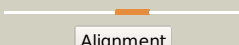
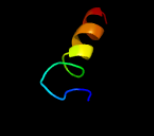
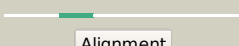

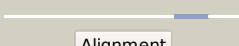

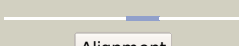

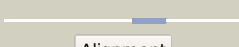
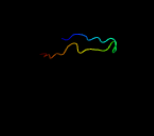



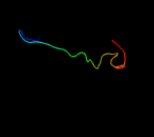



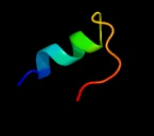

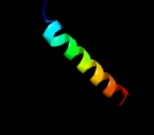

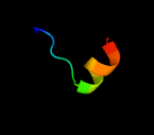




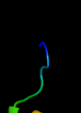

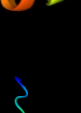
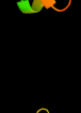
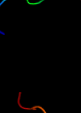


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1508c_(-)_1698101_1699900
Date	Fri Aug 2 13:30:09 BST 2019
Unique Job ID	8d9bc5b9b49ca8f9

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5t42A_</a>	 Alignment		86.3	67	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> envelope glycoprotein; <b>PDBTitle:</b> structure of the ebola virus envelope protein mper/tm domain and its2 interaction with the fusion loop explains their fusion activity
2	<a href="#">c1s1hN_</a>	 Alignment		46.2	40	<b>PDB header:</b> ribosome <b>Chain:</b> N: <b>PDB Molecule:</b> 40s ribosomal protein s29-b; <b>PDBTitle:</b> structure of the ribosomal 80s-eef2-sordarin complex from yeast2 obtained by docking atomic models for rna and protein components into3 a 11.7 a cryo-em map. this file, 1s1h, contains 40s subunit. the 60s4 ribosomal subunit is in file 1s1i.
3	<a href="#">c5a63D_</a>	 Alignment		28.6	35	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> gamma-secretase subunit pen-2; <b>PDBTitle:</b> cryo-em structure of the human gamma-secretase complex at 3.4 angstrom2 resolution.
4	<a href="#">c4e8uA_</a>	 Alignment		26.7	42	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein t8p19.180; <b>PDBTitle:</b> crystal structure of arabidopsis idn2 xs domain along with a small2 segment of adjacent coiled-coil region
5	<a href="#">c2vecA_</a>	 Alignment		24.6	24	<b>PDB header:</b> cytosolic protein <b>Chain:</b> A: <b>PDB Molecule:</b> pirin-like protein yhak; <b>PDBTitle:</b> the crystal structure of the protein yhak from escherichia2 coli
6	<a href="#">c6m8sM_</a>	 Alignment		24.0	47	<b>PDB header:</b> signaling protein <b>Chain:</b> M: <b>PDB Molecule:</b> btb/poz domain-containing protein kctd12; <b>PDBTitle:</b> crystal structure of the kctd12 h1 domain in complex with gbeta1gamma22 subunits
7	<a href="#">d1laja_</a>	 Alignment		23.3	38	<b>Fold:</b> Nucleoplasmin-like/VP (viral coat and capsid proteins) <b>Superfamily:</b> Positive stranded ssRNA viruses <b>Family:</b> Bromoviridae-like VP
8	<a href="#">c1lajA_</a>	 Alignment		23.3	38	<b>PDB header:</b> virus/rna <b>Chain:</b> A: <b>PDB Molecule:</b> capsid protein; <b>PDBTitle:</b> the structure of tomato aspermy virus by x-ray2 crystallography
9	<a href="#">c3cjsA_</a>	 Alignment		23.2	39	<b>PDB header:</b> transferase/ribosomal protein <b>Chain:</b> A: <b>PDB Molecule:</b> ribosomal protein l11 methyltransferase; <b>PDBTitle:</b> minimal recognition complex between prma and ribosomal protein l11
10	<a href="#">d1lgha_</a>	 Alignment		23.1	44	<b>Fold:</b> Light-harvesting complex subunits <b>Superfamily:</b> Light-harvesting complex subunits <b>Family:</b> Light-harvesting complex subunits
11	<a href="#">c3zey8_</a>	 Alignment		21.6	36	<b>PDB header:</b> ribosome <b>Chain:</b> 8: <b>PDB Molecule:</b> ribosomal protein s29, putative; <b>PDBTitle:</b> high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome

12	<a href="#">c5xyid</a>	Alignment		21.4	43	<b>PDB header:</b> ribosome <b>Chain:</b> D: <b>PDB Molecule:</b> ribosomal protein s3, putative; <b>PDBTitle:</b> small subunit of trichomonas vaginalis ribosome
13	<a href="#">c3j20P</a>	Alignment		20.4	43	<b>PDB header:</b> ribosome <b>Chain:</b> P: <b>PDB Molecule:</b> 30s ribosomal protein s14p type z; <b>PDBTitle:</b> promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit)
14	<a href="#">c2xznN</a>	Alignment		20.0	36	<b>PDB header:</b> ribosome <b>Chain:</b> N: <b>PDB Molecule:</b> rps29e; <b>PDBTitle:</b> crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2
15	<a href="#">c2zkgq</a>	Alignment		19.4	50	<b>PDB header:</b> ribosomal protein/rna <b>Chain:</b> N: <b>PDB Molecule:</b> <b>PDBTitle:</b> structure of a mammalian ribosomal 40s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
16	<a href="#">c6az1S</a>	Alignment		19.1	36	<b>PDB header:</b> ribosome/antibiotic <b>Chain:</b> S: <b>PDB Molecule:</b> ribosomal protein s14; <b>PDBTitle:</b> cryo-em structure of the small subunit of leishmania ribosome bound to2 paromomycin
17	<a href="#">c3jyvN</a>	Alignment		19.0	43	<b>PDB header:</b> ribosome <b>Chain:</b> N: <b>PDB Molecule:</b> 40s ribosomal protein s29(a); <b>PDBTitle:</b> structure of the 40s rrna and proteins and p/e trna for eukaryotic2 ribosome based on cryo-em map of thermomyces lanuginosus ribosome at3 8.9a resolution
18	<a href="#">c5xxud</a>	Alignment		17.9	36	<b>PDB header:</b> ribosome <b>Chain:</b> D: <b>PDB Molecule:</b> ribosomal protein us3; <b>PDBTitle:</b> small subunit of toxoplasma gondii ribosome
19	<a href="#">c5x8rx</a>	Alignment		17.9	43	<b>PDB header:</b> ribosome <b>Chain:</b> X: <b>PDB Molecule:</b> <b>PDBTitle:</b> structure of the 30s small subunit of chloroplast ribosome from2 spinach
20	<a href="#">c5mmjx</a>	Alignment		16.2	43	<b>PDB header:</b> ribosome <b>Chain:</b> X: <b>PDB Molecule:</b> <b>PDBTitle:</b> structure of the small subunit of the chloroplast ribosome
21	<a href="#">c1f15C</a>	Alignment	not modelled	15.2	38	<b>PDB header:</b> virus <b>Chain:</b> C: <b>PDB Molecule:</b> coat protein; <b>PDBTitle:</b> cucumber mosaic virus (strain fny)
22	<a href="#">d1f15b</a>	Alignment	not modelled	12.2	38	<b>Fold:</b> Nucleoplasmin-like/VP (viral coat and capsid proteins) <b>Superfamily:</b> Positive stranded ssRNA viruses <b>Family:</b> Bromoviridae-like VP
23	<a href="#">c5f8A</a>	Alignment	not modelled	12.1	42	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> nucleoside diphosphate-linked moiety x motif 17; <b>PDBTitle:</b> human nucleoside diphosphate-linked moiety x motif 17 (nudt17)
24	<a href="#">d2gmfa</a>	Alignment	not modelled	11.2	78	<b>Fold:</b> 4-helical cytokines <b>Superfamily:</b> 4-helical cytokines <b>Family:</b> Short-chain cytokines
25	<a href="#">c1scfA</a>	Alignment	not modelled	10.2	50	<b>PDB header:</b> hormone/growth factor <b>Chain:</b> A: <b>PDB Molecule:</b> stem cell factor; <b>PDBTitle:</b> human recombinant stem cell factor
26	<a href="#">d1scfa</a>	Alignment	not modelled	10.2	50	<b>Fold:</b> 4-helical cytokines <b>Superfamily:</b> 4-helical cytokines <b>Family:</b> Short-chain cytokines
27	<a href="#">d3nlaa</a>	Alignment	not modelled	10.1	33	<b>Fold:</b> beta-clip <b>Superfamily:</b> AFP III-like domain <b>Family:</b> AFP III-like domain
28	<a href="#">d1f15a</a>	Alignment	not modelled	9.2	38	<b>Fold:</b> Nucleoplasmin-like/VP (viral coat and capsid proteins) <b>Superfamily:</b> Positive stranded ssRNA viruses <b>Family:</b> Bromoviridae-like VP
						<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain)

29	<a href="#">d1x61a2</a>	Alignment	not modelled	8.9	38	<b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> LIM domain
30	<a href="#">c6a68A</a>	Alignment	not modelled	8.6	47	<b>PDB header:</b> exocytosis <b>Chain:</b> A: <b>PDB Molecule:</b> calcium-dependent secretion activator 1; <b>PDBTitle:</b> the crystal structure of rat calcium-dependent activator protein for2 secretion (caps) damh domain
31	<a href="#">c2lzsE</a>	Alignment	not modelled	8.6	24	<b>PDB header:</b> protein transport <b>Chain:</b> E: <b>PDB Molecule:</b> sec-independent protein translocase protein tata; <b>PDBTitle:</b> tata oligomer
32	<a href="#">c2momC</a>	Alignment	not modelled	8.5	61	<b>PDB header:</b> membrane protein <b>Chain:</b> C: <b>PDB Molecule:</b> lysosome-associated membrane glycoprotein 2; <b>PDBTitle:</b> structural insights of tm domain of lamp-2a in dpc micelles
33	<a href="#">c2momB</a>	Alignment	not modelled	8.5	61	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> lysosome-associated membrane glycoprotein 2; <b>PDBTitle:</b> structural insights of tm domain of lamp-2a in dpc micelles
34	<a href="#">c1ceeB</a>	Alignment	not modelled	8.5	17	<b>PDB header:</b> structural protein regulation <b>Chain:</b> B: <b>PDB Molecule:</b> wiskott-aldrich syndrome protein wasp; <b>PDBTitle:</b> solution structure of cdc42 in complex with the gtpase2 binding domain of wasp
35	<a href="#">c4pnbC</a>	Alignment	not modelled	8.5	67	<b>PDB header:</b> de novo protein <b>Chain:</b> C: <b>PDB Molecule:</b> cc-hex3; <b>PDBTitle:</b> a de novo designed hexameric coiled coil cc-hex3
36	<a href="#">c2k3mA</a>	Alignment	not modelled	8.2	60	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> rv1761c; <b>PDBTitle:</b> rv1761c
37	<a href="#">c3io5B</a>	Alignment	not modelled	8.2	33	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> recombination and repair protein; <b>PDBTitle:</b> crystal structure of a dimeric form of the uvx recombinase core2 domain from enterobacteria phage t4
38	<a href="#">c4pnbA</a>	Alignment	not modelled	8.2	67	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> cc-hex3; <b>PDBTitle:</b> a de novo designed hexameric coiled coil cc-hex3
39	<a href="#">c4pnbD</a>	Alignment	not modelled	8.2	67	<b>PDB header:</b> de novo protein <b>Chain:</b> D: <b>PDB Molecule:</b> cc-hex3; <b>PDBTitle:</b> a de novo designed hexameric coiled coil cc-hex3
40	<a href="#">c4pnbB</a>	Alignment	not modelled	7.8	67	<b>PDB header:</b> de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> cc-hex3; <b>PDBTitle:</b> a de novo designed hexameric coiled coil cc-hex3
41	<a href="#">d1scfc</a>	Alignment	not modelled	7.7	50	<b>Fold:</b> 4-helical cytokines <b>Superfamily:</b> 4-helical cytokines <b>Family:</b> Short-chain cytokines
42	<a href="#">c3lr4A</a>	Alignment	not modelled	7.6	29	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sensor protein; <b>PDBTitle:</b> periplasmic domain of the riss sensor protein from burkholderia2 pseudomallei, barium phased at low ph
43	<a href="#">c4mnoA</a>	Alignment	not modelled	7.4	58	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> translation initiation factor 1a; <b>PDBTitle:</b> crystal structure of aif1a from pyrococcus abyssi
44	<a href="#">c3ut7A</a>	Alignment	not modelled	7.3	26	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> structural view of a non pfam singleton and crystal packing analysis
45	<a href="#">d2k4xa1</a>	Alignment	not modelled	7.2	67	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zn-binding ribosomal proteins <b>Family:</b> Ribosomal protein S27a
46	<a href="#">c2mi2A</a>	Alignment	not modelled	7.2	22	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> sec-independent protein translocase protein tatb; <b>PDBTitle:</b> solution structure of the e. coli tatb protein in dpc micelles
47	<a href="#">c2a2bA</a>	Alignment	not modelled	6.9	43	<b>PDB header:</b> antibiotic <b>Chain:</b> A: <b>PDB Molecule:</b> bacteriocin curvacin a; <b>PDBTitle:</b> curvacin a
48	<a href="#">c6qb7A</a>	Alignment	not modelled	6.7	42	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> btb/poz domain-containing protein kctd16; <b>PDBTitle:</b> structure of the h1 domain of human kctd16
49	<a href="#">d1g72b</a>	Alignment	not modelled	6.7	80	<b>Fold:</b> Non-globular all-alpha subunits of globular proteins <b>Superfamily:</b> Methanol dehydrogenase subunit <b>Family:</b> Methanol dehydrogenase subunit
50	<a href="#">d1iarb1</a>	Alignment	not modelled	6.6	80	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Fibronectin type III <b>Family:</b> Fibronectin type III
51	<a href="#">c4apmA</a>	Alignment	not modelled	6.6	41	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> apical membrane antigen 1; <b>PDBTitle:</b> crystal structure of ama1 from babesia divergens
52	<a href="#">d2ad6b1</a>	Alignment	not modelled	6.5	80	<b>Fold:</b> Non-globular all-alpha subunits of globular proteins <b>Superfamily:</b> Methanol dehydrogenase subunit <b>Family:</b> Methanol dehydrogenase subunit
53	<a href="#">d1w6sb</a>	Alignment	not modelled	6.4	60	<b>Fold:</b> Non-globular all-alpha subunits of globular proteins <b>Superfamily:</b> Methanol dehydrogenase subunit <b>Family:</b> Methanol dehydrogenase subunit
54	<a href="#">c2lioA</a>	Alignment	not modelled	6.3	36	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution nmr structure of bfr322 from bacteroides fragilis, northeast2 structural genomics consortium target bfr322
55	<a href="#">d1luca</a>	Alignment	not modelled	6.3	60	<b>Fold:</b> beta-clip <b>Superfamily:</b> AFP III-like domain <b>Family:</b> AFP III-like domain

56	<a href="#">d1wj9a2</a>	Alignment	not modelled	6.2	38	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> CRISPR-associated protein <b>Family:</b> CRISPR-associated protein
57	<a href="#">c2lq1A</a>	Alignment	not modelled	6.2	53	<b>PDB header:</b> antifreeze protein <b>Chain:</b> A: <b>PDB Molecule:</b> de novo designed antifreeze peptide 3; <b>PDBTitle:</b> solution structure of de novo designed antifreeze peptide 3
58	<a href="#">c5wsuD</a>	Alignment	not modelled	6.1	67	<b>PDB header:</b> motor protein/calcium binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> unconventional myosin-viia; <b>PDBTitle:</b> crystal structure of myosin viia iq5-sah in complex with apo-cam
59	<a href="#">c6g72A</a>	Alignment	not modelled	6.0	38	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadh-ubiquinone oxidoreductase chain 3; <b>PDBTitle:</b> mouse mitochondrial complex i in the deactive state
60	<a href="#">c5gpdB</a>	Alignment	not modelled	6.0	44	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> sterol regulatory element-binding protein 1; <b>PDBTitle:</b> crystal structure of the binding domain of srebp from fission yeast
61	<a href="#">c1qhhD</a>	Alignment	not modelled	6.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> protein (pcra (subunit)); <b>PDBTitle:</b> structure of dna helicase with adpnp
62	<a href="#">d1l6ja1</a>	Alignment	not modelled	6.0	16	<b>Fold:</b> PGBD-like <b>Superfamily:</b> PGBD-like <b>Family:</b> MMP N-terminal domain
63	<a href="#">d1lrwb</a>	Alignment	not modelled	5.9	80	<b>Fold:</b> Non-globular all-alpha subunits of globular proteins <b>Superfamily:</b> Methanol dehydrogenase subunit <b>Family:</b> Methanol dehydrogenase subunit
64	<a href="#">c5nhqA</a>	Alignment	not modelled	5.9	32	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> agnoprotein; <b>PDBTitle:</b> nuclear magnetic resonance structure of the human polyoma jc virus2 agnoprotein
65	<a href="#">c2l16A</a>	Alignment	not modelled	5.7	26	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> sec-independent protein translocase protein tatad; <b>PDBTitle:</b> solution structure of bacillus subtilis tatad protein in dpc micelles
66	<a href="#">c3bmzA</a>	Alignment	not modelled	5.6	38	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> violacein biosynthetic enzyme vioe
67	<a href="#">c4wyhA</a>	Alignment	not modelled	5.6	31	<b>PDB header:</b> replication <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of prix from the hyperthermophilic archaeon2 sulfolobus solfataricus
68	<a href="#">c6f21B</a>	Alignment	not modelled	5.5	67	<b>PDB header:</b> toxin <b>Chain:</b> B: <b>PDB Molecule:</b> dendroaspis polylepis mt9; <b>PDBTitle:</b> crystal structure of toxin mt9 from mamba venom
69	<a href="#">c1ce4A</a>	Alignment	not modelled	5.5	67	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein (v3 loop of hiv-1 envelope protein); <b>PDBTitle:</b> conformational model for the consensus v3 loop of the envelope protein2 gp120 of hiv-1
70	<a href="#">c2odbB</a>	Alignment	not modelled	5.4	31	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> serine/threonine-protein kinase pak 6; <b>PDBTitle:</b> the crystal structure of human cdc42 in complex with the crib domain2 of human p21-activated kinase 6 (pak6)
71	<a href="#">c2pv9C</a>	Alignment	not modelled	5.3	83	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> proteinase-activated receptor 4; <b>PDBTitle:</b> crystal structure of murine thrombin in complex with the extracellular2 fragment of murine par4
72	<a href="#">c4b0fE</a>	Alignment	not modelled	5.2	71	<b>PDB header:</b> immune system <b>Chain:</b> E: <b>PDB Molecule:</b> c4b-binding protein alpha chain; <b>PDBTitle:</b> heptameric core complex structure of c4b-binding (c4bp) protein from2 human
73	<a href="#">c3hp7A</a>	Alignment	not modelled	5.2	100	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hemolysin, putative; <b>PDBTitle:</b> putative hemolysin from streptococcus thermophilus.
74	<a href="#">d1tq5a1</a>	Alignment	not modelled	5.1	24	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmIC-like cupins <b>Family:</b> Pirin-like