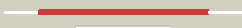
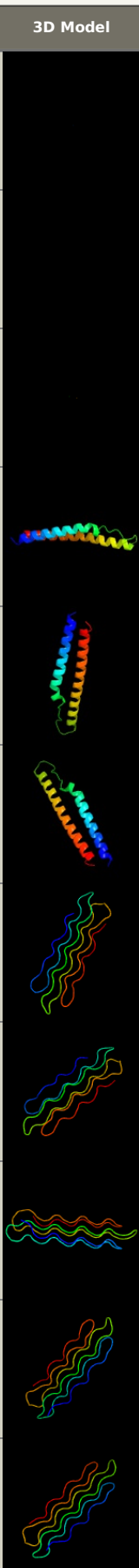












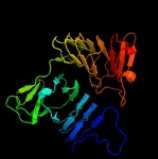
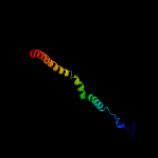

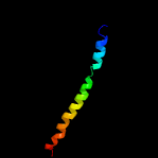
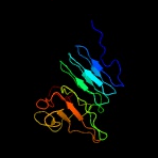
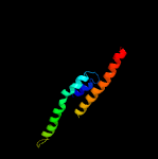
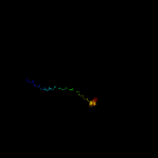


# Phyre2

Email [mdejesus@rockefeller.edu](mailto:mdejesus@rockefeller.edu)  
 Description RVBD3345c\_(PE\_PGRS50)\_3738329\_3742945  
 Date Thu Aug 8 16:20:55 BST 2019  
 Unique Job ID 9ea81385472b6237

Detailed template information

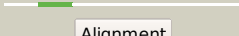
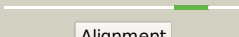
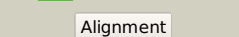






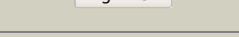


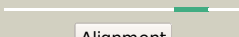
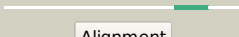


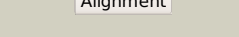

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1ygvA_</a>	 Alignment		100.0	48	<b>PDB header:</b> structural protein/contractile protein <b>Chain:</b> A: <b>PDB Molecule:</b> collagen i alpha 1; <b>PDBTitle:</b> the structure of collagen type i. single type i collagen2 molecule: rigid refinement
2	<a href="#">c3hqvB_</a>	 Alignment		100.0	26	<b>PDB header:</b> structural protein, contractile protein <b>Chain:</b> B: <b>PDB Molecule:</b> collagen alpha-2(i) chain; <b>PDBTitle:</b> low resolution, molecular envelope structure of type i2 collagen in situ determined by fiber diffraction. single3 type i collagen molecule, rigid body refinement
3	<a href="#">c1y0fB_</a>	 Alignment		99.9	26	<b>PDB header:</b> structural protein/contractile protein <b>Chain:</b> B: <b>PDB Molecule:</b> collagen i alpha 2; <b>PDBTitle:</b> the structure of collagen type i. single type i collagen2 molecule
4	<a href="#">c5xfxA_</a>	 Alignment		99.9	50	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> pe family protein pe8; <b>PDBTitle:</b> crystal structure of pe8-ppp15 in complex with esp95 from m.2 tuberculosis
5	<a href="#">d2g38a1</a>	 Alignment		99.9	30	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> PE/PPE dimer-like <b>Family:</b> PE
6	<a href="#">c2g38A_</a>	 Alignment		99.9	30	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> pe family protein; <b>PDBTitle:</b> a pe/ppp protein complex from mycobacterium tuberculosis
7	<a href="#">c3bogB_</a>	 Alignment		97.9	42	<b>PDB header:</b> antifreeze protein <b>Chain:</b> B: <b>PDB Molecule:</b> 6.5 kda glycine-rich antifreeze protein; <b>PDBTitle:</b> snow flea antifreeze protein quasi-racemate
8	<a href="#">c3bogA_</a>	 Alignment		97.9	42	<b>PDB header:</b> antifreeze protein <b>Chain:</b> A: <b>PDB Molecule:</b> 6.5 kda glycine-rich antifreeze protein; <b>PDBTitle:</b> snow flea antifreeze protein quasi-racemate
9	<a href="#">c2pneA_</a>	 Alignment		97.7	36	<b>PDB header:</b> antifreeze protein <b>Chain:</b> A: <b>PDB Molecule:</b> 6.5 kda glycine-rich antifreeze protein; <b>PDBTitle:</b> crystal structure of the snow flea antifreeze protein
10	<a href="#">c3boiB_</a>	 Alignment		97.7	36	<b>PDB header:</b> antifreeze protein <b>Chain:</b> B: <b>PDB Molecule:</b> 6.5 kda glycine-rich antifreeze protein; <b>PDBTitle:</b> snow flea antifreeze protein racemate
11	<a href="#">c3boiA_</a>	 Alignment		97.7	36	<b>PDB header:</b> antifreeze protein <b>Chain:</b> A: <b>PDB Molecule:</b> 6.5 kda glycine-rich antifreeze protein; <b>PDBTitle:</b> snow flea antifreeze protein racemate

12	<a href="#">c2qubG</a>	Alignment		97.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> G: <b>PDB Molecule:</b> extracellular lipase; <b>PDBTitle:</b> crystal structure of extracellular lipase lipa from serratia2 marcescens
13	<a href="#">c1nayC</a>	Alignment		96.7	25	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> gpp-foldon:x-ray structure
14	<a href="#">c2zj6A</a>	Alignment		96.3	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lipase; <b>PDBTitle:</b> crystal structure of d337a mutant of pseudomonas sp. mis38 lipase
15	<a href="#">c3j04A</a>	Alignment		95.9	10	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> myosin-11; <b>PDBTitle:</b> em structure of the heavy meromyosin subfragment of chick smooth2 muscle myosin with regulatory light chain in phosphorylated state
16	<a href="#">c1k7qA</a>	Alignment		95.5	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> secreted protease c; <b>PDBTitle:</b> prtC from erwinia chrysanthemi: e189a mutant
17	<a href="#">c2bkiA</a>	Alignment		95.4	10	<b>PDB header:</b> motor protein/metal-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> unconventional myosin; <b>PDBTitle:</b> myosin vi nucleotide-free (mdinsert2-iq) crystal structure
18	<a href="#">c2ml3A</a>	Alignment		95.4	16	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> poly(beta-d-mannuronate) c5 epimerase 6; <b>PDBTitle:</b> solution structure of alge6r3 subunit from the azotobacter vinelandii2 mannuronan c5-epimerase
19	<a href="#">c2ycuA</a>	Alignment		95.2	7	<b>PDB header:</b> motor protein <b>Chain:</b> A: <b>PDB Molecule:</b> non muscle myosin 2c, alpha-actinin; <b>PDBTitle:</b> crystal structure of human non muscle myosin 2c in pre-power stroke2 state
20	<a href="#">c5ctiC</a>	Alignment		95.2	22	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> collagen alpha-1(i) chain,collagen alpha-3(ix) chain; <b>PDBTitle:</b> crystal structure of the type ix collagen nc2 heterotrimerization2 domain with a guest fragment a2a1a1 of type i collagen (native form)
21	<a href="#">c5ctdB</a>	Alignment	not modelled	94.9	26	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> collagen alpha-2(i) chain,collagen alpha-2(ix) chain; <b>PDBTitle:</b> crystal structure of the type ix collagen nc2 heterotrimerization2 domain with a guest fragment a2a1a1 of type i collagen
22	<a href="#">c1i84V</a>	Alignment	not modelled	94.9	11	<b>PDB header:</b> contractile protein <b>Chain:</b> V: <b>PDB Molecule:</b> smooth muscle myosin heavy chain; <b>PDBTitle:</b> cryo-em structure of the heavy meromyosin subfragment of2 chicken gizzard smooth muscle myosin with regulatory light3 chain in the dephosphorylated state. only c alphas4 provided for regulatory light chain. only backbone atoms5 provided for s2 fragment.
23	<a href="#">c5ctdA</a>	Alignment	not modelled	94.7	25	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> collagen alpha-1(i) chain,collagen alpha-1(ix) chain; <b>PDBTitle:</b> crystal structure of the type ix collagen nc2 heterotrimerization2 domain with a guest fragment a2a1a1 of type i collagen
24	<a href="#">c5tbyA</a>	Alignment	not modelled	94.6	12	<b>PDB header:</b> contractile protein <b>Chain:</b> A: <b>PDB Molecule:</b> myosin-7; <b>PDBTitle:</b> human beta cardiac heavy meromyosin interacting-heads motif obtained2 by homology modeling (using swiss-model) of human sequence from3 aphonopelma homology model (pdb-3jbh), rigidly fitted to human beta-4 cardiac negatively stained thick filament 3d-reconstruction (emd-5 2240)
25	<a href="#">d1kapp1</a>	Alignment	not modelled	94.2	19	<b>Fold:</b> Single-stranded right-handed beta-helix <b>Superfamily:</b> beta-Roll <b>Family:</b> Serralysin-like metalloprotease, C-terminal domain
26	<a href="#">c2ml2A</a>	Alignment	not modelled	93.5	20	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> poly(beta-d-mannuronate) c5 epimerase 6;

						<b>PDBTitle:</b> solution structure of alge6r2 subunit from the azotobacter vinelandii2 mannuronan c5-epimerase
27	<a href="#">c1satA_</a>	Alignment	not modelled	93.3	20	<b>PDB header:</b> hydrolase (serine protease) <b>Chain:</b> A: <b>PDB Molecule:</b> serratia protease; <b>PDBTitle:</b> crystal structure of the 50 kda metallo protease from s.2 marcescens
28	<a href="#">d1k7ia1</a>	Alignment	not modelled	93.1	19	<b>Fold:</b> Single-stranded right-handed beta-helix <b>Superfamily:</b> beta-Roll <b>Family:</b> Serralysin-like metalloprotease, C-terminal domain
29	<a href="#">d1sata1</a>	Alignment	not modelled	92.5	18	<b>Fold:</b> Single-stranded right-handed beta-helix <b>Superfamily:</b> beta-Roll <b>Family:</b> Serralysin-like metalloprotease, C-terminal domain
30	<a href="#">c2agmA_</a>	Alignment	not modelled	92.5	25	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> poly(beta-d-mannuronate) c5 epimerase 4; <b>PDBTitle:</b> solution structure of the r-module from alge4
31	<a href="#">c1jiwP_</a>	Alignment	not modelled	92.1	26	<b>PDB header:</b> hydrolase/hyrolase inhibitor <b>Chain:</b> P: <b>PDB Molecule:</b> alkaline metalloproteinase; <b>PDBTitle:</b> crystal structure of the apr-aprin complex
32	<a href="#">c1o1aP_</a>	Alignment	not modelled	92.1	29	<b>PDB header:</b> contractile protein <b>Chain:</b> P: <b>PDB Molecule:</b> skeletal muscle myosin ii; <b>PDBTitle:</b> molecular models of averaged rigor crossbridges from tomograms of2 insect flight muscle
33	<a href="#">d1g9ka1</a>	Alignment	not modelled	91.4	19	<b>Fold:</b> Single-stranded right-handed beta-helix <b>Superfamily:</b> beta-Roll <b>Family:</b> Serralysin-like metalloprotease, C-terminal domain
34	<a href="#">c4pd3B_</a>	Alignment	not modelled	90.2	5	<b>PDB header:</b> contractile protein <b>Chain:</b> B: <b>PDB Molecule:</b> nonmuscle myosin heavy chain b, alpha-actinin a chimera <b>PDBTitle:</b> crystal structure of rigor-like human nonmuscle myosin-2b
35	<a href="#">c1om8A_</a>	Alignment	not modelled	89.8	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> serralysin; <b>PDBTitle:</b> crystal structure of a cold adapted alkaline protease from pseudomonas2 tac ii 18, co-crystallized with 10 mm edta
36	<a href="#">d1kk8a2</a>	Alignment	not modelled	89.4	11	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Motor proteins
37	<a href="#">c2klwA_</a>	Alignment	not modelled	89.2	30	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> (pkg)10; <b>PDBTitle:</b> solution structure of an abc collagen heterotrimer reveals a2 single-register helix stabilized by electrostatic3 interactions
38	<a href="#">c5i0iB_</a>	Alignment	not modelled	88.3	17	<b>PDB header:</b> motor protein <b>Chain:</b> B: <b>PDB Molecule:</b> unconventional myosin-x; <b>PDBTitle:</b> crystal structure of myosin x motor domain with 2iq motifs in pre-2 powerstroke state
39	<a href="#">c2otgA_</a>	Alignment	not modelled	87.2	11	<b>PDB header:</b> contractile protein <b>Chain:</b> A: <b>PDB Molecule:</b> myosin heavy chain; <b>PDBTitle:</b> rigor-like structures of muscle myosins reveal key2 mechanical elements in the transduction pathways of this3 allosteric motor
40	<a href="#">c2cuoF_</a>	Alignment	not modelled	86.6	33	<b>PDB header:</b> structural protein <b>Chain:</b> F: <b>PDB Molecule:</b> collagen model peptide (pro-pro-gly)9; <b>PDBTitle:</b> collagen model peptide (pro-pro-gly)9
41	<a href="#">c2cuoC_</a>	Alignment	not modelled	86.6	33	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> collagen model peptide (pro-pro-gly)9; <b>PDBTitle:</b> collagen model peptide (pro-pro-gly)9
42	<a href="#">c3dtpA_</a>	Alignment	not modelled	84.3	12	<b>PDB header:</b> contractile protein <b>Chain:</b> A: <b>PDB Molecule:</b> myosin 2 heavy chain chimera of smooth and cardiac muscle; <b>PDBTitle:</b> tarantula heavy meromyosin obtained by flexible docking to tarantula2 muscle thick filament cryo-em 3d-map
43	<a href="#">c1k6fC_</a>	Alignment	not modelled	84.2	31	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> collagen triple helix; <b>PDBTitle:</b> crystal structure of the collagen triple helix model [(pro-pro-gly)2 10]3
44	<a href="#">c1k6fE_</a>	Alignment	not modelled	84.2	31	<b>PDB header:</b> structural protein <b>Chain:</b> E: <b>PDB Molecule:</b> collagen triple helix; <b>PDBTitle:</b> crystal structure of the collagen triple helix model [(pro-pro-gly)2 10]3
45	<a href="#">c1k6fF_</a>	Alignment	not modelled	84.2	31	<b>PDB header:</b> structural protein <b>Chain:</b> F: <b>PDB Molecule:</b> collagen triple helix; <b>PDBTitle:</b> crystal structure of the collagen triple helix model [(pro-pro-gly)2 10]3
46	<a href="#">c1k6fB_</a>	Alignment	not modelled	84.2	31	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> collagen triple helix; <b>PDBTitle:</b> crystal structure of the collagen triple helix model [(pro-pro-gly)2 10]3
47	<a href="#">c1k6fA_</a>	Alignment	not modelled	84.2	31	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> collagen triple helix; <b>PDBTitle:</b> crystal structure of the collagen triple helix model [(pro-pro-gly)2 10]3
48	<a href="#">c1k6fD_</a>	Alignment	not modelled	84.2	31	<b>PDB header:</b> structural protein <b>Chain:</b> D: <b>PDB Molecule:</b> collagen triple helix; <b>PDBTitle:</b> crystal structure of the collagen triple helix model [(pro-pro-gly)2 10]3
49	<a href="#">c2dfsA_</a>	Alignment	not modelled	83.6	19	<b>PDB header:</b> contractile protein/transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> myosin-5a; <b>PDBTitle:</b> 3-d structure of myosin-v inhibited state
50	<a href="#">c3ah9A_</a>	Alignment	not modelled	82.4	33	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure of (pro-pro-gly)9 at 1.1 a resolution
51	<a href="#">c2cuoB_</a>	Alignment	not modelled	81.9	31	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> collagen model peptide (pro-pro-gly)9; <b>PDBTitle:</b> collagen model peptide (pro-pro-gly)9
						<b>PDB header:</b> structural protein

52	<a href="#">c2cuoA_</a>	Alignment	not modelled	81.9	31	<b>Chain:</b> A: <b>PDB Molecule:</b> collagen model peptide (pro-pro-gly)9; <b>PDBTitle:</b> collagen model peptide (pro-pro-gly)9
53	<a href="#">c2cuoD_</a>	Alignment	not modelled	81.9	31	<b>PDB header:</b> structural protein <b>Chain:</b> D: <b>PDB Molecule:</b> collagen model peptide (pro-pro-gly)9; <b>PDBTitle:</b> collagen model peptide (pro-pro-gly)9
54	<a href="#">c2cuoE_</a>	Alignment	not modelled	81.9	31	<b>PDB header:</b> structural protein <b>Chain:</b> E: <b>PDB Molecule:</b> collagen model peptide (pro-pro-gly)9; <b>PDBTitle:</b> collagen model peptide (pro-pro-gly)9
55	<a href="#">c3ah9D_</a>	Alignment	not modelled	81.2	36	<b>PDB header:</b> structural protein <b>Chain:</b> D: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure of (pro-pro-gly)9 at 1.1 a resolution
56	<a href="#">c3ah9F_</a>	Alignment	not modelled	80.7	33	<b>PDB header:</b> structural protein <b>Chain:</b> F: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure of (pro-pro-gly)9 at 1.1 a resolution
57	<a href="#">c5cxIA_</a>	Alignment	not modelled	80.7	30	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional hemolysin/adenylate cyclase; <b>PDBTitle:</b> crystal structure of rtx domain block v of adenylate cyclase toxin2 from bordetella pertussis
58	<a href="#">c3ah9B_</a>	Alignment	not modelled	79.9	32	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure of (pro-pro-gly)9 at 1.1 a resolution
59	<a href="#">c3ah9C_</a>	Alignment	not modelled	79.9	32	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure of (pro-pro-gly)9 at 1.1 a resolution
60	<a href="#">c3ah9E_</a>	Alignment	not modelled	79.9	32	<b>PDB header:</b> structural protein <b>Chain:</b> E: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure of (pro-pro-gly)9 at 1.1 a resolution
61	<a href="#">c2vb6A_</a>	Alignment	not modelled	79.3	12	<b>PDB header:</b> motor protein <b>Chain:</b> A: <b>PDB Molecule:</b> myosin vi; <b>PDBTitle:</b> myosin vi (md-insert2-cam, delta insert1) post-rigor state (2 crystal form 2)
62	<a href="#">c3w5mA_</a>	Alignment	not modelled	78.8	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative rhamnosidase; <b>PDBTitle:</b> crystal structure of streptomyces avermitilis alpha-l-rhamnosidase
63	<a href="#">c2bkhA_</a>	Alignment	not modelled	78.1	13	<b>PDB header:</b> motor protein/metal-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> unconventional myosin; <b>PDBTitle:</b> myosin vi nucleotide-free (mdinsert2) crystal structure
64	<a href="#">c4r8gE_</a>	Alignment	not modelled	76.9	21	<b>PDB header:</b> protein binding/calcium-binding protein <b>Chain:</b> E: <b>PDB Molecule:</b> unconventional myosin-ic; <b>PDBTitle:</b> crystal structure of myosin-1c tail in complex with calmodulin
65	<a href="#">c3p4gD_</a>	Alignment	not modelled	76.4	14	<b>PDB header:</b> antifreeze protein <b>Chain:</b> D: <b>PDB Molecule:</b> antifreeze protein; <b>PDBTitle:</b> x-ray crystal structure of a hyperactive, ca2+-dependent, beta-helical2 antifreeze protein from an antarctic bacterium
66	<a href="#">d2mysa2</a>	Alignment	not modelled	75.7	27	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Motor proteins
67	<a href="#">c3lphD_</a>	Alignment	not modelled	75.5	65	<b>PDB header:</b> viral protein <b>Chain:</b> D: <b>PDB Molecule:</b> protein rev; <b>PDBTitle:</b> crystal structure of the hiv-1 rev dimer
68	<a href="#">c3a0mF_</a>	Alignment	not modelled	74.5	33	<b>PDB header:</b> structural protein <b>Chain:</b> F: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> structure of (ppg)4-ovg-(ppg)4, monoclinic, twinned crystal
69	<a href="#">c3jbhA_</a>	Alignment	not modelled	73.8	14	<b>PDB header:</b> contractile protein <b>Chain:</b> A: <b>PDB Molecule:</b> myosin 2 heavy chain striated muscle; <b>PDBTitle:</b> two heavy meromyosin interacting-heads motifs flexible docked into2 tarantula thick filament 3d-map allows in depth study of intra- and3 intermolecular interactions
70	<a href="#">c5uz7R_</a>	Alignment	not modelled	73.0	21	<b>PDB header:</b> signaling protein <b>Chain:</b> R: <b>PDB Molecule:</b> calcitonin receptor; <b>PDBTitle:</b> volta phase plate cryo-electron microscopy structure of a calcitonin2 receptor-heterotrimeric gs protein complex
71	<a href="#">c5szsC_</a>	Alignment	not modelled	71.6	21	<b>PDB header:</b> viral protein <b>Chain:</b> C: <b>PDB Molecule:</b> spike glycoprotein; <b>PDBTitle:</b> glycan shield and epitope masking of a coronavirus spike protein2 observed by cryo-electron microscopy
72	<a href="#">c3j44h_</a>	Alignment	not modelled	71.4	53	<b>PDB header:</b> ribosome/protein transport <b>Chain:</b> H: <b>PDB Molecule:</b> 50s ribosomal protein l11p; <b>PDBTitle:</b> structure of the methanococcus jannaschii ribosome-secybeta channel2 complex (50s ribosomal subunit)
73	<a href="#">c3j21h_</a>	Alignment	not modelled	71.4	53	<b>PDB header:</b> ribosome <b>Chain:</b> H: <b>PDB Molecule:</b> 50s ribosomal protein l11p; <b>PDBTitle:</b> promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
74	<a href="#">c5jbh0_</a>	Alignment	not modelled	71.0	53	<b>PDB header:</b> transcription <b>Chain:</b> 0: <b>PDB Molecule:</b> 30s ribosomal protein e41; <b>PDBTitle:</b> cryo-em structure of a full archaeal ribosomal translation initiation2 complex in the p-in conformation
75	<a href="#">c5jb30_</a>	Alignment	not modelled	71.0	53	<b>PDB header:</b> translation <b>Chain:</b> 0: <b>PDB Molecule:</b> 30s ribosomal protein e41; <b>PDBTitle:</b> cryo-em structure of a full archaeal ribosomal translation initiation2 complex in the p-remote conformation
76	<a href="#">c6ar3A_</a>	Alignment	not modelled	70.0	35	<b>PDB header:</b> rna binding protein/rna/dna <b>Chain:</b> A: <b>PDB Molecule:</b> gsi-ii c rt; <b>PDBTitle:</b> structure of a thermostable group ii intron reverse transcriptase with2 template-primer and its functional and evolutionary implications3 (rt/duplex (se-met))
77	<a href="#">c3ob4A_</a>	Alignment	not modelled	69.1	17	<b>PDB header:</b> allergen <b>Chain:</b> A: <b>PDB Molecule:</b> maltose abc transporter periplasmic protein, arah 2; <b>PDBTitle:</b> mbp-fusion protein of the major peanut allergen ara h 2

78	<a href="#">c5xxum_</a>	Alignment	not modelled	69.0	52	<b>PDB header:</b> ribosome <b>Chain:</b> M: <b>PDB Molecule:</b> ribosomal protein es12; <b>PDBTitle:</b> small subunit of toxoplasma gondii ribosome
79	<a href="#">c2x7IP_</a>	Alignment	not modelled	68.5	59	<b>PDB header:</b> immune system <b>Chain:</b> P: <b>PDB Molecule:</b> protein rev; <b>PDBTitle:</b> implications of the hiv-1 rev dimer structure at 3.2a resolution for 2 multimeric binding to the rev response element
80	<a href="#">c6i9eE_</a>	Alignment	not modelled	66.7	42	<b>PDB header:</b> virus <b>Chain:</b> E: <b>PDB Molecule:</b> major head protein; <b>PDBTitle:</b> thermophage p23-45 empty expanded capsid
81	<a href="#">c4dwcA_</a>	Alignment	not modelled	66.1	50	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> e(rns) glycoprotein; <b>PDBTitle:</b> crystal structure of the glycoprotein erns from the pestivirus bvdv-12 in complex with zn ions
82	<a href="#">c5o5jO_</a>	Alignment	not modelled	64.5	30	<b>PDB header:</b> ribosome <b>Chain:</b> O: <b>PDB Molecule:</b> 30s ribosomal protein s15; <b>PDBTitle:</b> structure of the 30s small ribosomal subunit from mycobacterium2 smegmatis
83	<a href="#">d1g1xb_</a>	Alignment	not modelled	64.1	28	<b>Fold:</b> S15/NS1 RNA-binding domain <b>Superfamily:</b> S15/NS1 RNA-binding domain <b>Family:</b> Ribosomal protein S15
84	<a href="#">c4i79A_</a>	Alignment	not modelled	61.6	16	<b>PDB header:</b> motor protein/metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> unconventional myosin-ib; <b>PDBTitle:</b> crystal structure of nucleotide-free myosin 1b residues 1-728 with 2 bound calmodulin
85	<a href="#">c2lm4A_</a>	Alignment	not modelled	61.3	31	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> succinate dehydrogenase assembly factor 2, mitochondrial; <b>PDBTitle:</b> solution nmr structure of mitochondrial succinate dehydrogenase2 assembly factor 2 from saccharomyces cerevisiae, northeast structural3 genomics consortium target yt682a
86	<a href="#">c3admC_</a>	Alignment	not modelled	60.9	35	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure of (pro-pro-gly)4-hyp-ser-gly-(pro-pro-gly)4
87	<a href="#">c2d3fD_</a>	Alignment	not modelled	60.7	35	<b>PDB header:</b> structural protein <b>Chain:</b> D: <b>PDB Molecule:</b> collagen model peptides (pro-pro-gly)4-pro-hyp- <b>PDBTitle:</b> crystal structures of collagen model peptides (pro-pro-gly)2 4-pro-hyp-gly-(pro-pro-gly)4
88	<a href="#">c1x1kB_</a>	Alignment	not modelled	60.7	35	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> host-guest peptide (pro-pro-gly)4-(pro-allohyp- <b>PDBTitle:</b> host-guest peptide (pro-pro-gly)4-(pro-allohyp-gly)-(pro-2 pro-gly)4
89	<a href="#">c2d3fE_</a>	Alignment	not modelled	60.7	35	<b>PDB header:</b> structural protein <b>Chain:</b> E: <b>PDB Molecule:</b> collagen model peptides (pro-pro-gly)4-pro-hyp- <b>PDBTitle:</b> crystal structures of collagen model peptides (pro-pro-gly)2 4-pro-hyp-gly-(pro-pro-gly)4
90	<a href="#">c1x1kD_</a>	Alignment	not modelled	60.7	35	<b>PDB header:</b> structural protein <b>Chain:</b> D: <b>PDB Molecule:</b> host-guest peptide (pro-pro-gly)4-(pro-allohyp- <b>PDBTitle:</b> host-guest peptide (pro-pro-gly)4-(pro-allohyp-gly)-(pro-2 pro-gly)4
91	<a href="#">c1x1kC_</a>	Alignment	not modelled	60.7	35	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> host-guest peptide (pro-pro-gly)4-(pro-allohyp- <b>PDBTitle:</b> host-guest peptide (pro-pro-gly)4-(pro-allohyp-gly)-(pro-2 pro-gly)4
92	<a href="#">c1x1kA_</a>	Alignment	not modelled	60.7	35	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> host-guest peptide (pro-pro-gly)4-(pro-allohyp- <b>PDBTitle:</b> host-guest peptide (pro-pro-gly)4-(pro-allohyp-gly)-(pro-2 pro-gly)4
93	<a href="#">c2d3fF_</a>	Alignment	not modelled	60.7	35	<b>PDB header:</b> structural protein <b>Chain:</b> F: <b>PDB Molecule:</b> collagen model peptides (pro-pro-gly)4-pro-hyp- <b>PDBTitle:</b> crystal structures of collagen model peptides (pro-pro-gly)2 4-pro-hyp-gly-(pro-pro-gly)4
94	<a href="#">d2a5yb2</a>	Alignment	not modelled	58.7	23	<b>Fold:</b> DEATH domain <b>Superfamily:</b> DEATH domain <b>Family:</b> Caspase recruitment domain, CARD
95	<a href="#">c3nb0A_</a>	Alignment	not modelled	58.3	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glycogen [starch] synthase isoform 2; <b>PDBTitle:</b> glucose-6-phosphate activated form of yeast glycogen synthase
96	<a href="#">c2ds2C_</a>	Alignment	not modelled	58.0	43	<b>PDB header:</b> plant protein <b>Chain:</b> C: <b>PDB Molecule:</b> sweet protein mabinlin-2 chain a; <b>PDBTitle:</b> crystal structure of mabinlin ii
97	<a href="#">c3admA_</a>	Alignment	not modelled	55.4	35	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure of (pro-pro-gly)4-hyp-ser-gly-(pro-pro-gly)4
98	<a href="#">c3admF_</a>	Alignment	not modelled	55.4	35	<b>PDB header:</b> structural protein <b>Chain:</b> F: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure of (pro-pro-gly)4-hyp-ser-gly-(pro-pro-gly)4
99	<a href="#">c3admE_</a>	Alignment	not modelled	55.4	35	<b>PDB header:</b> structural protein <b>Chain:</b> E: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure of (pro-pro-gly)4-hyp-ser-gly-(pro-pro-gly)4
100	<a href="#">c3admB_</a>	Alignment	not modelled	55.4	35	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure of (pro-pro-gly)4-hyp-ser-gly-(pro-pro-gly)4
101	<a href="#">c5epmC_</a>	Alignment	not modelled	55.1	56	<b>PDB header:</b> toxin/immune system <b>Chain:</b> C: <b>PDB Molecule:</b> beta-theraphotoxin-cm1a; <b>PDBTitle:</b> ceratotoxin variant in complex with specific antibody fab fragment

102	<a href="#">c4clvB_</a>	 Alignment	not modelled	54.8	9	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> nickel-cobalt-cadmium resistance protein nccx; <b>PDBTitle:</b> crystal structure of dodecylphosphocholine-solubilized nccx2 from cupriavidus metallidurans 31a
103	<a href="#">c5b68A_</a>	 Alignment	not modelled	54.3	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-alpha-glucanotransferase; <b>PDBTitle:</b> crystal structure of apo amylomaltase from corynebacterium glutamicum
104	<a href="#">c3a08D_</a>	 Alignment	not modelled	53.7	41	<b>PDB header:</b> structural protein <b>Chain:</b> D: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> structure of (ppg)4-oog-(ppg)4, monoclinic, twinned crystal
105	<a href="#">c3a19F_</a>	 Alignment	not modelled	53.7	41	<b>PDB header:</b> structural protein <b>Chain:</b> F: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> structure of (ppg)4-oog-(ppg)4_h monoclinic, twinned crystal
106	<a href="#">c2d3hD_</a>	 Alignment	not modelled	53.7	41	<b>PDB header:</b> structural protein <b>Chain:</b> D: <b>PDB Molecule:</b> collagen model peptides (pro-pro-gly)4-hyp-hyp- <b>PDBTitle:</b> crystal structures of collagen model peptides (pro-pro-gly)2 4-hyp-hyp-gly-(pro-pro-gly)4
107	<a href="#">c3ulwA_</a>	 Alignment	not modelled	53.3	9	<b>PDB header:</b> ribosomal protein <b>Chain:</b> A: <b>PDB Molecule:</b> 30s ribosomal protein s15; <b>PDBTitle:</b> 30s ribosomal protein s15 from campylobacter jejuni
108	<a href="#">c3abnA_</a>	 Alignment	not modelled	52.8	35	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure of (pro-pro-gly)4-hyp-asp-gly-(pro-pro-gly)4 at 1.022 a
109	<a href="#">c5dg3D_</a>	 Alignment	not modelled	51.9	19	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> acyl-[acyl-carrier-protein]-udp-n-acetylglucosamine o- <b>PDBTitle:</b> structure of pseudomonas aeruginosa lpxa in complex with udp-3-o-(r-3-2 hydroxydecanoyl)-glnac
110	<a href="#">d1a32a_</a>	 Alignment	not modelled	51.8	22	<b>Fold:</b> S15/NS1 RNA-binding domain <b>Superfamily:</b> S15/NS1 RNA-binding domain <b>Family:</b> Ribosomal protein S15
111	<a href="#">c2jr5A_</a>	 Alignment	not modelled	50.9	38	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> upf0350 protein vc_2471; <b>PDBTitle:</b> solution structure of upf0350 protein vc_2471. northeast structural2 genomics target vcr36
112	<a href="#">c3a0mA_</a>	 Alignment	not modelled	49.2	32	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> structure of (ppg)4-ovg-(ppg)4, monoclinic, twinned crystal
113	<a href="#">d1vs5o1</a>	 Alignment	not modelled	48.7	22	<b>Fold:</b> S15/NS1 RNA-binding domain <b>Superfamily:</b> S15/NS1 RNA-binding domain <b>Family:</b> Ribosomal protein S15
114	<a href="#">c3a0mE_</a>	 Alignment	not modelled	47.4	33	<b>PDB header:</b> structural protein <b>Chain:</b> E: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> structure of (ppg)4-ovg-(ppg)4, monoclinic, twinned crystal
115	<a href="#">c2m1aA_</a>	 Alignment	not modelled	47.3	52	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> hiv-1 rev arginine-rich motif (arm); <b>PDBTitle:</b> hiv-1 rev arm peptide (residues t34-r50)
116	<a href="#">c3skqA_</a>	 Alignment	not modelled	47.3	13	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> mitochondrial distribution and morphology protein 38; <b>PDBTitle:</b> mdm38 is a 14-3-3-like receptor and associates with the protein2 synthesis machinery at the inner mitochondrial membrane
117	<a href="#">d1niya_</a>	 Alignment	not modelled	46.8	44	<b>Fold:</b> Knottins (small inhibitors, toxins, lectins) <b>Superfamily:</b> omega toxin-like <b>Family:</b> Spider toxins
118	<a href="#">d1mb6a_</a>	 Alignment	not modelled	46.6	56	<b>Fold:</b> Knottins (small inhibitors, toxins, lectins) <b>Superfamily:</b> omega toxin-like <b>Family:</b> Spider toxins
119	<a href="#">c1etfB_</a>	 Alignment	not modelled	46.4	52	<b>PDB header:</b> viral protein/rna <b>Chain:</b> B: <b>PDB Molecule:</b> rev peptide; <b>PDBTitle:</b> rev response element (rre) rna complexed with rev peptide,2 nmr, minimized average structure
120	<a href="#">c1etgB_</a>	 Alignment	not modelled	46.4	52	<b>PDB header:</b> viral protein/rna <b>Chain:</b> B: <b>PDB Molecule:</b> rev peptide; <b>PDBTitle:</b> rev response element (rre) rna complexed with rev peptide,2 nmr, 19 structures