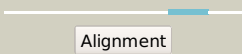

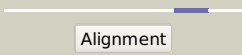

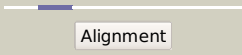
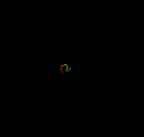
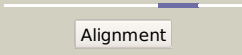
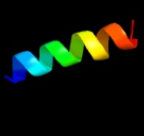


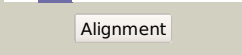

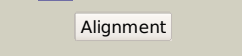

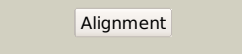
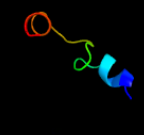
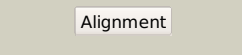

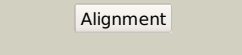

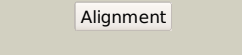








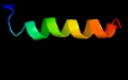



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1892_(-)_2140172_2140483
Date	Fri Aug 2 13:30:51 BST 2019
Unique Job ID	c21b6b4d8c687458

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2wvrB_	 Alignment		33.0	21	PDB header: replication Chain: B: PDB Molecule: geminin; PDBTitle: human cdt1:geminin complex
2	d2h8pc1	 Alignment		16.9	25	Fold: Voltage-gated potassium channels Superfamily: Voltage-gated potassium channels Family: Voltage-gated potassium channels
3	c5z58w_	 Alignment		15.8	67	PDB header: splicing Chain: W: PDB Molecule: PDBTitle: cryo-em structure of a human activated spliceosome (early bact) at 4.92 angstrom.
4	c5oqtC_	 Alignment		13.5	50	PDB header: transport protein Chain: C: PDB Molecule: uncharacterized protein ynem; PDBTitle: crystal structure of a bacterial cationic amino acid transporter (cat)2 homologue
5	c1hk7A_	 Alignment		13.4	58	PDB header: chaperone Chain: A: PDB Molecule: heat shock protein hsp82; PDBTitle: middle domain of hsp90
6	c6g90T_	 Alignment		13.2	50	PDB header: splicing Chain: T: PDB Molecule: pre-mrna-splicing factor prp9; PDBTitle: prespliceosome structure provides insight into spliceosome assembly2 and regulation (map a2)
7	c1y6zA_	 Alignment		13.2	50	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: heat shock protein, putative; PDBTitle: middle domain of plasmodium falciparum putative heat shock protein2 pf14_0417
8	c5jygA_	 Alignment		13.1	43	PDB header: structural protein Chain: A: PDB Molecule: actin-like atpase; PDBTitle: cryo-em structure of the mamk filament at 6.5 a
9	c6f34C_	 Alignment		12.4	50	PDB header: membrane protein Chain: C: PDB Molecule: mgts; PDBTitle: crystal structure of a bacterial cationic amino acid transporter (cat)2 homologue bound to arginine.
10	c2qw6A_	 Alignment		12.1	33	PDB header: hydrolase Chain: A: PDB Molecule: aaa atpase, central region; PDBTitle: crystal structure of the c-terminal domain of an aaa atpase from2 enterococcus faecium do
11	d2qw6a1	 Alignment		12.1	33	Fold: post-AAA+ oligomerization domain-like Superfamily: post-AAA+ oligomerization domain-like Family: MgsA/YrvN C-terminal domain-like

12	d1usua_	Alignment		11.6	50	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Hsp90 middle domain
13	c2ww9O_	Alignment		11.5	50	PDB header: ribosome Chain: O: PDB Molecule: 60s ribosomal protein l39; PDBTitle: cryo-em structure of the active yeast ssh1 complex bound to the yeast2 80s ribosome
14	c2o1tB_	Alignment		11.4	33	PDB header: chaperone Chain: B: PDB Molecule: endoplasmic; PDBTitle: structure of middle plus c-terminal domains (m+c) of grp94
15	d1dxsa_	Alignment		11.1	62	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
16	c4xb6D_	Alignment		10.7	35	PDB header: transferase Chain: D: PDB Molecule: alpha-d-ribose 1-methylphosphonate 5-phosphate c-p lyase; PDBTitle: structure of the e. coli c-p lyase core complex
17	c3prvA_	Alignment		9.8	33	PDB header: chaperone Chain: A: PDB Molecule: heat shock protein hsp 90-beta; PDBTitle: crystal structure of the middle domain of human hsp90-beta refined at 2.3 a resolution
18	c2xuvB_	Alignment		9.7	54	PDB header: unknown function Chain: B: PDB Molecule: hdeb; PDBTitle: the structure of hdeb
19	d1rg6a_	Alignment		9.5	26	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
20	c2zkr3_	Alignment		9.3	63	PDB header: ribosomal protein/rna Chain: 3: PDB Molecule: 60s ribosomal protein l39e; PDBTitle: structure of a mammalian ribosomal 60s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an 3.8.7 a cryo-em map
21	c2gq0B_	Alignment	not modelled	8.6	50	PDB header: chaperone, hydrolase Chain: B: PDB Molecule: chaperone protein htpg; PDBTitle: crystal structure of the middle domain of htpg, the e. coli hsp90
22	c3q6nF_	Alignment	not modelled	8.5	42	PDB header: chaperone Chain: F: PDB Molecule: heat shock protein hsp 90-alpha; PDBTitle: crystal structure of human mc-hsp90 in p21 space group
23	c5xfmD_	Alignment	not modelled	8.5	50	PDB header: hydrolase Chain: D: PDB Molecule: alpha-glucosidase; PDBTitle: crystal structure of beta-arabinopyranosidase
24	c2la3A_	Alignment	not modelled	8.1	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: the nmr structure of the protein np_344798.1 reveals a cca-adding2 enzyme head domain
25	c2cgeD_	Alignment	not modelled	8.0	58	PDB header: chaperone Chain: D: PDB Molecule: atp-dependent molecular chaperone hsp82; PDBTitle: crystal structure of an hsp90-sba1 closed chaperone complex
26	c3hjcA_	Alignment	not modelled	7.9	50	PDB header: chaperone Chain: A: PDB Molecule: heat shock protein 83-1; PDBTitle: crystal structure of the carboxy-terminal domain of hsp90 from2 leishmania major, lmjf33.0312
27	c3a24A_	Alignment	not modelled	6.9	50	PDB header: hydrolase Chain: A: PDB Molecule: alpha-galactosidase; PDBTitle: crystal structure of bt1871 retaining glycosidase
28	c2n90A_	Alignment	not modelled	6.8	67	PDB header: transferase Chain: A: PDB Molecule: high affinity nerve growth factor receptor; PDBTitle: trka transmembrane domain nmr structure in dpc micelles

29	c2n90B_	Alignment	not modelled	6.8	67	PDB header: transferase Chain: B: PDB Molecule: high affinity nerve growth factor receptor; PDBTitle: trka transmembrane domain nmr structure in dpc micelles
30	c3zf7q_	Alignment	not modelled	6.7	40	PDB header: ribosome Chain: Q: PDB Molecule: ribosomal protein l15; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
31	c3r9jD_	Alignment	not modelled	6.6	18	PDB header: cell cycle,hydrolase/cell cycle Chain: D: PDB Molecule: cell division topological specificity factor; PDBTitle: 4.3a resolution structure of a mind-mine(i24n) protein complex
32	c3izso_	Alignment	not modelled	6.4	40	PDB header: ribosome Chain: O: PDB Molecule: 60s ribosomal protein rpl28 (l15p); PDBTitle: localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
33	d1xmec1	Alignment	not modelled	6.3	23	Fold: Single transmembrane helix Superfamily: Bacterial ba3 type cytochrome c oxidase subunit Ila Family: Bacterial ba3 type cytochrome c oxidase subunit Ila
34	c3bvdC_	Alignment	not modelled	6.3	23	PDB header: oxidoreductase Chain: C: PDB Molecule: cytochrome c oxidase polypeptide 2a; PDBTitle: structure of surface-engineered cytochrome ba3 oxidase from thermus2 thermophilus under xenon pressure, 100psi 5min
35	c6adqP_	Alignment	not modelled	6.2	23	PDB header: electron transport Chain: P: PDB Molecule: prokaryotic respiratory supercomplex associate factor 1 PDBTitle: respiratory complex ciii2civ2sod2 from mycobacterium smegmatis
36	c2iopD_	Alignment	not modelled	5.9	50	PDB header: chaperone Chain: D: PDB Molecule: chaperone protein htpg; PDBTitle: crystal structure of full-length htpg, the escherichia coli2 hsp90, bound to adp
37	c2wfoA_	Alignment	not modelled	5.7	43	PDB header: viral protein Chain: A: PDB Molecule: glycoprotein 1; PDBTitle: crystal structure of machupo virus envelope glycoprotein gp1
38	c5tthA_	Alignment	not modelled	5.6	42	PDB header: chaperone Chain: A: PDB Molecule: c-terminal spycatcher fusion of wildtype zebrafish tnf PDBTitle: heterodimeric spycatcher/spytag-fused zebrafish trap1 in atp/adp-2 hybrid state
39	c2ariA_	Alignment	not modelled	5.5	50	PDB header: viral protein Chain: A: PDB Molecule: envelope polyprotein gp160; PDBTitle: solution structure of micelle-bound fusion domain of hiv-12 gp41
40	c2wseE_	Alignment	not modelled	5.1	40	PDB header: photosynthesis Chain: E: PDB Molecule: photosystem i reaction center subunit iv a, chloroplastic; PDBTitle: improved model of plant photosystem i