





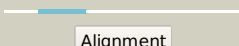
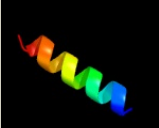
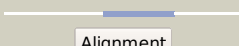
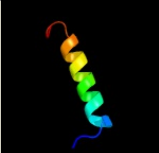
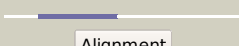

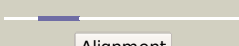


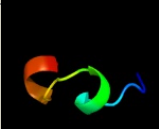



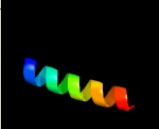

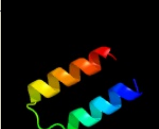


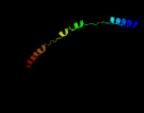


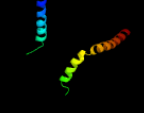
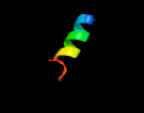




# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2520c_(-)_2837398_2837625
Date	Wed Aug 7 12:50:15 BST 2019
Unique Job ID	96943a3d90c5c4db

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4fi5A_</a>	 Alignment		33.7	27	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> nucleoprotein; <b>PDBTitle:</b> crystal structure of the n-terminal domain of hantaan virus strain 76-2 118 nucleoprotein
2	<a href="#">d1mrza1</a>	 Alignment		33.3	20	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Riboflavin kinase-like <b>Family:</b> ATP-dependent riboflavin kinase-like
3	<a href="#">c3bnwA_</a>	 Alignment		30.9	47	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> riboflavin kinase, putative; <b>PDBTitle:</b> crystal structure of riboflavin kinase from trypanosoma brucei
4	<a href="#">d1n08a_</a>	 Alignment		30.3	12	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Riboflavin kinase-like <b>Family:</b> ATP-dependent riboflavin kinase-like
5	<a href="#">c3ff5B_</a>	 Alignment		28.7	13	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> peroxisomal biogenesis factor 14; <b>PDBTitle:</b> crystal structure of the conserved n-terminal domain of the2 peroxisomal matrix-protein-import receptor, pex14p
6	<a href="#">c4pu4C_</a>	 Alignment		17.1	21	<b>PDB header:</b> toxin/antitoxin/dna <b>Chain:</b> C: <b>PDB Molecule:</b> toxin-antitoxin system antidote transcriptional repressor <b>PDBTitle:</b> shewanella oneidensis mr-1 toxin antitoxin system hipa, hipb and its2 operator dna complex (space group p21)
7	<a href="#">d1nb9a_</a>	 Alignment		16.8	20	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Riboflavin kinase-like <b>Family:</b> ATP-dependent riboflavin kinase-like
8	<a href="#">c4cc9C_</a>	 Alignment		15.6	50	<b>PDB header:</b> protein binding <b>Chain:</b> C: <b>PDB Molecule:</b> deoxynucleoside triphosphate triphosphohydrolase samhd1; <b>PDBTitle:</b> crystal structure of human samhd1 (amino acid residues 582-626) bound2 to vpx isolated from sooty mangabey and human dcaf1 (amino acid3 residues 1058-1396)
9	<a href="#">c4xngC_</a>	 Alignment		14.2	44	<b>PDB header:</b> unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized protein mg218.1; <b>PDBTitle:</b> central domain of mycoplasma genitalium terminal organelle protein2 mg491
10	<a href="#">c6adqP_</a>	 Alignment		13.3	32	<b>PDB header:</b> electron transport <b>Chain:</b> P: <b>PDB Molecule:</b> prokaryotic respiratory supercomplex associate factor 1 <b>PDBTitle:</b> respiratory complex ciii2civ2sod2 from mycobacterium smegmatis
11	<a href="#">c5ikfA_</a>	 Alignment		12.8	25	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> chromatin remodeling factor mit1; <b>PDBTitle:</b> crystal structure of the c-terminal domain of the mit1 nucleosome2 remodeler in complex with clr1

12	<a href="#">c5aonB_</a>	Alignment		12.6	18	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> peroxin 14; <b>PDBTitle:</b> crystal structure of the conserved n-terminal domain of2 pex14 from trypanosoma brucei
13	<a href="#">c2x0kB_</a>	Alignment		11.9	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> riboflavin biosynthesis protein ribf; <b>PDBTitle:</b> crystal structure of modular fad synthetase from2 corynebacterium ammoniagenes
14	<a href="#">c3hd7A_</a>	Alignment		11.8	18	<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
15	<a href="#">c1sfcl_</a>	Alignment		10.0	20	<b>PDB header:</b> transport protein <b>Chain:</b> I: <b>PDB Molecule:</b> protein (synaptobrevin 2); <b>PDBTitle:</b> neuronal synaptic fusion complex
16	<a href="#">d1k1fa_</a>	Alignment		9.9	13	<b>Fold:</b> Bcr-Abl oncoprotein oligomerization domain <b>Superfamily:</b> Bcr-Abl oncoprotein oligomerization domain <b>Family:</b> Bcr-Abl oncoprotein oligomerization domain
17	<a href="#">c2kogA_</a>	Alignment		9.9	18	<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
18	<a href="#">c2w85A_</a>	Alignment		9.7	18	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> peroxisomal membrane anchor protein pex14; <b>PDBTitle:</b> structure of pex14 in complex with pex19
19	<a href="#">c5l87A_</a>	Alignment		9.4	18	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> peroxin 14; <b>PDBTitle:</b> targeting the pex14-pex5 interaction by small molecules provides novel2 therapeutic routes to treat trypanosomiasis.
20	<a href="#">c1n7sA_</a>	Alignment		9.3	20	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> vesicle-associated membrane protein 2; <b>PDBTitle:</b> high resolution structure of a truncated neuronal snare complex
21	<a href="#">c4z1ml_</a>	Alignment	not modelled	9.3	44	<b>PDB header:</b> hydrolase <b>Chain:</b> I: <b>PDB Molecule:</b> atpase inhibitor, mitochondrial; <b>PDBTitle:</b> bovine f1-atpase inhibited by three copies of the inhibitor protein2 if1 crystallised in the presence of thiophosphate.
22	<a href="#">c4tt3l_</a>	Alignment	not modelled	9.3	44	<b>PDB header:</b> hydrolase <b>Chain:</b> I: <b>PDB Molecule:</b> atpase inhibitor, mitochondrial; <b>PDBTitle:</b> the pathway of binding of the intrinsically disordered mitochondrial2 inhibitor protein to f1-atpase
23	<a href="#">c4zigB_</a>	Alignment	not modelled	9.2	19	<b>PDB header:</b> apoptosis <b>Chain:</b> B: <b>PDB Molecule:</b> bh3-interacting domain death agonist; <b>PDBTitle:</b> crystal structure of core/latch dimer of bax in complex with2 bidbh3mini
24	<a href="#">c2qdgB_</a>	Alignment	not modelled	9.0	31	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> talins-1; <b>PDBTitle:</b> crystal structure of the talin dimerisation domain
25	<a href="#">c2v7sA_</a>	Alignment	not modelled	8.7	30	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> probable conserved lipoprotein lppa; <b>PDBTitle:</b> crystal structure of the putative lipoprotein lppa from2 mycobacterium tuberculosis
26	<a href="#">c5j0lC_</a>	Alignment	not modelled	8.5	24	<b>PDB header:</b> de novo protein <b>Chain:</b> C: <b>PDB Molecule:</b> designed protein 3l6hc2_2; <b>PDBTitle:</b> de novo design of protein homo-oligomers with modular hydrogen bond2 network-mediated specificity
27	<a href="#">c1gl2A_</a>	Alignment	not modelled	8.5	8	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> endobrevin; <b>PDBTitle:</b> crystal structure of an endosomal snare core complex
28	<a href="#">c3vepC_</a>	Alignment	not modelled	8.1	69	<b>PDB header:</b> membrane protein/transcription <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized protein rv3413c/mt3522; <b>PDBTitle:</b> crystal structure of sigd4 in complex with its negative regulator rsda <b>PDB header:</b> membrane protein/transcription

29	<a href="#">c3vepX_</a>	Alignment	not modelled	8.1	69	<b>Chain:</b> X; <b>PDB Molecule:</b> uncharacterized protein rv3413c/mt3522; <b>PDBTitle:</b> crystal structure of sigd4 in complex with its negative regulator rsda
30	<a href="#">c3j2wE_</a>	Alignment	not modelled	8.0	30	<b>PDB header:</b> virus <b>Chain:</b> E; <b>PDB Molecule:</b> glycoprotein e1; <b>PDBTitle:</b> electron cryo-microscopy of chikungunya virus
31	<a href="#">c3j2wH_</a>	Alignment	not modelled	8.0	30	<b>PDB header:</b> virus <b>Chain:</b> H; <b>PDB Molecule:</b> glycoprotein e1; <b>PDBTitle:</b> electron cryo-microscopy of chikungunya virus
32	<a href="#">c2myxA_</a>	Alignment	not modelled	7.2	17	<b>PDB header:</b> ubiquitin-binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> coupling of ubiquitin conjugation to er degradation protein <b>PDBTitle:</b> structure of the cue domain of yeast cue1
33	<a href="#">d1zkea1</a>	Alignment	not modelled	7.1	30	<b>Fold:</b> ROP-like <b>Superfamily:</b> HP1531-like <b>Family:</b> HP1531-like
34	<a href="#">c1t6zB_</a>	Alignment	not modelled	6.9	24	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> riboflavin kinase/fmn adenyllyltransferase; <b>PDBTitle:</b> crystal structure of riboflavin bound tm379
35	<a href="#">c3r84F_</a>	Alignment	not modelled	6.8	31	<b>PDB header:</b> transcription <b>Chain:</b> F; <b>PDB Molecule:</b> mediator of rna polymerase ii transcription subunit 22; <b>PDBTitle:</b> structure of the mediator head subcomplex med11/22
36	<a href="#">c4k08A_</a>	Alignment	not modelled	6.7	17	<b>PDB header:</b> signaling protein <b>Chain:</b> A; <b>PDB Molecule:</b> methyl-accepting chemotaxis sensory transducer; <b>PDBTitle:</b> periplasmic sensor domain of chemotaxis protein, adeh_3718
37	<a href="#">c1hf9B_</a>	Alignment	not modelled	6.7	13	<b>PDB header:</b> atpase inhibitor <b>Chain:</b> B; <b>PDB Molecule:</b> atpase inhibitor (mitochondrial); <b>PDBTitle:</b> c-terminal coiled-coil domain from bovine if1
38	<a href="#">c5z2wB_</a>	Alignment	not modelled	6.4	29	<b>PDB header:</b> cell cycle <b>Chain:</b> B; <b>PDB Molecule:</b> cell division protein ftsb; <b>PDBTitle:</b> crystal structure of the bacterial cell division protein ftsq and ftsb
39	<a href="#">c2npsA_</a>	Alignment	not modelled	6.2	20	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> vesicle-associated membrane protein 4; <b>PDBTitle:</b> crystal structure of the early endosomal snare complex
40	<a href="#">c5i7cA_</a>	Alignment	not modelled	6.1	21	<b>PDB header:</b> structural protein <b>Chain:</b> A; <b>PDB Molecule:</b> centrosomin; <b>PDBTitle:</b> centrosomin-motif 2 (cm2) domain of drosophila melanogaster2 centrosomin (cnn)
41	<a href="#">c1zv8B_</a>	Alignment	not modelled	6.0	40	<b>PDB header:</b> viral protein <b>Chain:</b> B; <b>PDB Molecule:</b> e2 glycoprotein; <b>PDBTitle:</b> a structure-based mechanism of sars virus membrane fusion
42	<a href="#">c1avoA_</a>	Alignment	not modelled	5.9	24	<b>PDB header:</b> proteasome activator <b>Chain:</b> A; <b>PDB Molecule:</b> 11s regulator; <b>PDBTitle:</b> proteasome activator reg(alpha)
43	<a href="#">c3bbzA_</a>	Alignment	not modelled	5.9	36	<b>PDB header:</b> viral protein, replication <b>Chain:</b> A; <b>PDB Molecule:</b> p protein; <b>PDBTitle:</b> structure of the nucleocapsid-binding domain from the mumps2 virus phosphoprotein
44	<a href="#">c2v51E_</a>	Alignment	not modelled	5.8	38	<b>PDB header:</b> structural protein/contractile protein <b>Chain:</b> E; <b>PDB Molecule:</b> mk1/myocardin-like protein 1; <b>PDBTitle:</b> structure of mal-rpel1 complexed to actin
45	<a href="#">c2v51F_</a>	Alignment	not modelled	5.8	38	<b>PDB header:</b> structural protein/contractile protein <b>Chain:</b> F; <b>PDB Molecule:</b> mk1/myocardin-like protein 1; <b>PDBTitle:</b> structure of mal-rpel1 complexed to actin
46	<a href="#">d1wglA_</a>	Alignment	not modelled	5.7	24	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> CUE domain
47	<a href="#">c4c0xA_</a>	Alignment	not modelled	5.6	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> fmn-dependent nadh-azoreductase 1; <b>PDBTitle:</b> the crystal structure of ppazor in complex with anthraquinone-2-2 sulfonate
48	<a href="#">d1t6aa_</a>	Alignment	not modelled	5.6	20	<b>Fold:</b> TBP-like <b>Superfamily:</b> Rbstp2229 protein <b>Family:</b> Rbstp2229 protein
49	<a href="#">c4gqmA_</a>	Alignment	not modelled	5.3	7	<b>PDB header:</b> unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> ct009; <b>PDBTitle:</b> crystal structure of a helix-turn-helix containing hypothetical2 protein (ct009) from chlamydia trachomatis in a sub-domain swap3 conformation
50	<a href="#">c5xauD_</a>	Alignment	not modelled	5.2	11	<b>PDB header:</b> cell adhesion <b>Chain:</b> D; <b>PDB Molecule:</b> laminin subunit alpha-5; <b>PDBTitle:</b> crystal structure of integrin binding fragment of laminin-511