



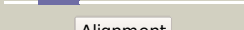








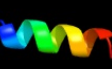


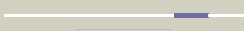






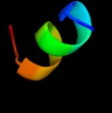









# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1517_(-)_1708877_1709641
Date	Fri Aug 2 13:30:10 BST 2019
Unique Job ID	10709d86191658cc

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5kvA_</a>	 Alignment		96.4	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome c-type biogenesis protein ccda; <b>PDBTitle:</b> solution nmr structure of the membrane electron transporter ccda
2	<a href="#">d2o8pa1</a>	 Alignment		18.0	30	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> 14-3-3 protein <b>Family:</b> 14-3-3 protein
3	<a href="#">d1rc2a_</a>	 Alignment		17.8	26	<b>Fold:</b> Aquaporin-like <b>Superfamily:</b> Aquaporin-like <b>Family:</b> Aquaporin-like
4	<a href="#">c5wlbF_</a>	 Alignment		17.4	50	<b>PDB header:</b> protein binding <b>Chain:</b> F: <b>PDB Molecule:</b> 225-15 b; <b>PDBTitle:</b> kras g12v, bound to gppnhp and miniprotein 225-15a/b
5	<a href="#">c5wlbC_</a>	 Alignment		15.6	50	<b>PDB header:</b> protein binding <b>Chain:</b> C: <b>PDB Molecule:</b> 225-15 b; <b>PDBTitle:</b> kras g12v, bound to gppnhp and miniprotein 225-15a/b
6	<a href="#">c6o4mA_</a>	 Alignment		13.8	21	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> melittin; <b>PDBTitle:</b> racemic melittin
7	<a href="#">c6o4mB_</a>	 Alignment		13.8	21	<b>PDB header:</b> toxin <b>Chain:</b> B: <b>PDB Molecule:</b> melittin; <b>PDBTitle:</b> racemic melittin
8	<a href="#">c6dstA_</a>	 Alignment		13.8	21	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> melittin; <b>PDBTitle:</b> recombinant melittin
9	<a href="#">c2mltB_</a>	 Alignment		13.8	21	<b>PDB header:</b> toxin (hemolytic polypeptide) <b>Chain:</b> B: <b>PDB Molecule:</b> melittin; <b>PDBTitle:</b> melittin
10	<a href="#">c2mltA_</a>	 Alignment		13.8	21	<b>PDB header:</b> toxin (hemolytic polypeptide) <b>Chain:</b> A: <b>PDB Molecule:</b> melittin; <b>PDBTitle:</b> melittin
11	<a href="#">d3efza1</a>	 Alignment		13.0	27	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> 14-3-3 protein <b>Family:</b> 14-3-3 protein

12	<a href="#">c3efzA</a>	Alignment		13.0	27	<b>PDB header:</b> signaling protein <b>Chain:</b> A; <b>PDB Molecule:</b> 14-3-3 protein; <b>PDBTitle:</b> crystal structure of a 14-3-3 protein from cryptosporidium parvum2 (cgd1_2980)
13	<a href="#">c6a9wA</a>	Alignment		12.4	45	<b>PDB header:</b> replication <b>Chain:</b> A; <b>PDB Molecule:</b> primase; <b>PDBTitle:</b> structure of the bifunctional dna primase-polymerase from phage nrs-1
14	<a href="#">c2mw6A</a>	Alignment		12.2	25	<b>PDB header:</b> toxin <b>Chain:</b> A; <b>PDB Molecule:</b> melittin; <b>PDBTitle:</b> structure of the bee venom toxin melittin with [(c5h5)ru]+ fragment2 attached to the tryptophan residue
15	<a href="#">c2npmB</a>	Alignment		10.8	60	<b>PDB header:</b> protein binding <b>Chain:</b> B; <b>PDB Molecule:</b> 14-3-3 domain containing protein; <b>PDBTitle:</b> crystal structure of cryptosporidium parvum 14-3-3 protein in complex2 with peptide
16	<a href="#">c1bh1A</a>	Alignment		10.6	27	<b>PDB header:</b> toxin <b>Chain:</b> A; <b>PDB Molecule:</b> melittin; <b>PDBTitle:</b> structural studies of d-pro melittin, nmr, 20 structures
17	<a href="#">c2n1pA</a>	Alignment		10.3	31	<b>PDB header:</b> viral protein <b>Chain:</b> A; <b>PDB Molecule:</b> non-structural protein 5b, ns5b; <b>PDBTitle:</b> structure of the c-terminal membrane domain of hcv ns5b protein
18	<a href="#">d1o9da</a>	Alignment		10.2	60	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> 14-3-3 protein <b>Family:</b> 14-3-3 protein
19	<a href="#">c3bvdC</a>	Alignment		9.5	31	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C; <b>PDB Molecule:</b> cytochrome c oxidase polypeptide 2a; <b>PDBTitle:</b> structure of surface-engineered cytochrome ba3 oxidase from thermus2 thermophilus under xenon pressure, 100psi 5min
20	<a href="#">d1xmec1</a>	Alignment		9.5	31	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Bacterial ba3 type cytochrome c oxidase subunit IIa <b>Family:</b> Bacterial ba3 type cytochrome c oxidase subunit IIa
21	<a href="#">d2o02a1</a>	Alignment	not modelled	9.5	60	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> 14-3-3 protein <b>Family:</b> 14-3-3 protein
22	<a href="#">c3bjrA</a>	Alignment	not modelled	9.4	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> putative carboxylesterase; <b>PDBTitle:</b> crystal structure of a putative carboxylesterase (lp_1002) from2 lactobacillus plantarum wcf1 at 2.09 a resolution
23	<a href="#">c2c1nA</a>	Alignment	not modelled	9.1	60	<b>PDB header:</b> signaling protein <b>Chain:</b> A; <b>PDB Molecule:</b> 14-3-3 protein zeta/delta; <b>PDBTitle:</b> molecular basis for the recognition of phosphorylated and2 phosphoacetylated histone h3 by 14-3-3
24	<a href="#">c3kl4B</a>	Alignment	not modelled	8.8	71	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> signal peptide of yeast dipeptidyl aminopeptidase b; <b>PDBTitle:</b> recognition of a signal peptide by the signal recognition particle
25	<a href="#">c6iz4G</a>	Alignment	not modelled	8.6	13	<b>PDB header:</b> membrane protein <b>Chain:</b> G; <b>PDB Molecule:</b> trimeric intracellular cation channel type b-b; <b>PDBTitle:</b> crystal structure analysis of tric counter-ion channels in calcium2 release
26	<a href="#">c3e6yB</a>	Alignment	not modelled	8.4	60	<b>PDB header:</b> signaling protein <b>Chain:</b> B; <b>PDB Molecule:</b> 14-3-3-like protein c; <b>PDBTitle:</b> structure of 14-3-3 in complex with the differentiation-inducing agent2 cotylenin a
27	<a href="#">c1izlC</a>	Alignment	not modelled	8.1	45	<b>PDB header:</b> photosynthesis <b>Chain:</b> C; <b>PDB Molecule:</b> photosystem ii: subunit psbc; <b>PDBTitle:</b> crystal structure of photosystem ii
28	<a href="#">c6iz0A</a>	Alignment	not modelled	7.5	18	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> trimeric intracellular cation channel type a;

						<b>PDBTitle:</b> crystal structure analysis of a eukaryotic membrane protein
29	<a href="#">c1zIM_</a>	Alignment	not modelled	7.4	45	<b>PDB header:</b> photosynthesis <b>Chain:</b> M: <b>PDB Molecule:</b> photosystem ii: subunit psbc; <b>PDBTitle:</b> crystal structure of photosystem ii
30	<a href="#">c2kv5A_</a>	Alignment	not modelled	6.6	47	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein rna1; <b>PDBTitle:</b> solution structure of the par toxin fst in dpc micelles
31	<a href="#">d2axtc1</a>	Alignment	not modelled	6.5	45	<b>Fold:</b> Photosystem II antenna protein-like <b>Superfamily:</b> Photosystem II antenna protein-like <b>Family:</b> Photosystem II antenna protein-like
32	<a href="#">c2axtc_</a>	Alignment	not modelled	6.5	45	<b>PDB header:</b> electron transport <b>Chain:</b> C: <b>PDB Molecule:</b> photosystem ii cp43 protein; <b>PDBTitle:</b> crystal structure of photosystem ii from thermosynechococcus elongatus
33	<a href="#">d1uptb_</a>	Alignment	not modelled	6.0	41	<b>Fold:</b> GRIP domain <b>Superfamily:</b> GRIP domain <b>Family:</b> GRIP domain
34	<a href="#">c5x42B_</a>	Alignment	not modelled	5.7	31	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> icmo (dotl); <b>PDBTitle:</b> structure of dotl(590-659)-dotn derived from legionella pneumophila
35	<a href="#">c5ykaA_</a>	Alignment	not modelled	5.6	25	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein kdo0; <b>PDBTitle:</b> crystal structure of the kdo hydroxylase kdo0, a non-heme fe(ii)2 alphaketoglutarate dependent dioxygenase in complex with cobalt(ii)
36	<a href="#">c2l1nA_</a>	Alignment	not modelled	5.5	26	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution nmr structure of the protein yp_399305.1
37	<a href="#">c4ct0B_</a>	Alignment	not modelled	5.5	17	<b>PDB header:</b> circadian clock protein <b>Chain:</b> B: <b>PDB Molecule:</b> period circadian protein homolog 2; <b>PDBTitle:</b> crystal structure of mouse cryptochrome1 in complex with period2