b>Chain:</b> B; <b>PDB Molecule:</b> atp-binding cassette sub-family g member 2; <b>PDBTitle:</b> structure of an abc transporter: complete structure
7	<a href="#">c5xjvA_</a>	 Alignment		92.2	8	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> atp-binding cassette sub-family a member 1; <b>PDBTitle:</b> cryo-em structure of human abca1
8	<a href="#">c6e11F_</a>	 Alignment		11.4	14	<b>PDB header:</b> protein transport <b>Chain:</b> F; <b>PDB Molecule:</b> exported protein 2; <b>PDBTitle:</b> ptex core complex in the resetting (compact) state
9	<a href="#">c6f0kD_</a>	 Alignment		9.9	7	<b>PDB header:</b> membrane protein <b>Chain:</b> D; <b>PDB Molecule:</b> actd; <b>PDBTitle:</b> alternative complex iii
10	<a href="#">c5wufA_</a>	 Alignment		9.8	15	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> putative membrane protein; <b>PDBTitle:</b> structural basis for conductance through tric cation channels
11	<a href="#">c4nawG_</a>	 Alignment		8.9	17	<b>PDB header:</b> protein transport/ligase <b>Chain:</b> G; <b>PDB Molecule:</b> autophagy-related protein 16-1; <b>PDBTitle:</b> crystal structure of human atg12~atg5-atg16n in complex with a2 fragment of atg3

12	<a href="#">c4nawO_</a>	 Alignment		8.9	17	<b>PDB header:</b> protein transport/ligase <b>Chain:</b> O: <b>PDB Molecule:</b> autophagy-related protein 16-1; <b>PDBTitle:</b> crystal structure of human atg12~atg5-atg16n in complex with a2 fragment of atg3
13	<a href="#">c4nawC_</a>	 Alignment		8.9	17	<b>PDB header:</b> protein transport/ligase <b>Chain:</b> C: <b>PDB Molecule:</b> autophagy-related protein 16-1; <b>PDBTitle:</b> crystal structure of human atg12~atg5-atg16n in complex with a2 fragment of atg3
14	<a href="#">c4gdlC_</a>	 Alignment		8.9	17	<b>PDB header:</b> protein binding <b>Chain:</b> C: <b>PDB Molecule:</b> autophagy-related protein 16-1; <b>PDBTitle:</b> crystal structure of human atg12~atg5 conjugate in complex with an n-2 terminal fragment of atg16l1
15	<a href="#">c4nawK_</a>	 Alignment		8.9	17	<b>PDB header:</b> protein transport/ligase <b>Chain:</b> K: <b>PDB Molecule:</b> autophagy-related protein 16-1; <b>PDBTitle:</b> crystal structure of human atg12~atg5-atg16n in complex with a2 fragment of atg3
16	<a href="#">c4gdkC_</a>	 Alignment		8.9	17	<b>PDB header:</b> protein binding <b>Chain:</b> C: <b>PDB Molecule:</b> autophagy-related protein 16-1; <b>PDBTitle:</b> crystal structure of human atg12~atg5 conjugate in complex with an n-2 terminal fragment of atg16l1
17	<a href="#">c4gdkF_</a>	 Alignment		8.8	17	<b>PDB header:</b> protein binding <b>Chain:</b> F: <b>PDB Molecule:</b> autophagy-related protein 16-1; <b>PDBTitle:</b> crystal structure of human atg12~atg5 conjugate in complex with an n-2 terminal fragment of atg16l1
18	<a href="#">c4y0IA_</a>	 Alignment		7.2	30	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative membrane protein mmp111; <b>PDBTitle:</b> mycobacterial membrane protein mmp111d2
19	<a href="#">c2na6C_</a>	 Alignment		7.0	33	<b>PDB header:</b> apoptosis <b>Chain:</b> C: <b>PDB Molecule:</b> tumor necrosis factor receptor superfamily member 6; <b>PDBTitle:</b> transmembrane domain of mouse fas/cd95 death receptor
20	<a href="#">c2na6A_</a>	 Alignment		7.0	33	<b>PDB header:</b> apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> tumor necrosis factor receptor superfamily member 6; <b>PDBTitle:</b> transmembrane domain of mouse fas/cd95 death receptor
21	<a href="#">c2na6B_</a>	 Alignment	not modelled	7.0	33	<b>PDB header:</b> apoptosis <b>Chain:</b> B: <b>PDB Molecule:</b> tumor necrosis factor receptor superfamily member 6; <b>PDBTitle:</b> transmembrane domain of mouse fas/cd95 death receptor
22	<a href="#">c4ftfA_</a>	 Alignment	not modelled	6.9	32	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> alternate secretin pathway subunit s (vc395_1821, vc1703); <b>PDBTitle:</b> structure of the type ii secretion system pilotin asps from vibrio2 cholerae
23	<a href="#">c2olvA_</a>	 Alignment	not modelled	6.9	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> penicillin-binding protein 2; <b>PDBTitle:</b> structural insight into the transglycosylation step of bacterial cell2 wall biosynthesis : donor ligand complex