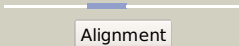

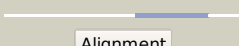

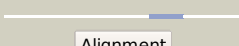


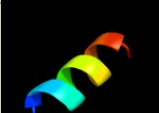





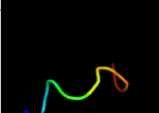








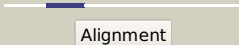




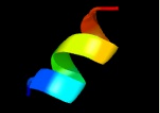




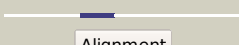




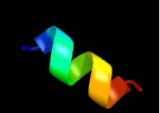


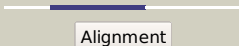

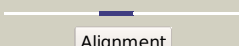
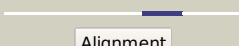
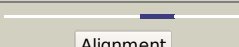


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2433c_(-)_2728854_2729144
Date	Wed Aug 7 12:50:05 BST 2019
Unique Job ID	b36890118a9e28a7

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1o82a_</a>	 Alignment		27.9	41	<b>Fold:</b> Saposin-like <b>Superfamily:</b> Bacteriocin AS-48 <b>Family:</b> Bacteriocin AS-48
2	<a href="#">c5kw2A_</a>	 Alignment		21.2	16	<b>PDB header:</b> fatty acid binding protein/hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> free fatty acid receptor 1,lysozyme,free fatty acid <b>PDBTitle:</b> the extra-helical binding site of gpr40 and the structural basis for2 allosteric agonism and incretin stimulation
3	<a href="#">c2kk1A_</a>	 Alignment		20.7	9	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine-protein kinase abl2; <b>PDBTitle:</b> solution structure of c-terminal domain of tyrosine-protein2 kinase abl2 from homo sapiens, northeast structural3 genomics consortium (nesg) target hr5537a
4	<a href="#">c1ijjA_</a>	 Alignment		16.3	33	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> erbB-2 receptor protein-tyrosine kinase; <b>PDBTitle:</b> solution structure of the neu/erbB-2 membrane spanning2 segment
5	<a href="#">d1jmx2</a>	 Alignment		16.3	22	<b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
6	<a href="#">d1pbya2</a>	 Alignment		15.0	24	<b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
7	<a href="#">c2mmjA_</a>	 Alignment		11.9	40	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> maculatin g15; <b>PDBTitle:</b> structure of a peptoid analogue of maculatin g15 in dpc micelles
8	<a href="#">c4wrpB_</a>	 Alignment		11.8	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> the c-terminal domain of gene product lpg0944 from legionella2 pneumophila subsp. pneumophila str. philadelphia 1
9	<a href="#">c1jmxA_</a>	 Alignment		10.4	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> amine dehydrogenase; <b>PDBTitle:</b> crystal structure of a quinohemoprotein amine dehydrogenase2 from pseudomonas putida
10	<a href="#">c5lc5c_</a>	 Alignment		9.1	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> nadH dehydrogenase [ubiquinone] iron-sulfur protein 3, <b>PDBTitle:</b> structure of mammalian respiratory complex i, class2
11	<a href="#">c2ld7B_</a>	 Alignment		8.3	12	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> paired amphipathic helix protein sin3a; <b>PDBTitle:</b> solution structure of the mSin3a-pah3-sap30 sid complex

12	<a href="#">c2l53B_</a>	 Alignment		7.9	29	<b>PDB header:</b> ca-binding protein/proton transport <b>Chain:</b> B: <b>PDB Molecule:</b> voltage-gated sodium channel type v alpha isoform b <b>PDBTitle:</b> solution nmr structure of apo-calmodulin in complex with the iq motif2 of human cardiac sodium channel nav1.5
13	<a href="#">c2kpeB_</a>	 Alignment		7.2	40	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> glycophorin-a; <b>PDBTitle:</b> refined structure of glycophorin a transmembrane segment dimer in dpc2 micelles
14	<a href="#">c2kpeA_</a>	 Alignment		7.2	40	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> glycophorin-a; <b>PDBTitle:</b> refined structure of glycophorin a transmembrane segment dimer in dpc2 micelles
15	<a href="#">c2amnA_</a>	 Alignment		7.1	21	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> cathelicidin; <b>PDBTitle:</b> solution structure of fowlicidin-1, a novel cathelicidin2 antimicrobial peptide from chicken
16	<a href="#">c5eh6A_</a>	 Alignment		6.9	36	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> glycophorin-a; <b>PDBTitle:</b> crystal structure of the glycophorin a transmembrane monomer in2 lipidic cubic phase
17	<a href="#">c5eh4A_</a>	 Alignment		6.9	36	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> glycophorin-a; <b>PDBTitle:</b> crystal structure of the glycophorin a transmembrane dimer in lipidic2 cubic phase
18	<a href="#">c5eh4B_</a>	 Alignment		6.9	36	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> glycophorin-a; <b>PDBTitle:</b> crystal structure of the glycophorin a transmembrane dimer in lipidic2 cubic phase
19	<a href="#">c5eh4D_</a>	 Alignment		6.9	36	<b>PDB header:</b> membrane protein <b>Chain:</b> D: <b>PDB Molecule:</b> glycophorin-a; <b>PDBTitle:</b> crystal structure of the glycophorin a transmembrane dimer in lipidic2 cubic phase
20	<a href="#">c5eh4C_</a>	 Alignment		6.9	36	<b>PDB header:</b> membrane protein <b>Chain:</b> C: <b>PDB Molecule:</b> glycophorin-a; <b>PDBTitle:</b> crystal structure of the glycophorin a transmembrane dimer in lipidic2 cubic phase
21	<a href="#">c6ca8A_</a>	 Alignment	not modelled	6.8	13	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> dna topoisomerase 2; <b>PDBTitle:</b> crystal structure of plasmodium falciparum topoisomerase ii dna-2 binding, cleavage and re-ligation domain
22	<a href="#">c5ldwc_</a>	 Alignment	not modelled	6.3	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> nadh dehydrogenase [ubiquinone] iron-sulfur protein 3, <b>PDBTitle:</b> structure of mammalian respiratory complex i, class1
23	<a href="#">c3j47R_</a>	 Alignment	not modelled	5.6	36	<b>PDB header:</b> protein binding <b>Chain:</b> R: <b>PDB Molecule:</b> 26s proteasome regulatory subunit rpn7; <b>PDBTitle:</b> formation of an intricate helical bundle dictates the assembly of the2 26s proteasome lid
24	<a href="#">c3ixzB_</a>	 Alignment	not modelled	5.5	28	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> potassium-transporting atpase subunit beta; <b>PDBTitle:</b> pig gastric h+/k+-atpase complexed with aluminium fluoride
25	<a href="#">c4oojB_</a>	 Alignment	not modelled	5.2	27	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> sidc, interaptin; <b>PDBTitle:</b> crystal structure of the n-terminal domain of the legionella2 pneumophila protein sidc at 2.4a resolution