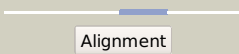
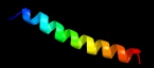
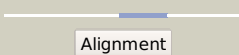
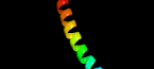
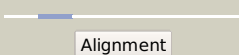

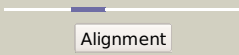
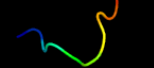
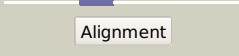

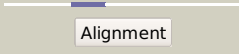

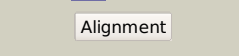

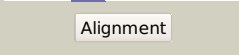
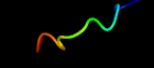
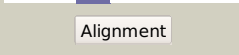

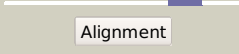
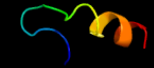
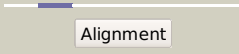
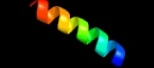


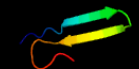
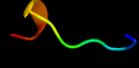



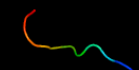



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0912_(-)_1016240_1016689
Date	Fri Jul 26 01:50:50 BST 2019
Unique Job ID	9bf3c7aee5fe2aeb

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2l9uA_</a>	 Alignment		20.1	32	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> receptor tyrosine-protein kinase erbB-3; <b>PDBTitle:</b> spatial structure of dimeric erbB3 transmembrane domain
2	<a href="#">c2l9uB_</a>	 Alignment		20.1	32	<b>PDB header:</b> membrane protein <b>Chain:</b> B; <b>PDB Molecule:</b> receptor tyrosine-protein kinase erbB-3; <b>PDBTitle:</b> spatial structure of dimeric erbB3 transmembrane domain
3	<a href="#">d1vf5c3</a>	 Alignment		20.0	26	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Cytochrome f subunit of the cytochrome b6f complex, transmembrane anchor <b>Family:</b> Cytochrome f subunit of the cytochrome b6f complex, transmembrane anchor
4	<a href="#">c4k0qC_</a>	 Alignment		17.8	55	<b>PDB header:</b> ribosome <b>Chain:</b> C; <b>PDB Molecule:</b> 50s ribosomal protein l1; <b>PDBTitle:</b> crystal structure of thermus thermophilus 70s containing trnas and2 mrna stop codon with pseudouridine
5	<a href="#">c2memA_</a>	 Alignment		17.5	42	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> sex comb on midleg-like protein 2; <b>PDBTitle:</b> solution nmr structure of sled domain of scm12
6	<a href="#">c4k0mC_</a>	 Alignment		17.4	55	<b>PDB header:</b> ribosome <b>Chain:</b> C; <b>PDB Molecule:</b> 50s ribosomal protein l1; <b>PDBTitle:</b> crystal structure of thermus thermophilus 70s containing trnas and2 mrna stop codon with pseudouridine
7	<a href="#">c4wwtA_</a>	 Alignment		15.2	55	<b>PDB header:</b> ribosome <b>Chain:</b> A; <b>PDB Molecule:</b> 50s ribosomal protein l1; <b>PDBTitle:</b> crystal structure of bactobolin a bound to 70s ribosome-trna complex
8	<a href="#">c4wweA_</a>	 Alignment		13.1	55	<b>PDB header:</b> ribosome <b>Chain:</b> A; <b>PDB Molecule:</b> 50s ribosomal protein l1; <b>PDBTitle:</b> crystal structure of bactobolin a bound to 70s ribosome-trna complex
9	<a href="#">c2jx5A_</a>	 Alignment		13.0	56	<b>PDB header:</b> ribosomal protein <b>Chain:</b> A; <b>PDB Molecule:</b> glub(s27a); <b>PDBTitle:</b> solution structure of the ubiquitin domain n-terminal to2 the s27a ribosomal subunit of giardia lamblia
10	<a href="#">c5tszA_</a>	 Alignment		10.9	25	<b>PDB header:</b> cell invasion <b>Chain:</b> A; <b>PDB Molecule:</b> pv cell-traversal protein; <b>PDBTitle:</b> crystal structure of plasmodium vivax celtsos
11	<a href="#">d1q90a3</a>	 Alignment		10.9	16	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Cytochrome f subunit of the cytochrome b6f complex, transmembrane anchor <b>Family:</b> Cytochrome f subunit of the cytochrome b6f complex, transmembrane anchor

12	<a href="#">c4ndvB_</a>	Alignment		10.7	20	<b>PDB header:</b> sugar binding protein <b>Chain:</b> B; <b>PDB Molecule:</b> alpha-galactosyl-binding lectin; <b>PDBTitle:</b> crystal structure of l. decastes alpha-galactosyl-binding lectin in2 complex with globotriose
13	<a href="#">c2jpkA_</a>	Alignment		10.4	40	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A; <b>PDB Molecule:</b> bacteriocin lactococcin-g subunit beta; <b>PDBTitle:</b> lactococcin g-b in dpc
14	<a href="#">c3a5pD_</a>	Alignment		10.3	36	<b>PDB header:</b> sugar binding protein <b>Chain:</b> D; <b>PDB Molecule:</b> haemagglutinin i; <b>PDBTitle:</b> crystal structure of hemagglutinin
15	<a href="#">c1alnA_</a>	Alignment		10.3	60	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> cytidine deaminase; <b>PDBTitle:</b> crystal structure of cytidine deaminase complexed with 3-deazacytidine
16	<a href="#">d1r5ta_</a>	Alignment		9.9	60	<b>Fold:</b> Cytidine deaminase-like <b>Superfamily:</b> Cytidine deaminase-like <b>Family:</b> Cytidine deaminase
17	<a href="#">c2jpmA_</a>	Alignment		9.1	40	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A; <b>PDB Molecule:</b> bacteriocin lactococcin-g subunit beta; <b>PDBTitle:</b> lactococcin g-b in tfe
18	<a href="#">c5lnkn_</a>	Alignment		9.0	35	<b>PDB header:</b> oxidoreductase <b>Chain:</b> N; <b>PDB Molecule:</b> mitochondrial complex i, nd2 subunit; <b>PDBTitle:</b> entire ovine respiratory complex i
19	<a href="#">c3qoyA_</a>	Alignment		8.2	64	<b>PDB header:</b> ribosomal protein <b>Chain:</b> A; <b>PDB Molecule:</b> 50s ribosomal protein l1; <b>PDBTitle:</b> crystal structure of ribosomal protein l1 from aquifex aeolicus
20	<a href="#">d1alna2</a>	Alignment		8.0	60	<b>Fold:</b> Cytidine deaminase-like <b>Superfamily:</b> Cytidine deaminase-like <b>Family:</b> Cytidine deaminase
21	<a href="#">d1jb0a_</a>	Alignment	not modelled	7.8	36	<b>Fold:</b> Photosystem I subunits PsaA/PsaB <b>Superfamily:</b> Photosystem I subunits PsaA/PsaB <b>Family:</b> Photosystem I subunits PsaA/PsaB
22	<a href="#">d1mzpa_</a>	Alignment	not modelled	7.7	18	<b>Fold:</b> Ribosomal protein L1 <b>Superfamily:</b> Ribosomal protein L1 <b>Family:</b> Ribosomal protein L1
23	<a href="#">c3bboD_</a>	Alignment	not modelled	7.4	36	<b>PDB header:</b> ribosome <b>Chain:</b> D; <b>PDB Molecule:</b> ribosomal protein l1; <b>PDBTitle:</b> homology model for the spinach chloroplast 50s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome
24	<a href="#">d2j01c1</a>	Alignment	not modelled	7.4	55	<b>Fold:</b> Ribosomal protein L1 <b>Superfamily:</b> Ribosomal protein L1 <b>Family:</b> Ribosomal protein L1
25	<a href="#">d1mq0a_</a>	Alignment	not modelled	7.2	60	<b>Fold:</b> Cytidine deaminase-like <b>Superfamily:</b> Cytidine deaminase-like <b>Family:</b> Cytidine deaminase
26	<a href="#">c4eg2G_</a>	Alignment	not modelled	7.1	60	<b>PDB header:</b> hydrolase <b>Chain:</b> G; <b>PDB Molecule:</b> cytidine deaminase; <b>PDBTitle:</b> 2.2 angstrom crystal structure of cytidine deaminase from vibrio2 cholerae in complex with zinc and uridine
27	<a href="#">d1ad2a_</a>	Alignment	not modelled	6.7	55	<b>Fold:</b> Ribosomal protein L1 <b>Superfamily:</b> Ribosomal protein L1 <b>Family:</b> Ribosomal protein L1
28	<a href="#">c5dm7Q_</a>	Alignment	not modelled	6.5	55	<b>PDB header:</b> ribosome <b>Chain:</b> 0; <b>PDB Molecule:</b> 50s ribosomal protein l1; <b>PDBTitle:</b> crystal structure of the 50s ribosomal subunit from deinococcus2 radiodurans in complex with hygromycin a
						<b>PDB header:</b> transport protein <b>Chain:</b> B; <b>PDB Molecule:</b> potassium voltage-gated channel

29	<a href="#">c1s6cB_</a>	Alignment	not modelled	6.1	20	subfamily d member 2; <b>PDBTitle:</b> crystal structure of the complex between kchip1 and kv4.2 n1-30
30	<a href="#">c2gyc2_</a>	Alignment	not modelled	6.0	55	<b>PDB header:</b> ribosome <b>Chain:</b> 2; <b>PDB Molecule:</b> 50s ribosomal protein l1; <b>PDBTitle:</b> structure of the 50s subunit of a secm-stalled e. coli ribosome2 complex obtained by fitting atomic models for rna and protein3 components into cryo-em map emd-1143
31	<a href="#">c1mq5B_</a>	Alignment	not modelled	5.9	38	<b>PDB header:</b> endocytosis/exocytosis <b>Chain:</b> B; <b>PDB Molecule:</b> integral membrane protein sed5; <b>PDBTitle:</b> crystal structure of sly1p in complex with an n-terminal peptide of2 sed5p
32	<a href="#">d2fr5a1</a>	Alignment	not modelled	5.9	60	<b>Fold:</b> Cytidine deaminase-like <b>Superfamily:</b> Cytidine deaminase-like <b>Family:</b> Cytidine deaminase
33	<a href="#">d1uwza_</a>	Alignment	not modelled	5.6	40	<b>Fold:</b> Cytidine deaminase-like <b>Superfamily:</b> Cytidine deaminase-like <b>Family:</b> Cytidine deaminase
34	<a href="#">d1lgha_</a>	Alignment	not modelled	5.5	60	<b>Fold:</b> Light-harvesting complex subunits <b>Superfamily:</b> Light-harvesting complex subunits <b>Family:</b> Light-harvesting complex subunits
35	<a href="#">c2zkr5_</a>	Alignment	not modelled	5.2	45	<b>PDB header:</b> ribosomal protein/rna <b>Chain:</b> 5; <b>PDB Molecule:</b> 60s ribosomal protein l10a; <b>PDBTitle:</b> structure of a mammalian ribosomal 60s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
36	<a href="#">c4gyxA_</a>	Alignment	not modelled	5.1	100	<b>PDB header:</b> structural protein, blood clotting <b>Chain:</b> A; <b>PDB Molecule:</b> type iii collagen fragment in a host peptide stabilized by <b>PDBTitle:</b> the von willebrand factor a3 domain binding region of type iii2 collagen stabilized by the cysteine knot
37	<a href="#">c4gyxB_</a>	Alignment	not modelled	5.1	100	<b>PDB header:</b> structural protein, blood clotting <b>Chain:</b> B; <b>PDB Molecule:</b> type iii collagen fragment in a host peptide stabilized by <b>PDBTitle:</b> the von willebrand factor a3 domain binding region of type iii2 collagen stabilized by the cysteine knot
38	<a href="#">c6et5u_</a>	Alignment	not modelled	5.1	22	<b>PDB header:</b> photosynthesis <b>Chain:</b> U; <b>PDB Molecule:</b> light-harvesting protein b-1015 gamma chain; <b>PDBTitle:</b> reaction centre light harvesting complex 1 from blc. viridis