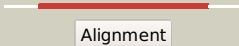
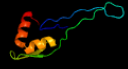


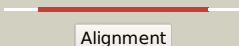

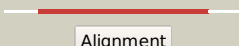
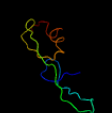
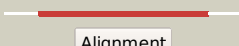

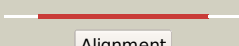
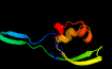
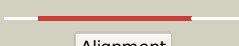


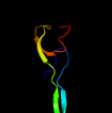

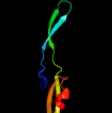

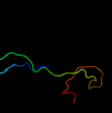

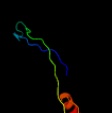
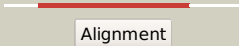

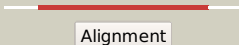
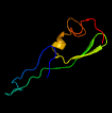

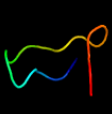
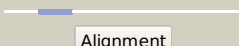

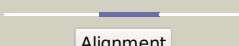
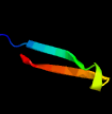
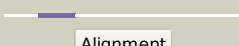

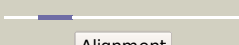



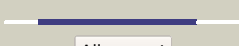


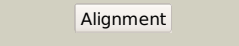

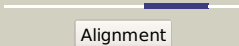
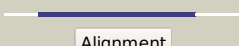

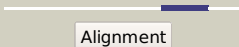



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2058c_(rpmB)_2314833_2315069
Date	Mon Aug 5 13:25:17 BST 2019
Unique Job ID	d16b655a91c91ebb

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6dzpy_</a>	 Alignment		100.0	83	<b>PDB header:</b> ribosome <b>Chain:</b> Y; <b>PDB Molecule:</b> <b>PDBTitle:</b> cryo-em structure of mycobacterium smegmatis c(minus) 50s ribosomal2 subunit
2	<a href="#">d2qamz1</a>	 Alignment		100.0	45	<b>Fold:</b> L28p-like <b>Superfamily:</b> L28p-like <b>Family:</b> Ribosomal protein L28
3	<a href="#">c1vw4S_</a>	 Alignment		100.0	24	<b>PDB header:</b> ribosome <b>Chain:</b> S; <b>PDB Molecule:</b> 54s ribosomal protein l24, mitochondrial; <b>PDBTitle:</b> structure of the yeast mitochondrial large ribosomal subunit
4	<a href="#">c3bboY_</a>	 Alignment		100.0	33	<b>PDB header:</b> ribosome <b>Chain:</b> Y; <b>PDB Molecule:</b> ribosomal protein l28; <b>PDBTitle:</b> homology model for the spinach chloroplast 50s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome
5	<a href="#">d2jz6a1</a>	 Alignment		99.9	37	<b>Fold:</b> L28p-like <b>Superfamily:</b> L28p-like <b>Family:</b> Ribosomal protein L28
6	<a href="#">c4v191_</a>	 Alignment		99.9	20	<b>PDB header:</b> ribosome <b>Chain:</b> 1; <b>PDB Molecule:</b> mitoribosomal protein bl28m, mrpl28; <b>PDBTitle:</b> structure of the large subunit of the mammalian mitoribosome, part 12 of 2
7	<a href="#">c5o60Y_</a>	 Alignment		99.9	44	<b>PDB header:</b> ribosome <b>Chain:</b> Y; <b>PDB Molecule:</b> 50s ribosomal protein l28; <b>PDBTitle:</b> structure of the 50s large ribosomal subunit from mycobacterium2 smegmatis
8	<a href="#">c6ddgl_</a>	 Alignment		99.9	33	<b>PDB header:</b> ribosome/antibiotic <b>Chain:</b> J; <b>PDB Molecule:</b> 50s ribosomal protein l28; <b>PDBTitle:</b> structure of the 50s ribosomal subunit from methicillin resistant2 staphylococcus aureus in complex with the oxazolidinone antibiotic3 lzd-6
9	<a href="#">c2j181_</a>	 Alignment		99.8	26	<b>PDB header:</b> ribosome <b>Chain:</b> 1; <b>PDB Molecule:</b> 50s ribosomal protein l28; <b>PDBTitle:</b> insights into translational termination from the structure2 of rf2 bound to the ribosome (part 4 of 4).3 this file contains the 50s subunit.
10	<a href="#">c4wfaU_</a>	 Alignment		99.4	30	<b>PDB header:</b> ribosome <b>Chain:</b> U; <b>PDB Molecule:</b> 50s ribosomal protein l28; <b>PDBTitle:</b> the crystal structure of the large ribosomal subunit of staphylococcus2 aureus in complex with linezolid
11	<a href="#">d2zjru1</a>	 Alignment		99.2	10	<b>Fold:</b> L28p-like <b>Superfamily:</b> L28p-like <b>Family:</b> Ribosomal protein L28

12	<a href="#">c4ce41_</a>	 Alignment		98.4	27	<b>PDB header:</b> ribosome <b>Chain:</b> 1: <b>PDB Molecule:</b> mrpl28; <b>PDBTitle:</b> 39s large subunit of the porcine mitochondrial ribosome
13	<a href="#">d2j0111</a>	 Alignment		97.6	27	<b>Fold:</b> L28p-like <b>Superfamily:</b> L28p-like <b>Family:</b> Ribosomal protein L28
14	<a href="#">d2cu8a1</a>	 Alignment		38.3	21	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> LIM domain
15	<a href="#">c2k5cA_</a>	 Alignment		20.1	22	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein pf0385; <b>PDBTitle:</b> nmr structure for pf0385
16	<a href="#">c2uz0B_</a>	 Alignment		16.6	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> tributyrin esterase; <b>PDBTitle:</b> the crystal crystal structure of the esta protein, a2 virulence factor esta protein from streptococcus pneumonia
17	<a href="#">c4n0oC_</a>	 Alignment		15.6	43	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> C: <b>PDB Molecule:</b> replicase polyprotein 1ab; <b>PDBTitle:</b> complex structure of arterivirus nonstructural protein 10 (helicase)2 with dna
18	<a href="#">c2elrA_</a>	 Alignment		10.3	43	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> zinc finger protein 406; <b>PDBTitle:</b> solution structure of the 15th c2h2 zinc finger of human2 zinc finger protein 406
19	<a href="#">d2yt9a2</a>	 Alignment		10.1	33	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> Classic zinc finger, C2H2
20	<a href="#">c1dvpA_</a>	 Alignment		9.4	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hepatocyte growth factor-regulated tyrosine <b>PDBTitle:</b> crystal structure of the vhs and fyve tandem domains of hrs,2 a protein involved in membrane trafficking and signal3 transduction
21	<a href="#">c4zxsC_</a>	 Alignment	not modelled	8.8	21	<b>PDB header:</b> viral protein <b>Chain:</b> C: <b>PDB Molecule:</b> virion egress protein ul34; <b>PDBTitle:</b> hsv-1 nuclear egress complex
22	<a href="#">c2fs1A_</a>	 Alignment	not modelled	8.2	21	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> psd-1; <b>PDBTitle:</b> solution structure of psd-1
23	<a href="#">c2oz5A_</a>	 Alignment	not modelled	8.0	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> phosphotyrosine protein phosphatase ptpb; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis protein tyrosine2 phosphatase ptpb in complex with the specific inhibitor omts
24	<a href="#">d1acoa1</a>	 Alignment	not modelled	7.7	8	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> LeuD/IlvD-like <b>Family:</b> LeuD-like
25	<a href="#">c3zyqA_</a>	 Alignment	not modelled	7.4	15	<b>PDB header:</b> signaling <b>Chain:</b> A: <b>PDB Molecule:</b> hepatocyte growth factor-regulated tyrosine kinase <b>PDBTitle:</b> crystal structure of the tandem vhs and fyve domains of hepatocyte2 growth factor-regulated tyrosine kinase substrate (hgs-hrs) at 1.48 a3 resolution
26	<a href="#">d2dmda2</a>	 Alignment	not modelled	7.2	43	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> Classic zinc finger, C2H2
27	<a href="#">d1ywfa1</a>	 Alignment	not modelled	7.0	12	<b>Fold:</b> (Phosphotyrosine protein) phosphatases II <b>Superfamily:</b> (Phosphotyrosine protein) phosphatases II <b>Family:</b> Mycobacterial PtpB-like
		 Alignment				<b>Fold:</b> Cdc48 domain 2-like

28	<a href="#">d1cz5a2</a>	Alignment	not modelled	6.7	50	<b>Superfamily:</b> Cdc48 domain 2-like <b>Family:</b> Cdc48 domain 2-like
29	<a href="#">c5zwnY_</a>	Alignment	not modelled	6.5	43	<b>PDB header:</b> splicing <b>Chain:</b> Y; <b>PDB Molecule:</b> protein luc7; <b>PDBTitle:</b> cryo-em structure of the yeast pre-b complex at an average resolution2 of 3.3 angstrom (part ii: u1 snrnp region)
30	<a href="#">d1gjsa_</a>	Alignment	not modelled	6.3	13	<b>Fold:</b> immunoglobulin/albumin-binding domain-like <b>Superfamily:</b> Bacterial immunoglobulin/albumin-binding domains <b>Family:</b> GA module, an albumin-binding domain
31	<a href="#">d1ej5a_</a>	Alignment	not modelled	5.7	53	<b>Fold:</b> Wiscott-Aldrich syndrome protein, WASP, C-terminal domain <b>Superfamily:</b> Wiscott-Aldrich syndrome protein, WASP, C-terminal domain <b>Family:</b> Wiscott-Aldrich syndrome protein, WASP, C-terminal domain
32	<a href="#">c3iufA_</a>	Alignment	not modelled	5.5	25	<b>PDB header:</b> protein binding <b>Chain:</b> A; <b>PDB Molecule:</b> zinc finger protein ubi-d4; <b>PDBTitle:</b> crystal structure of the c2h2-type zinc finger domain of human ubi-d4
33	<a href="#">c5uwaB_</a>	Alignment	not modelled	5.3	25	<b>PDB header:</b> transport protein <b>Chain:</b> B; <b>PDB Molecule:</b> probable phospholipid-binding protein mlac; <b>PDBTitle:</b> structure of e. coli phospholipid binding protein mlac
34	<a href="#">d2htna1</a>	Alignment	not modelled	5.2	13	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ferritin
35	<a href="#">c2qm0B_</a>	Alignment	not modelled	5.1	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> bes; <b>PDBTitle:</b> crystal structure of bes protein from bacillus cereus