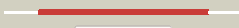

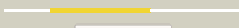
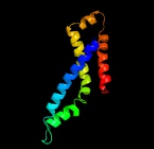


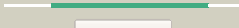



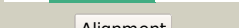
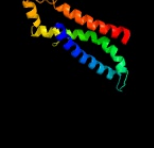
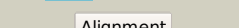
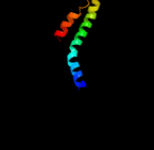
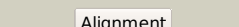

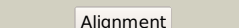

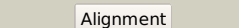





# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1964_(yrbE3A)_2207708_2208505
Date	Mon Aug 5 13:25:06 BST 2019
Unique Job ID	be5f11e6a7d26e28

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6ic4H_</a>	 Alignment		100.0	23	<b>PDB header:</b> protein transport <b>Chain:</b> H: <b>PDB Molecule:</b> abc transporter permease; <b>PDBTitle:</b> cryo-em structure of the a. baumannii mla complex at 8.7 a resolution
2	<a href="#">c5x5yG_</a>	 Alignment		75.1	16	<b>PDB header:</b> membrane protein <b>Chain:</b> G: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> a membrane protein complex
3	<a href="#">c5l75G_</a>	 Alignment		57.7	27	<b>PDB header:</b> transport protein <b>Chain:</b> G: <b>PDB Molecule:</b> fig000906: predicted permease; <b>PDBTitle:</b> a protein structure
4	<a href="#">c6qvcB_</a>	 Alignment		44.7	15	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> chloride channel protein 1; <b>PDBTitle:</b> cryoem structure of the human clc-1 chloride channel, cbs state 1
5	<a href="#">c5l75F_</a>	 Alignment		42.8	14	<b>PDB header:</b> transport protein <b>Chain:</b> F: <b>PDB Molecule:</b> fig000988: predicted permease; <b>PDBTitle:</b> a protein structure
6	<a href="#">c6mjpF_</a>	 Alignment		40.5	10	<b>PDB header:</b> lipid transport <b>Chain:</b> F: <b>PDB Molecule:</b> fig000988: predicted permease; <b>PDBTitle:</b> lptb(e163q)fgc from vibrio cholerae
7	<a href="#">c6f2dJ_</a>	 Alignment		38.0	15	<b>PDB header:</b> protein transport <b>Chain:</b> J: <b>PDB Molecule:</b> flagellar biosynthetic protein flq; <b>PDBTitle:</b> a flipqr complex forms the core of the salmonella type iii secretion2 system export apparatus.
8	<a href="#">c6f2dI_</a>	 Alignment		38.0	15	<b>PDB header:</b> protein transport <b>Chain:</b> I: <b>PDB Molecule:</b> flagellar biosynthetic protein flq; <b>PDBTitle:</b> a flipqr complex forms the core of the salmonella type iii secretion2 system export apparatus.
9	<a href="#">c6mjpG_</a>	 Alignment		35.7	11	<b>PDB header:</b> lipid transport <b>Chain:</b> G: <b>PDB Molecule:</b> lps export abc transporter permease lptg; <b>PDBTitle:</b> lptb(e163q)fgc from vibrio cholerae
10	<a href="#">c6r6bl_</a>	 Alignment		30.0	9	<b>PDB header:</b> protein transport <b>Chain:</b> I: <b>PDB Molecule:</b> surface presentation of antigens protein spaq; <b>PDBTitle:</b> structure of the core shigella flexneri type iii secretion system2 export gate complex sctrst (spa24/spa9/spa29).
11	<a href="#">c6coyB_</a>	 Alignment		26.6	14	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> chloride channel protein 1; <b>PDBTitle:</b> human clc-1 chloride ion channel, transmembrane domain

12	<a href="#">c5x5yF_</a>	Alignment		21.6	13	<b>PDB header:</b> membrane protein <b>Chain:</b> F: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> a membrane protein complex
13	<a href="#">c5ghaF_</a>	Alignment		21.5	40	<b>PDB header:</b> transferase/transport protein <b>Chain:</b> F: <b>PDB Molecule:</b> sulfur carrier ttub; <b>PDBTitle:</b> sulfur transferase ttua in complex with sulfur carrier ttub
14	<a href="#">d2hafa1</a>	Alignment		19.1	40	<b>Fold:</b> VC0467-like <b>Superfamily:</b> VC0467-like <b>Family:</b> VC0467-like
15	<a href="#">c5xu1M_</a>	Alignment		18.7	14	<b>PDB header:</b> transport protein <b>Chain:</b> M: <b>PDB Molecule:</b> abc transporter permeae; <b>PDBTitle:</b> structure of a non-canonical abc transporter from streptococcus2 pneumoniae r6
16	<a href="#">c2m67A_</a>	Alignment		18.4	6	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> merf; <b>PDBTitle:</b> full-length mercury transporter protein merf in lipid bilayer2 membranes
17	<a href="#">c2kn8A_</a>	Alignment		15.5	25	<b>PDB header:</b> protein binding, dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna cleavage and packaging protein large subunit, ul89; <b>PDBTitle:</b> nmr structure of the c-terminal domain of pul89
18	<a href="#">c5ws4A_</a>	Alignment		14.3	11	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> macrolide export atp-binding/permease protein macb; <b>PDBTitle:</b> crystal structure of tripartite-type abc transporter macb from2 acinetobacter baumannii
19	<a href="#">c2aj2A_</a>	Alignment		14.2	40	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical upf0301 protein vc0467; <b>PDBTitle:</b> x-ray crystal structure of protein vc0467 from vibrio2 cholerae. northeast structural genomics consortium target3 vcr8.
20	<a href="#">c2hv8D_</a>	Alignment		13.5	16	<b>PDB header:</b> protein transport <b>Chain:</b> D: <b>PDB Molecule:</b> rab11 family-interacting protein 3; <b>PDBTitle:</b> crystal structure of gtp-bound rab11 in complex with fip3
21	<a href="#">c1abzA_</a>	Alignment	not modelled	12.3	31	<b>PDB header:</b> de novo design <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-t-alpha; <b>PDBTitle:</b> alpha-t-alpha, a de novo designed peptide, nmr, 232 structures
22	<a href="#">c2hg5D_</a>	Alignment	not modelled	11.4	17	<b>PDB header:</b> membrane protein <b>Chain:</b> D: <b>PDB Molecule:</b> kcsa channel; <b>PDBTitle:</b> cs+ complex of a k channel with an amide to ester substitution in the2 selectivity filter
23	<a href="#">c4migC_</a>	Alignment	not modelled	10.7	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> pyranose 2-oxidase; <b>PDBTitle:</b> pyranose 2-oxidase from phanerochaete chrysosporium, recombinant wild2 type
24	<a href="#">d1z96a1</a>	Alignment	not modelled	10.4	24	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> UBA domain
25	<a href="#">c2yvxD_</a>	Alignment	not modelled	9.9	18	<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
26	<a href="#">d3dhwa1</a>	Alignment	not modelled	8.7	13	<b>Fold:</b> MetI-like <b>Superfamily:</b> MetI-like <b>Family:</b> MetI-like
27	<a href="#">c2mfrA_</a>	Alignment	not modelled	8.1	9	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> insulin receptor; <b>PDBTitle:</b> solution structure of the transmembrane domain of the insulin receptor2 in micelles
28	<a href="#">d1q74a_</a>	Alignment	not modelled	7.5	36	<b>Fold:</b> LmbE-like <b>Superfamily:</b> LmbE-like <b>Family:</b> LmbE-like
						<b>PDB header:</b> oxidoreductase(flavoprotein)

29	<a href="#">c1cf3A_</a>	Alignment	not modelled	7.3	13	<b>Chain:</b> A: <b>PDB Molecule:</b> protein (glucose oxidase); <b>PDBTitle:</b> glucose oxidase from apergillus niger
30	<a href="#">c1vmaA_</a>	Alignment	not modelled	7.3	25	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> cell division protein ftsy; <b>PDBTitle:</b> crystal structure of cell division protein ftsy (tm0570) from2 thermotoga maritima at 1.60 a resolution
31	<a href="#">d2k0bx1</a>	Alignment	not modelled	7.1	27	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> UBA domain
32	<a href="#">c1gw4A_</a>	Alignment	not modelled	7.0	45	<b>PDB header:</b> high density lipoproteins <b>Chain:</b> A: <b>PDB Molecule:</b> apoa-i; <b>PDBTitle:</b> the helix-hinge-helix structural motif in human2 apolipoprotein a-i determined by nmr spectroscopy, 13 structure
33	<a href="#">d2do8a1</a>	Alignment	not modelled	7.0	30	<b>Fold:</b> VC0467-like <b>Superfamily:</b> VC0467-like <b>Family:</b> VC0467-like
34	<a href="#">d1g7oa1</a>	Alignment	not modelled	6.7	12	<b>Fold:</b> GST C-terminal domain-like <b>Superfamily:</b> GST C-terminal domain-like <b>Family:</b> Glutathione S-transferase (GST), C-terminal domain
35	<a href="#">c3n4qA_</a>	Alignment	not modelled	6.5	30	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> terminase subunit ul89 protein; <b>PDBTitle:</b> human cytomegalovirus terminase nuclease domain, mn soaked
36	<a href="#">d2hjqal</a>	Alignment	not modelled	6.2	20	<b>Fold:</b> LEM/SAP HeH motif <b>Superfamily:</b> Rho N-terminal domain-like <b>Family:</b> YqbF C-terminal domain-like
37	<a href="#">c5l1xH_</a>	Alignment	not modelled	6.2	53	<b>PDB header:</b> viral protein <b>Chain:</b> H: <b>PDB Molecule:</b> hmpv f1 subunit; <b>PDBTitle:</b> structure of the human metapneumovirus fusion protein in the2 postfusion conformation
38	<a href="#">c4ak9A_</a>	Alignment	not modelled	6.0	25	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> cpfts;y; <b>PDBTitle:</b> structure of chloroplast ftsy from physcomitrella patens
39	<a href="#">c6bs7A_</a>	Alignment	not modelled	5.9	35	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> adenylosuccinate synthetase; <b>PDBTitle:</b> crystal structure of adenylosuccinate synthetase from legionella2 pneumophila philadelphia 1
40	<a href="#">c4dagA_</a>	Alignment	not modelled	5.8	53	<b>PDB header:</b> viral protein/immune system <b>Chain:</b> A: <b>PDB Molecule:</b> fusion glycoprotein f0; <b>PDBTitle:</b> structure of the human metapneumovirus fusion protein with2 neutralizing antibody identifies a pneumovirus antigenic site
41	<a href="#">c5l3sF_</a>	Alignment	not modelled	5.7	33	<b>PDB header:</b> protein transport <b>Chain:</b> F: <b>PDB Molecule:</b> signal recognition particle receptor ftsy; <b>PDBTitle:</b> structure of the gtpase heterodimer of crenarchaeal srp54 and ftsy
42	<a href="#">c2jy8A_</a>	Alignment	not modelled	5.7	27	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin-binding protein p62; <b>PDBTitle:</b> nmr structure of the ubiquitin associated (uba) domain of2 p62 (sqstm1) in complex with ubiquitin. rdc refined
43	<a href="#">c2j7pA_</a>	Alignment	not modelled	5.6	25	<b>PDB header:</b> signal recognition <b>Chain:</b> A: <b>PDB Molecule:</b> signal recognition particle protein; <b>PDBTitle:</b> gmppnp-stabilized ng domain complex of the srp gtpases ffh2 and ftsy
44	<a href="#">c3n4pA_</a>	Alignment	not modelled	5.6	30	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> terminase subunit ul89 protein; <b>PDBTitle:</b> human cytomegalovirus terminase nuclease domain
45	<a href="#">c5egiB_</a>	Alignment	not modelled	5.6	9	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein y57a10a.10; <b>PDBTitle:</b> structure of a trimeric intracellular cation channel from c. elegans2 with bound ca2+
46	<a href="#">c5wb0F_</a>	Alignment	not modelled	5.5	53	<b>PDB header:</b> viral protein <b>Chain:</b> F: <b>PDB Molecule:</b> fusion glycoprotein f0; <b>PDBTitle:</b> crystal structure of human metapneumovirus fusion glycoprotein2 stabilized in the prefusion state
47	<a href="#">c3b9qA_</a>	Alignment	not modelled	5.5	25	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> chloroplast srp receptor homolog, alpha subunit <b>PDBTitle:</b> the crystal structure of cpfts; from arabidopsis thaliana
48	<a href="#">c6cy1B_</a>	Alignment	not modelled	5.5	33	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> signal recognition particle receptor ftsy; <b>PDBTitle:</b> crystal structure of signal recognition particle receptor ftsy from2 elizabethkingia anophelis
49	<a href="#">c5eikA_</a>	Alignment	not modelled	5.4	11	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein y57a10a.28; <b>PDBTitle:</b> structure of a trimeric intracellular cation channel from c. elegans2 in the absence of ca2+
50	<a href="#">c3dfmA_</a>	Alignment	not modelled	5.4	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> teicoplanin pseudoaglycone deacetylase orf2; <b>PDBTitle:</b> the crystal structure of the zinc inhibited form of2 teicoplanin deacetylase orf2
51	<a href="#">c1w1nA_</a>	Alignment	not modelled	5.2	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphatidylinositol 3-kinase tor1; <b>PDBTitle:</b> the solution structure of the fatc domain of the protein kinase tor12 from yeast
52	<a href="#">c2kitA_</a>	Alignment	not modelled	5.2	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> serine/threonine-protein kinase tor1; <b>PDBTitle:</b> the solution structure of the reduced yeast tor1 fatc domain bound to2 dpc micelles at 298k