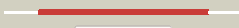

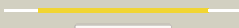
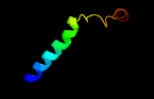
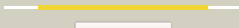

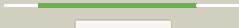



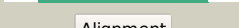

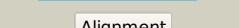

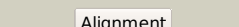

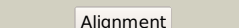

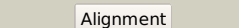









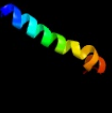




# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1792A_(RVBD1792A)_2030531_2030650
Date	Fri Aug 2 13:30:40 BST 2019
Unique Job ID	96097a2d2455a056

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3ogiD_</a>	 Alignment		99.9	97	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> putative esat-6-like protein 7; <b>PDBTitle:</b> crystal structure of the mycobacterium tuberculosis h37rv esxop2 complex (rv2346c-rv2347c)
2	<a href="#">d1wa8a1</a>	 Alignment		76.2	21	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> EsxAB dimer-like <b>Family:</b> ESAT-6 like
3	<a href="#">c4lwsA_</a>	 Alignment		73.8	32	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> esxa : esxb (semet) hetero-dimer from thermomonospora curvata
4	<a href="#">c3zbc_</a>	 Alignment		58.6	23	<b>PDB header:</b> unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> esxa; <b>PDBTitle:</b> geobacillus thermodenitrificans esxa crystal form i
5	<a href="#">c3m0dC_</a>	 Alignment		53.7	20	<b>PDB header:</b> signaling protein <b>Chain:</b> C: <b>PDB Molecule:</b> tnf receptor-associated factor 1; <b>PDBTitle:</b> crystal structure of the traf1:traf2:ciap2 complex
6	<a href="#">c3m06F_</a>	 Alignment		42.0	23	<b>PDB header:</b> protein binding <b>Chain:</b> F: <b>PDB Molecule:</b> tnf receptor-associated factor 2; <b>PDBTitle:</b> crystal structure of traf2
7	<a href="#">c3gvmA_</a>	 Alignment		38.2	17	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein sag1039; <b>PDBTitle:</b> structure of the homodimeric wxg-100 family protein from streptococcus2 agalactiae
8	<a href="#">c2la2A_</a>	 Alignment		34.7	27	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> cecropin; <b>PDBTitle:</b> solution structure of papiliocin isolated from the swallowtail2 butterfly, papilio xuthus
9	<a href="#">c2vs0B_</a>	 Alignment		30.9	11	<b>PDB header:</b> cell invasion <b>Chain:</b> B: <b>PDB Molecule:</b> virulence factor esxa; <b>PDBTitle:</b> structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
10	<a href="#">d2j01h1</a>	 Alignment		15.3	45	<b>Fold:</b> Ribosomal protein L6 <b>Superfamily:</b> Ribosomal protein L6 <b>Family:</b> Ribosomal protein L6
11	<a href="#">d2zjre2</a>	 Alignment		14.8	45	<b>Fold:</b> Ribosomal protein L6 <b>Superfamily:</b> Ribosomal protein L6 <b>Family:</b> Ribosomal protein L6

12	<a href="#">d2qamg1</a>	Alignment		13.6	36	<b>Fold:</b> Ribosomal protein L6 <b>Superfamily:</b> Ribosomal protein L6 <b>Family:</b> Ribosomal protein L6
13	<a href="#">d1vqoe1</a>	Alignment		13.2	64	<b>Fold:</b> Ribosomal protein L6 <b>Superfamily:</b> Ribosomal protein L6 <b>Family:</b> Ribosomal protein L6
14	<a href="#">d1rl6a1</a>	Alignment		11.4	45	<b>Fold:</b> Ribosomal protein L6 <b>Superfamily:</b> Ribosomal protein L6 <b>Family:</b> Ribosomal protein L6
15	<a href="#">c487dj_</a>	Alignment		11.3	42	<b>PDB header:</b> ribosome <b>Chain:</b> J; <b>PDB Molecule:</b> protein (50s l6 ribosomal protein); <b>PDBTitle:</b> seven ribosomal proteins fitted to a cryo-electron2 microscopic map of the large 50s subunit at 7.5 angstroms3 resolution
16	<a href="#">d2cqla1</a>	Alignment		10.7	45	<b>Fold:</b> Ribosomal protein L6 <b>Superfamily:</b> Ribosomal protein L6 <b>Family:</b> Ribosomal protein L6
17	<a href="#">c5o60G_</a>	Alignment		10.4	42	<b>PDB header:</b> ribosome <b>Chain:</b> G; <b>PDB Molecule:</b> 50s ribosomal protein l6; <b>PDBTitle:</b> structure of the 50s large ribosomal subunit from mycobacterium2 smegmatis
18	<a href="#">d1wa8b1</a>	Alignment		9.7	10	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> EsxAB dimer-like <b>Family:</b> ESAT-6 like
19	<a href="#">c2hguH_</a>	Alignment		9.0	42	<b>PDB header:</b> ribosome <b>Chain:</b> H; <b>PDB Molecule:</b> 50s ribosomal protein l6; <b>PDBTitle:</b> 70s t.th. ribosome functional complex with mrna and e- and p-site2 trnas at 4.5a. this entry 2hgu contains 50s ribosomal subunit. the3 30s ribosomal subunit can be found in pdb entry 2hgr.
20	<a href="#">c2i2vG_</a>	Alignment		8.9	33	<b>PDB header:</b> ribosome <b>Chain:</b> G; <b>PDB Molecule:</b> 50s ribosomal protein l6; <b>PDBTitle:</b> crystal structure of ribosome with messenger rna and the anticodon2 stem-loop of p-site trna. this file contains the 50s subunit of one3 70s ribosome. the entire crystal structure contains two 70s ribosomes4 and is described in remark 400.
21	<a href="#">c1sm1E_</a>	Alignment	not modelled	8.4	42	<b>PDB header:</b> ribosome/antibiotic <b>Chain:</b> E; <b>PDB Molecule:</b> 50s ribosomal protein l6; <b>PDBTitle:</b> complex of the large ribosomal subunit from deinococcus radiodurans2 with quinupristin and dalfopristin
22	<a href="#">c1pnuE_</a>	Alignment	not modelled	8.4	42	<b>PDB header:</b> ribosome <b>Chain:</b> E; <b>PDB Molecule:</b> 50s ribosomal protein l6; <b>PDBTitle:</b> crystal structure of a streptomycin dependent ribosome from2 escherichia coli, 50s subunit of 70s ribosome. this file, 1pnu,3 contains only molecules of the 50s ribosomal subunit. the 30s4 subunit, mrna, p-site trna, and a-site trna are in the pdb file 1pns.
23	<a href="#">c1vw4F_</a>	Alignment	not modelled	8.4	42	<b>PDB header:</b> ribosome <b>Chain:</b> F; <b>PDB Molecule:</b> 54s ribosomal protein l6, mitochondrial; <b>PDBTitle:</b> structure of the yeast mitochondrial large ribosomal subunit
24	<a href="#">c2bbrA_</a>	Alignment	not modelled	8.0	44	<b>PDB header:</b> viral protein <b>Chain:</b> A; <b>PDB Molecule:</b> viral casp8 and fadd-like apoptosis regulator; <b>PDBTitle:</b> crystal structure of mc159 reveals molecular mechanism of2 disc assembly and vflip inhibition
25	<a href="#">c2zkre_</a>	Alignment	not modelled	8.0	42	<b>PDB header:</b> ribosomal protein/rna <b>Chain:</b> E; <b>PDB Molecule:</b> rna expansion segment es7 part ii; <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
26	<a href="#">c3ccmE_</a>	Alignment	not modelled	7.9	64	<b>PDB header:</b> ribosome <b>Chain:</b> E; <b>PDB Molecule:</b> 50s ribosomal protein l6p; <b>PDBTitle:</b> structure of anisomycin resistant 50s ribosomal subunit: 23s rrna2 mutation g2611u
27	<a href="#">c5an9B_</a>	Alignment	not modelled	7.6	50	<b>PDB header:</b> translation <b>Chain:</b> B; <b>PDB Molecule:</b> 60s ribosomal protein l9; <b>PDBTitle:</b> mechanism of eif6 release from the nascent 60s ribosomal subunit

28	<a href="#">c4iogD_</a>	 Alignment	not modelled	7.4	26	<b>PDB header:</b> unknown function <b>Chain:</b> D; <b>PDB Molecule:</b> secreted protein esxb; <b>PDBTitle:</b> the crystal structure of a secreted protein esxb (wild-type, in p212 space group) from bacillus anthracis str. sterne
29	<a href="#">c4a1eE_</a>	 Alignment	not modelled	7.1	55	<b>PDB header:</b> ribosome <b>Chain:</b> E; <b>PDB Molecule:</b> 60s ribosomal protein l9; <b>PDBTitle:</b> t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna, 5.8s rrna3 and proteins of molecule 1
30	<a href="#">c4wf9E_</a>	 Alignment	not modelled	6.9	45	<b>PDB header:</b> ribosome <b>Chain:</b> E; <b>PDB Molecule:</b> 50s ribosomal protein l6; <b>PDBTitle:</b> the crystal structure of the large ribosomal subunit of staphylococcus2 aureus in complex with telithromycin
31	<a href="#">c3j39H_</a>	 Alignment	not modelled	6.5	55	<b>PDB header:</b> ribosome <b>Chain:</b> H; <b>PDB Molecule:</b> 60s ribosomal protein l9; <b>PDBTitle:</b> structure of the d. melanogaster 60s ribosomal proteins
32	<a href="#">d1xbla_</a>	 Alignment	not modelled	6.4	14	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Chaperone J-domain <b>Family:</b> Chaperone J-domain
33	<a href="#">c3j21F_</a>	 Alignment	not modelled	6.1	55	<b>PDB header:</b> ribosome <b>Chain:</b> F; <b>PDB Molecule:</b> 50s ribosomal protein l6p; <b>PDBTitle:</b> promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
34	<a href="#">c2bbzC_</a>	 Alignment	not modelled	6.0	53	<b>PDB header:</b> viral protein <b>Chain:</b> C; <b>PDB Molecule:</b> viral casp8 and fadd-like apoptosis regulator; <b>PDBTitle:</b> crystal structure of mc159 reveals molecular mechanism of2 disc assembly and vflip inhibition
35	<a href="#">c3zf7y_</a>	 Alignment	not modelled	5.7	45	<b>PDB header:</b> ribosome <b>Chain:</b> Y; <b>PDB Molecule:</b> 60s ribosomal protein l24, putative; <b>PDBTitle:</b> high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
36	<a href="#">c6fe8D_</a>	 Alignment	not modelled	5.5	42	<b>PDB header:</b> dna binding protein <b>Chain:</b> D; <b>PDB Molecule:</b> centromere dna-binding protein complex cbf3 subunit c; <b>PDBTitle:</b> cryo-em structure of the core centromere binding factor 3 complex
37	<a href="#">c3bbol_</a>	 Alignment	not modelled	5.5	45	<b>PDB header:</b> ribosome <b>Chain:</b> l; <b>PDB Molecule:</b> ribosomal protein l6; <b>PDBTitle:</b> homology model for the spinach chloroplast 50s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome