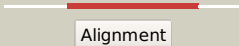
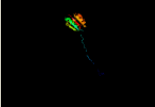

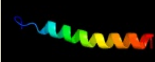


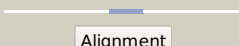

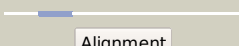

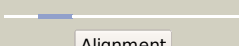

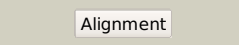

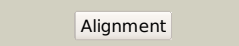













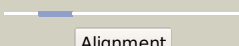

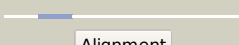

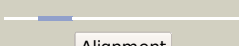

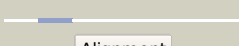
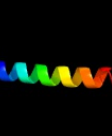









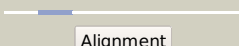
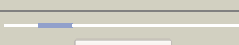



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2700_(-)_3015213_3015863
Date	Wed Aug 7 12:50:35 BST 2019
Unique Job ID	98c288503356a58f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2m5yA_</a>	 Alignment		99.6	17	<b>PDB header:</b> unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> putative tuberculin related peptide; <b>PDBTitle:</b> solution structure of the c-terminal domain of rv0431
2	<a href="#">c2kogA_</a>	 Alignment		65.8	13	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> vesicle-associated membrane protein 2; <b>PDBTitle:</b> lipid-bound synaptobrevin solution nmr structure
3	<a href="#">c2n28A_</a>	 Alignment		41.1	19	<b>PDB header:</b> viral protein <b>Chain:</b> A; <b>PDB Molecule:</b> protein vpu; <b>PDBTitle:</b> solid-state nmr structure of vpu
4	<a href="#">c4b2oB_</a>	 Alignment		28.3	29	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> ymdb phosphodiesterase; <b>PDBTitle:</b> crystal structure of bacillus subtilis ymdb, a global2 regulator of late adaptive responses.
5	<a href="#">c3hd7A_</a>	 Alignment		27.6	13	<b>PDB header:</b> exocytosis <b>Chain:</b> A; <b>PDB Molecule:</b> vesicle-associated membrane protein 2; <b>PDBTitle:</b> helical extension of the neuronal snare complex into the membrane,2 spacegroup c 1 2 1
6	<a href="#">c6mctF_</a>	 Alignment		26.3	10	<b>PDB header:</b> de novo protein <b>Chain:</b> F; <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> a designed pentameric membrane protein stabilized by van der waals2 interaction
7	<a href="#">c6mctJ_</a>	 Alignment		26.3	10	<b>PDB header:</b> de novo protein <b>Chain:</b> J; <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> a designed pentameric membrane protein stabilized by van der waals2 interaction
8	<a href="#">c6mctD_</a>	 Alignment		26.3	10	<b>PDB header:</b> de novo protein <b>Chain:</b> D; <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> a designed pentameric membrane protein stabilized by van der waals2 interaction
9	<a href="#">c6mctN_</a>	 Alignment		26.3	10	<b>PDB header:</b> de novo protein <b>Chain:</b> N; <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> a designed pentameric membrane protein stabilized by van der waals2 interaction
10	<a href="#">c6mctC_</a>	 Alignment		26.3	10	<b>PDB header:</b> de novo protein <b>Chain:</b> C; <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> a designed pentameric membrane protein stabilized by van der waals2 interaction
11	<a href="#">c6mctB_</a>	 Alignment		26.3	10	<b>PDB header:</b> de novo protein <b>Chain:</b> B; <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> a designed pentameric membrane protein stabilized by van der waals2 interaction

12	<a href="#">c6mctA_</a>			26.3	10	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> a designed pentameric membrane protein stabilized by van der waals2 interaction
13	<a href="#">c6mctK_</a>			26.3	10	<b>PDB header:</b> de novo protein <b>Chain:</b> K: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> a designed pentameric membrane protein stabilized by van der waals2 interaction
14	<a href="#">c6mctI_</a>			26.3	10	<b>PDB header:</b> de novo protein <b>Chain:</b> I: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> a designed pentameric membrane protein stabilized by van der waals2 interaction
15	<a href="#">c6mctH_</a>			26.3	10	<b>PDB header:</b> de novo protein <b>Chain:</b> H: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> a designed pentameric membrane protein stabilized by van der waals2 interaction
16	<a href="#">c6mctL_</a>			26.3	10	<b>PDB header:</b> de novo protein <b>Chain:</b> L: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> a designed pentameric membrane protein stabilized by van der waals2 interaction
17	<a href="#">c6mq2D_</a>			26.3	10	<b>PDB header:</b> de novo protein <b>Chain:</b> D: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> de novo design of membrane protein--mini-evgl membrane protein, c22212 form-2
18	<a href="#">c6mctM_</a>			26.3	10	<b>PDB header:</b> de novo protein <b>Chain:</b> M: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> a designed pentameric membrane protein stabilized by van der waals2 interaction
19	<a href="#">c6mctE_</a>			26.3	10	<b>PDB header:</b> de novo protein <b>Chain:</b> E: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> a designed pentameric membrane protein stabilized by van der waals2 interaction
20	<a href="#">c6mctO_</a>			26.3	10	<b>PDB header:</b> de novo protein <b>Chain:</b> O: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> a designed pentameric membrane protein stabilized by van der waals2 interaction
21	<a href="#">c6mpwA_</a>		not modelled	26.3	10	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> de novo design of membrane protein--mini-evgl membrane protein, c22212 form-1
22	<a href="#">c6mctG_</a>		not modelled	26.1	10	<b>PDB header:</b> de novo protein <b>Chain:</b> G: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> a designed pentameric membrane protein stabilized by van der waals2 interaction
23	<a href="#">c6mq2A_</a>		not modelled	25.2	10	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> de novo design of membrane protein--mini-evgl membrane protein, c22212 form-2
24	<a href="#">c6mq2C_</a>		not modelled	25.2	10	<b>PDB header:</b> de novo protein <b>Chain:</b> C: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> de novo design of membrane protein--mini-evgl membrane protein, c22212 form-2
25	<a href="#">c6mpwE_</a>		not modelled	25.2	10	<b>PDB header:</b> de novo protein <b>Chain:</b> E: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> de novo design of membrane protein--mini-evgl membrane protein, c22212 form-1
26	<a href="#">c6mq2B_</a>		not modelled	25.2	10	<b>PDB header:</b> de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> de novo design of membrane protein--mini-evgl membrane protein, c22212 form-2
27	<a href="#">c6mpwD_</a>		not modelled	25.2	10	<b>PDB header:</b> de novo protein <b>Chain:</b> D: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> de novo design of membrane protein--mini-evgl membrane protein, c22212 form-1
28	<a href="#">c6mpwB_</a>		not modelled	25.2	10	<b>PDB header:</b> de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> de novo design of membrane protein--mini-evgl membrane protein, c22212 form-1

29	<a href="#">c6mpwC_</a>	Alignment	not modelled	25.2	10	<b>PDB header:</b> de novo protein <b>Chain:</b> C: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> de novo design of membrane protein--mini-evgl membrane protein, c22212 form-1
30	<a href="#">c6mq2E_</a>	Alignment	not modelled	25.2	10	<b>PDB header:</b> de novo protein <b>Chain:</b> E: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> de novo design of membrane protein--mini-evgl membrane protein, c22212 form-2
31	<a href="#">d1t71a_</a>	Alignment	not modelled	25.1	18	<b>Fold:</b> Metallo-dependent phosphatases <b>Superfamily:</b> Metallo-dependent phosphatases <b>Family:</b> DR1281-like
32	<a href="#">d2z06a1</a>	Alignment	not modelled	23.8	17	<b>Fold:</b> Metallo-dependent phosphatases <b>Superfamily:</b> Metallo-dependent phosphatases <b>Family:</b> TTHA0625-like
33	<a href="#">d1t70a_</a>	Alignment	not modelled	21.2	22	<b>Fold:</b> Metallo-dependent phosphatases <b>Superfamily:</b> Metallo-dependent phosphatases <b>Family:</b> DR1281-like
34	<a href="#">c2m59A_</a>	Alignment	not modelled	16.7	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> vascular endothelial growth factor receptor 2; <b>PDBTitle:</b> spatial structure of dimeric vegfr2 membrane domain in dpc micelles
35	<a href="#">c2m59B_</a>	Alignment	not modelled	16.7	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> vascular endothelial growth factor receptor 2; <b>PDBTitle:</b> spatial structure of dimeric vegfr2 membrane domain in dpc micelles
36	<a href="#">c3hfxA_</a>	Alignment	not modelled	16.1	14	<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
37	<a href="#">c1pi8A_</a>	Alignment	not modelled	15.5	26	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> vpu protein; <b>PDBTitle:</b> structure of the channel-forming trans-membrane domain of2 virus protein "u" (vpu) from hiv-1
38	<a href="#">c2gohA_</a>	Alignment	not modelled	15.5	26	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> vpu protein; <b>PDBTitle:</b> three-dimensional structure of the trans-membrane domain of2 vpu from hiv-1 in aligned phospholipid bicelles
39	<a href="#">c1pjeA_</a>	Alignment	not modelled	15.5	26	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> vpu protein; <b>PDBTitle:</b> structure of the channel-forming trans-membrane domain of2 virus protein "u"(vpu) from hiv-1
40	<a href="#">c1pi7A_</a>	Alignment	not modelled	15.5	26	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> vpu protein; <b>PDBTitle:</b> structure of the channel-forming trans-membrane domain of2 virus protein "u" (vpu) from hiv-1
41	<a href="#">c2gofA_</a>	Alignment	not modelled	15.5	26	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> vpu protein; <b>PDBTitle:</b> three-dimensional structure of the trans-membrane domain of2 vpu from hiv-1 in aligned phospholipid bicelles
42	<a href="#">c5yq7C_</a>	Alignment	not modelled	12.8	21	<b>PDB header:</b> photosynthesis <b>Chain:</b> C: <b>PDB Molecule:</b> cytochrome subunit of photosynthetic reaction center; <b>PDBTitle:</b> cryo-em structure of the rc-lh core complex from roseiflexus2 castenholzii
43	<a href="#">c6f0kA_</a>	Alignment	not modelled	12.8	17	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome c family protein; <b>PDBTitle:</b> alternative complex iii
44	<a href="#">c2xagA_</a>	Alignment	not modelled	11.8	16	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> lysine-specific histone demethylase 1; <b>PDBTitle:</b> crystal structure of lsd1-corest in complex with para-bromo-2 (-)-trans-2-phenylcyclopropyl-1-amine
45	<a href="#">c2v1dA_</a>	Alignment	not modelled	11.8	16	<b>PDB header:</b> oxidoreductase/repressor <b>Chain:</b> A: <b>PDB Molecule:</b> lysine-specific histone demethylase 1; <b>PDBTitle:</b> structural basis of lsd1-corest selectivity in histone h32 recognition
46	<a href="#">c2voyE_</a>	Alignment	not modelled	10.1	12	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> sarcoplasmic/endoplasmic reticulum calcium atpase 1; <b>PDBTitle:</b> cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus
47	<a href="#">c3dinD_</a>	Alignment	not modelled	8.9	26	<b>PDB header:</b> membrane protein, protein transport <b>Chain:</b> D: <b>PDB Molecule:</b> preprotein translocase subunit sece; <b>PDBTitle:</b> crystal structure of the protein-translocation complex formed by the2 secy channel and the seca atpase
48	<a href="#">d1qf6a1</a>	Alignment	not modelled	8.7	17	<b>Fold:</b> Anticodon-binding domain-like <b>Superfamily:</b> Class II aaRS ABD-related <b>Family:</b> Anticodon-binding domain of Class II aaRS
49	<a href="#">c1yaxB_</a>	Alignment	not modelled	8.6	18	<b>PDB header:</b> transferase, signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> virulence sensor protein phoq, sensor domain; <b>PDBTitle:</b> cystal structure analysis of s.typhimurium phoq sensor domain with2 calcium
50	<a href="#">c5gnnA_</a>	Alignment	not modelled	8.3	38	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> lipid binding protein; <b>PDBTitle:</b> crystal structure of lipid binding protein nakanori at 1.6a
51	<a href="#">c4alzA_</a>	Alignment	not modelled	7.8	19	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> yop proteins translocation protein d; <b>PDBTitle:</b> the yersinia t3ss basal body component yscd reveals a different2 structural periplasmatic domain organization to known homologue prgh
52	<a href="#">c4ainB_</a>	Alignment	not modelled	7.2	21	<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.
53	<a href="#">c2w8aC_</a>	Alignment	not modelled	6.7	21	<b>PDB header:</b> membrane protein <b>Chain:</b> C: <b>PDB Molecule:</b> glycine betaine transporter betp; <b>PDBTitle:</b> crystal structure of the sodium-coupled glycine betaine2

						symporter betp from corynebacterium glutamicum with bound3 substrate
54	<a href="#">c5eulE_</a>	Alignment	not modelled	6.3	22	<b>PDB header:</b> protein transport <b>Chain:</b> E; <b>PDB Molecule:</b> preprotein translocase sece subunit; <b>PDBTitle:</b> structure of the seca-secy complex with a translocating polypeptide2 substrate
55	<a href="#">c2jwaA_</a>	Alignment	not modelled	6.2	39	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> receptor tyrosine-protein kinase erbb-2; <b>PDBTitle:</b> erbb2 transmembrane segment dimer spatial structure
56	<a href="#">c2ks1A_</a>	Alignment	not modelled	6.2	39	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> receptor tyrosine-protein kinase erbb-2; <b>PDBTitle:</b> heterodimeric association of transmembrane domains of erbb1 and erbb2 receptors enabling kinase activation
57	<a href="#">c6btmA_</a>	Alignment	not modelled	5.8	5	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> alternative complex iii subunit a; <b>PDBTitle:</b> structure of alternative complex iii from flavobacterium johnsoniae2 (wild type)
58	<a href="#">c4ainE_</a>	Alignment	not modelled	5.5	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E; <b>PDB Molecule:</b> enoyl-[acyl-carrier-protein] reductase [nadph]; <b>PDBTitle:</b> crystal structure of s. aureus fabi (p32)
59	<a href="#">c4tqvJ_</a>	Alignment	not modelled	5.4	27	<b>PDB header:</b> transport protein <b>Chain:</b> J; <b>PDB Molecule:</b> algm2; <b>PDBTitle:</b> crystal structure of a bacterial abc transporter involved in the2 import of the acidic polysaccharide alginate
60	<a href="#">c6cztA_</a>	Alignment	not modelled	5.1	27	<b>PDB header:</b> cell adhesion <b>Chain:</b> A; <b>PDB Molecule:</b> alginate biosynthesis protein algf; <b>PDBTitle:</b> cs-rosetta determined structures of the n-terminal domain of algf from2 p. aeruginosa
61	<a href="#">c2ptgA_</a>	Alignment	not modelled	5.1	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> enoyl-acyl carrier reductase; <b>PDBTitle:</b> crystal structure of eimeria tenella enoyl reductase
62	<a href="#">d1bcga_</a>	Alignment	not modelled	5.1	33	<b>Fold:</b> Knottins (small inhibitors, toxins, lectins) <b>Superfamily:</b> Scorpion toxin-like <b>Family:</b> Long-chain scorpion toxins
63	<a href="#">d1yt8a4</a>	Alignment	not modelled	5.0	16	<b>Fold:</b> Rhodanese/Cell cycle control phosphatase <b>Superfamily:</b> Rhodanese/Cell cycle control phosphatase <b>Family:</b> Multidomain sulfurtransferase (rhodanese)