






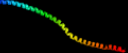







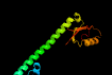






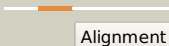
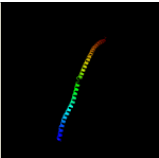
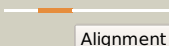


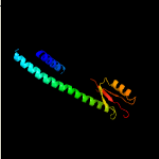

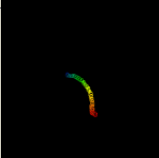
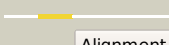
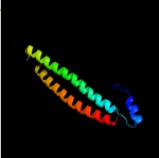
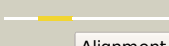
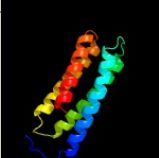
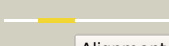
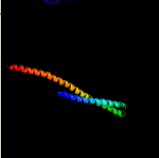
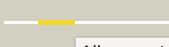
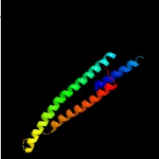

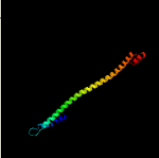
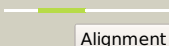

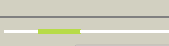

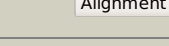

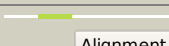



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2082_(-)_2338717_2340882
Date	Mon Aug 5 13:25:19 BST 2019
Unique Job ID	ddf270afe011ab9f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5imuA</a>	 Alignment		100.0	63	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> tat (twin-arginine translocation) pathway signal sequence <b>PDBTitle:</b> a fragment of conserved hypothetical protein rv3899c (residues 184-2 410) from mycobacterium tuberculosis
2	<a href="#">c3ojaB</a>	 Alignment		94.3	10	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> anopheles plasmodium-responsive leucine-rich repeat protein <b>PDBTitle:</b> crystal structure of Irim1/apl1c complex
3	<a href="#">c1ei3E</a>	 Alignment		92.9	4	<b>PDB header:</b> blood clotting <b>Chain:</b> E: <b>PDB Molecule:</b> fibrinogen; <b>PDBTitle:</b> crystal structure of native chicken fibrinogen
4	<a href="#">c1ei3C</a>	 Alignment		91.9	8	<b>PDB header:</b> blood clotting <b>Chain:</b> C: <b>PDB Molecule:</b> fibrinogen; <b>PDBTitle:</b> crystal structure of native chicken fibrinogen
5	<a href="#">c1degO</a>	 Alignment		91.8	7	<b>PDB header:</b> blood clotting <b>Chain:</b> O: <b>PDB Molecule:</b> fibrinogen (beta chain); <b>PDBTitle:</b> the crystal structure of modified bovine fibrinogen (at ~42 angstrom resolution)
6	<a href="#">c1degF</a>	 Alignment		89.4	6	<b>PDB header:</b> blood clotting <b>Chain:</b> F: <b>PDB Molecule:</b> fibrinogen (gamma chain); <b>PDBTitle:</b> the crystal structure of modified bovine fibrinogen (at ~42 angstrom resolution)
7	<a href="#">c3ghgI</a>	 Alignment		89.1	9	<b>PDB header:</b> blood clotting <b>Chain:</b> I: <b>PDB Molecule:</b> fibrinogen gamma chain; <b>PDBTitle:</b> crystal structure of human fibrinogen
8	<a href="#">c6o7xa</a>	 Alignment		89.1	4	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> vacuolar atp synthase catalytic subunit a; <b>PDBTitle:</b> saccharomyces cerevisiae v-atpase stv1-v1vo state 3
9	<a href="#">c5tbyA</a>	 Alignment		88.6	10	<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)
10	<a href="#">c3dtpA</a>	 Alignment		88.5	10	<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
11	<a href="#">c3ghgK</a>	 Alignment		86.6	5	<b>PDB header:</b> blood clotting <b>Chain:</b> K: <b>PDB Molecule:</b> fibrinogen beta chain; <b>PDBTitle:</b> crystal structure of human fibrinogen

12	<a href="#">c6flnE_</a>	 Alignment		85.9	8	<b>PDB header:</b> protein binding <b>Chain:</b> E: <b>PDB Molecule:</b> e3 ubiquitin/isg15 ligase trim25; <b>PDBTitle:</b> crystal structure of the human trim25 coiled-coil and pryspry domains
13	<a href="#">c5yz0C_</a>	 Alignment		85.1	11	<b>PDB header:</b> cell cycle <b>Chain:</b> C: <b>PDB Molecule:</b> atr-interacting protein; <b>PDBTitle:</b> cryo-em structure of human atr-atrip complex
14	<a href="#">c6o7ua_</a>	 Alignment		82.8	5	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> <b>PDBTitle:</b> saccharomyces cerevisiae v-atpase stv1-vo
15	<a href="#">c2dfsA_</a>	 Alignment		81.7	7	<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
16	<a href="#">c3lssA_</a>	 Alignment		77.9	11	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> seryl-trna synthetase; <b>PDBTitle:</b> trypanosoma brucei seryl-trna synthetase in complex with atp
17	<a href="#">c1y4cA_</a>	 Alignment		74.9	11	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> maltose binding protein fused with designed <b>PDBTitle:</b> designed helical protein fusion mbp
18	<a href="#">c5ew5C_</a>	 Alignment		74.0	5	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> colicin-e9; <b>PDBTitle:</b> crystal structure of colicin e9 in complex with its immunity protein2 im9
19	<a href="#">c1bf5A_</a>	 Alignment		71.2	7	<b>PDB header:</b> gene regulation/dna <b>Chain:</b> A: <b>PDB Molecule:</b> signal transducer and activator of transcription 1- <b>PDBTitle:</b> tyrosine phosphorylated stat-1/dna complex
20	<a href="#">c4cgkA_</a>	 Alignment		70.4	8	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> secreted 45 kda protein; <b>PDBTitle:</b> crystal structure of the essential protein pcsb from streptococcus2 pneumoniae
21	<a href="#">c6b3rE_</a>	 Alignment	not modelled	68.1	9	<b>PDB header:</b> transport protein <b>Chain:</b> E: <b>PDB Molecule:</b> piezo-type mechanosensitive ion channel component 1; <b>PDBTitle:</b> structure of the mechanosensitive channel piezo1
22	<a href="#">c4cg4D_</a>	 Alignment	not modelled	66.5	9	<b>PDB header:</b> actin-binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> pyrin; <b>PDBTitle:</b> crystal structure of the chs-b30.2 domains of trim20
23	<a href="#">c5gasN_</a>	 Alignment	not modelled	66.1	9	<b>PDB header:</b> hydrolase <b>Chain:</b> N: <b>PDB Molecule:</b> archaeal/vacuolar-type h+-atpase subunit i; <b>PDBTitle:</b> thermus thermophilus v/a-atpase, conformation 2
24	<a href="#">c6iu3A_</a>	 Alignment	not modelled	65.1	9	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> vit1; <b>PDBTitle:</b> crystal structure of iron transporter vit1 with zinc ions
25	<a href="#">c4rh7A_</a>	 Alignment	not modelled	63.9	9	<b>PDB header:</b> motor protein <b>Chain:</b> A: <b>PDB Molecule:</b> green fluorescent protein/cytoplasmic dynein 2 heavy chain <b>PDBTitle:</b> crystal structure of human cytoplasmic dynein 2 motor domain in2 complex with adp.vi
26	<a href="#">c3ojaA_</a>	 Alignment	not modelled	63.0	6	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> leucine-rich immune molecule 1; <b>PDBTitle:</b> crystal structure of lrim1/apl1c complex
27	<a href="#">c3cwgA_</a>	 Alignment	not modelled	61.1	10	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> signal transducer and activator of transcription <b>PDBTitle:</b> unphosphorylated mouse stat3 core fragment <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
28	<a href="#">c3jbaA_</a>	 Alignment	not modelled	60.5	4	

						of intra- and 3 intermolecular interactions
29	<a href="#">c4ll8E_</a>	Alignment	not modelled	58.1	8	<b>PDB header:</b> motor protein/transport protein <b>Chain:</b> E: <b>PDB Molecule:</b> swi5-dependent ho expression protein 3; <b>PDBTitle:</b> complex of carboxy terminal domain of myo4p and she3p middle fragment
30	<a href="#">c3vkhA_</a>	Alignment	not modelled	57.1	9	<b>PDB header:</b> motor protein <b>Chain:</b> A: <b>PDB Molecule:</b> dynein heavy chain, cytoplasmic; <b>PDBTitle:</b> x-ray structure of a functional full-length dynein motor domain
31	<a href="#">c2zv4O_</a>	Alignment	not modelled	57.0	15	<b>PDB header:</b> structural protein <b>Chain:</b> O: <b>PDB Molecule:</b> major vault protein; <b>PDBTitle:</b> the structure of rat liver vault at 3.5 angstrom resolution
32	<a href="#">d2jf2a1</a>	Alignment	not modelled	52.9	20	<b>Fold:</b> Single-stranded left-handed beta-helix <b>Superfamily:</b> Trimeric LpxA-like enzymes <b>Family:</b> UDP N-acetylglucosamine acyltransferase
33	<a href="#">c6gapB_</a>	Alignment	not modelled	52.0	9	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> outer capsid protein sigma-1; <b>PDBTitle:</b> crystal structure of the t3d reovirus sigma1 coiled coil tail and body
34	<a href="#">c3ipkA_</a>	Alignment	not modelled	50.3	4	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> agi/ii; <b>PDBTitle:</b> crystal structure of a3vp1 of agi/ii of streptococcus mutans
35	<a href="#">c1m1jA_</a>	Alignment	not modelled	50.3	7	<b>PDB header:</b> blood clotting <b>Chain:</b> A: <b>PDB Molecule:</b> fibrinogen alpha subunit; <b>PDBTitle:</b> crystal structure of native chicken fibrinogen with two different 2 bound ligands
36	<a href="#">c6gajA_</a>	Alignment	not modelled	49.5	10	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> outer capsid protein sigma-1; <b>PDBTitle:</b> crystal structure of the t1l reovirus sigma1 coiled coil tail (iodide)
37	<a href="#">c6gaoC_</a>	Alignment	not modelled	45.9	9	<b>PDB header:</b> viral protein <b>Chain:</b> C: <b>PDB Molecule:</b> outer capsid protein sigma-1; <b>PDBTitle:</b> crystal structure of the t1l reovirus sigma1 coiled coil tail and body
38	<a href="#">c5dfzD_</a>	Alignment	not modelled	44.4	11	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> vacuolar protein sorting-associated protein 30; <b>PDBTitle:</b> structure of vps34 complex ii from <i>s. cerevisiae</i> .
39	<a href="#">c4pd3B_</a>	Alignment	not modelled	43.3	10	<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
40	<a href="#">c1jchC_</a>	Alignment	not modelled	40.2	7	<b>PDB header:</b> ribosome inhibitor, hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> colicin e3; <b>PDBTitle:</b> crystal structure of colicin e3 in complex with its immunity protein
41	<a href="#">c5mg8B_</a>	Alignment	not modelled	39.3	8	<b>PDB header:</b> recombination <b>Chain:</b> B: <b>PDB Molecule:</b> structural maintenance of chromosomes protein 6; <b>PDBTitle:</b> crystal structure of the <i>s.pombe</i> smc5/6 hinge domain
42	<a href="#">c1d7mA_</a>	Alignment	not modelled	39.3	13	<b>PDB header:</b> contractile protein <b>Chain:</b> A: <b>PDB Molecule:</b> cortexillin i; <b>PDBTitle:</b> coiled-coil dimerization domain from cortexillin i
43	<a href="#">c3vkgB_</a>	Alignment	not modelled	39.1	11	<b>PDB header:</b> motor protein <b>Chain:</b> B: <b>PDB Molecule:</b> dynein heavy chain, cytoplasmic; <b>PDBTitle:</b> x-ray structure of an mtbd truncation mutant of dynein motor domain
44	<a href="#">c1i84V_</a>	Alignment	not modelled	38.5	6	<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 of 2 chicken gizzard smooth muscle myosin with regulatory light 3 chain in the dephosphorylated state. only c alphas 4 provided for regulatory light chain. only backbone atoms 5 provided for s 2 fragment.
45	<a href="#">c1kmiZ_</a>	Alignment	not modelled	37.6	8	<b>PDB header:</b> signaling protein <b>Chain:</b> Z: <b>PDB Molecule:</b> chemotaxis protein chez; <b>PDBTitle:</b> crystal structure of an e.coli chemotaxis protein, chez
46	<a href="#">c5voxb_</a>	Alignment	not modelled	36.5	4	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> v-type proton atpase subunit b; <b>PDBTitle:</b> yeast v-atpase in complex with legionella pneumophila effector sidk2 (rotational state 1)
47	<a href="#">c2i1kA_</a>	Alignment	not modelled	36.4	9	<b>PDB header:</b> cell adhesion, membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> moesin; <b>PDBTitle:</b> moesin from spodoptera frugiperda reveals the coiled-coil domain at 2 3.0 angstrom resolution
48	<a href="#">c5nf8A_</a>	Alignment	not modelled	36.2	15	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> respiratory supercomplex factor 1, mitochondrial; <b>PDBTitle:</b> solution structure of detergent-solubilized rcf1, a yeast 2 mitochondrial inner membrane protein involved in respiratory complex 3 iii/iv supercomplex formation
49	<a href="#">c6ogdB_</a>	Alignment	not modelled	34.2	8	<b>PDB header:</b> toxin <b>Chain:</b> B: <b>PDB Molecule:</b> toxin subunit yena2; <b>PDBTitle:</b> cryo-em structure of yentca in its prepore state
50	<a href="#">c5jxfA_</a>	Alignment	not modelled	32.6	5	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> asp/glu-specific dipeptidyl-peptidase; <b>PDBTitle:</b> crystal structure of flavobacterium psychrophilum dpp11 in complex 2 with dipeptide arg-asp
51	<a href="#">c2xzrA_</a>	Alignment	not modelled	32.6	9	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> immunoglobulin-binding protein eibd; <b>PDBTitle:</b> escherichia coli immunoglobulin-binding protein eibd 391-438 fused 2 to gcn4 adaptors
52	<a href="#">c3qo8A_</a>	Alignment	not modelled	32.5	7	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> seryl-trna synthetase, cytoplasmic; <b>PDBTitle:</b> crystal structure of seryl-trna synthetase from candida albicans
						<b>PDB header:</b> chaperone

53	<a href="#">c2ncaA</a>	Alignment	not modelled	29.8	10	<b>Chain:</b> A: <b>PDB Molecule:</b> hsp90 co-chaperone cdc37; <b>PDBTitle:</b> structural model for the n-terminal domain of human cdc37
54	<a href="#">c2gl2B</a>	Alignment	not modelled	29.3	13	<b>PDB header:</b> cell adhesion <b>Chain:</b> B: <b>PDB Molecule:</b> adhesion a; <b>PDBTitle:</b> crystal structure of the tetra mutant (t66g,r67g,f68g,y69g) of2 bacterial adhesin fada
55	<a href="#">c6cfzC</a>	Alignment	not modelled	27.3	21	<b>PDB header:</b> nuclear protein <b>Chain:</b> C: <b>PDB Molecule:</b> dad2; <b>PDBTitle:</b> structure of the dash/dam1 complex shows its role at the yeast2 kinetochore-microtubule interface
56	<a href="#">c3vkgA</a>	Alignment	not modelled	26.3	12	<b>PDB header:</b> motor protein <b>Chain:</b> A: <b>PDB Molecule:</b> dynein heavy chain, cytoplasmic; <b>PDBTitle:</b> x-ray structure of an mtbd truncation mutant of dynein motor domain
57	<a href="#">c6ezvX</a>	Alignment	not modelled	26.1	11	<b>PDB header:</b> toxin <b>Chain:</b> X: <b>PDB Molecule:</b> non-hemolytic enterotoxin lytic component I1; <b>PDBTitle:</b> the cytotoxin maka from vibrio cholerae
58	<a href="#">c2qzvB</a>	Alignment	not modelled	25.4	13	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> major vault protein; <b>PDBTitle:</b> draft crystal structure of the vault shell at 9 angstroms2 resolution
59	<a href="#">c3lvgD</a>	Alignment	not modelled	25.4	7	<b>PDB header:</b> structural protein <b>Chain:</b> D: <b>PDB Molecule:</b> clathrin light chain b; <b>PDBTitle:</b> crystal structure of a clathrin heavy chain and clathrin light chain2 complex
60	<a href="#">c5tvbB</a>	Alignment	not modelled	24.6	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> nucleoprotein tpr; <b>PDBTitle:</b> structure of the tpr oligomerization domain
61	<a href="#">c1wleB</a>	Alignment	not modelled	24.4	16	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> seryl-trna synthetase; <b>PDBTitle:</b> crystal structure of mammalian mitochondrial seryl-trna2 synthetase complexed with seryl-adenylate
62	<a href="#">c3u59C</a>	Alignment	not modelled	24.0	11	<b>PDB header:</b> contractile protein <b>Chain:</b> C: <b>PDB Molecule:</b> tropomyosin beta chain; <b>PDBTitle:</b> n-terminal 98-aa fragment of smooth muscle tropomyosin beta
63	<a href="#">c3vkhB</a>	Alignment	not modelled	23.6	11	<b>PDB header:</b> motor protein <b>Chain:</b> B: <b>PDB Molecule:</b> dynein heavy chain, cytoplasmic; <b>PDBTitle:</b> x-ray structure of a functional full-length dynein motor domain
64	<a href="#">c5jxpA</a>	Alignment	not modelled	23.0	10	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> asp/glu-specific dipeptidyl-peptidase; <b>PDBTitle:</b> crystal structure of porphyromonas endodontalis dpp11 in alternate2 conformation
65	<a href="#">c6nr84</a>	Alignment	not modelled	23.0	21	<b>PDB header:</b> chaperone <b>Chain:</b> 4: <b>PDB Molecule:</b> prefoldin subunit 4; <b>PDBTitle:</b> htric-hpfd class6
66	<a href="#">c5bu8A</a>	Alignment	not modelled	22.2	13	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna stabilization protein; <b>PDBTitle:</b> hk620 tail needle crystallized at ph 7.5 and derivatized with xenon
67	<a href="#">c6bwfB</a>	Alignment	not modelled	22.1	10	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> trpm7; <b>PDBTitle:</b> 4.1 angstrom mg2+-unbound structure of mouse trpm7
68	<a href="#">c6bwfA</a>	Alignment	not modelled	22.1	10	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> trpm7; <b>PDBTitle:</b> 4.1 angstrom mg2+-unbound structure of mouse trpm7
69	<a href="#">c6bwfD</a>	Alignment	not modelled	22.1	10	<b>PDB header:</b> membrane protein <b>Chain:</b> D: <b>PDB Molecule:</b> trpm7; <b>PDBTitle:</b> 4.1 angstrom mg2+-unbound structure of mouse trpm7
70	<a href="#">c6bwfC</a>	Alignment	not modelled	22.1	10	<b>PDB header:</b> membrane protein <b>Chain:</b> C: <b>PDB Molecule:</b> trpm7; <b>PDBTitle:</b> 4.1 angstrom mg2+-unbound structure of mouse trpm7
71	<a href="#">c5mqfK</a>	Alignment	not modelled	21.1	11	<b>PDB header:</b> splicing <b>Chain:</b> K: <b>PDB Molecule:</b> pre-mrna-splicing factor spf27; <b>PDBTitle:</b> cryo-em structure of a human spliceosome activated for step 2 of2 splicing (c* complex)
72	<a href="#">c3iv1F</a>	Alignment	not modelled	20.9	8	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> tumor susceptibility gene 101 protein; <b>PDBTitle:</b> coiled-coil domain of tumor susceptibility gene 101
73	<a href="#">c3rx6A</a>	Alignment	not modelled	20.3	17	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> polarity suppression protein; <b>PDBTitle:</b> crystal structure of polarity suppression protein from enterobacteria2 phage p4
74	<a href="#">c2ycuA</a>	Alignment	not modelled	20.2	13	<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
75	<a href="#">c2y3aB</a>	Alignment	not modelled	20.2	9	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphatidylinositol 3-kinase regulatory subunit beta; <b>PDBTitle:</b> crystal structure of p110beta in complex with icsh2 of p85beta and the2 drug gdc-0941
76	<a href="#">c4xa1D</a>	Alignment	not modelled	20.0	9	<b>PDB header:</b> motor protein <b>Chain:</b> D: <b>PDB Molecule:</b> gp7-myh7(1173-1238)-eb1 chimera protein; <b>PDBTitle:</b> crystal structure of the coiled-coil surrounding skip 1 of myh7
77	<a href="#">c4v1av</a>	Alignment	not modelled	19.1	20	<b>PDB header:</b> ribosome <b>Chain:</b> V: <b>PDB Molecule:</b> <b>PDBTitle:</b> structure of the large subunit of the mammalian mitoribosome, part 22 of 2
78	<a href="#">c5vgzC</a>	Alignment	not modelled	18.5	16	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> 26s proteasome regulatory subunit 8; <b>PDBTitle:</b> conformational landscape of the p28-bound human proteasome regulatory2 particle

79	<a href="#">c3j99M</a>	Alignment	not modelled	18.5	14	<b>PDB header:</b> hydrolase <b>Chain:</b> M: <b>PDB Molecule:</b> synaptosomal-associated protein 25; <b>PDBTitle:</b> structure of 20s supercomplex determined by single particle2 cryoelectron microscopy (state iiib)
80	<a href="#">c3ghgD</a>	Alignment	not modelled	18.5	8	<b>PDB header:</b> blood clotting <b>Chain:</b> D: <b>PDB Molecule:</b> fibrinogen alpha chain; <b>PDBTitle:</b> crystal structure of human fibrinogen
81	<a href="#">c1a92B</a>	Alignment	not modelled	18.1	14	<b>PDB header:</b> leucine zipper <b>Chain:</b> B: <b>PDB Molecule:</b> delta antigen; <b>PDBTitle:</b> oligomerization domain of hepatitis delta antigen
82	<a href="#">c1vw2H</a>	Alignment	not modelled	18.1	11	<b>PDB header:</b> toxin <b>Chain:</b> H: <b>PDB Molecule:</b> tcda1; <b>PDBTitle:</b> crystal structure of tcda1
83	<a href="#">c5jxxC</a>	Alignment	not modelled	18.1	10	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> acyl-[acyl-carrier-protein]-udp-n-acetylglucosamine o- <b>PDBTitle:</b> crystal structure of udp-n-acetylglucosamine o-acyltransferase (lpxa)2 from moraxella catarrhalis rh4.
84	<a href="#">c6bwdA</a>	Alignment	not modelled	17.3	18	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> transient receptor potential cation channel subfamily m <b>PDBTitle:</b> 3.7 angstrom cryoem structure of truncated mouse trpm7
85	<a href="#">c6bwdD</a>	Alignment	not modelled	17.3	18	<b>PDB header:</b> membrane protein <b>Chain:</b> D: <b>PDB Molecule:</b> transient receptor potential cation channel subfamily m <b>PDBTitle:</b> 3.7 angstrom cryoem structure of truncated mouse trpm7
86	<a href="#">c6bwdC</a>	Alignment	not modelled	17.3	18	<b>PDB header:</b> membrane protein <b>Chain:</b> C: <b>PDB Molecule:</b> transient receptor potential cation channel subfamily m <b>PDBTitle:</b> 3.7 angstrom cryoem structure of truncated mouse trpm7
87	<a href="#">c6bwdB</a>	Alignment	not modelled	17.3	18	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> transient receptor potential cation channel subfamily m <b>PDBTitle:</b> 3.7 angstrom cryoem structure of truncated mouse trpm7
88	<a href="#">c2v71A</a>	Alignment	not modelled	17.1	11	<b>PDB header:</b> nuclear protein <b>Chain:</b> A: <b>PDB Molecule:</b> nuclear distribution protein nude-like 1; <b>PDBTitle:</b> coiled-coil region of nudel
89	<a href="#">c2pohA</a>	Alignment	not modelled	16.7	14	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> head completion protein; <b>PDBTitle:</b> structure of phage p22 tail needle gp26
90	<a href="#">c3ni0A</a>	Alignment	not modelled	16.6	13	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> bone marrow stromal antigen 2; <b>PDBTitle:</b> crystal structure of mouse bst-2/tetherin ectodomain
91	<a href="#">c5cwsE</a>	Alignment	not modelled	16.6	10	<b>PDB header:</b> protein transport <b>Chain:</b> E: <b>PDB Molecule:</b> nucleoporin nup57; <b>PDBTitle:</b> crystal structure of the intact chaetomium thermophilum nsp1-nup49-2 nup57 channel nucleoporin heterotrimer bound to its nic96 nuclear3 pore complex attachment site
92	<a href="#">c6mi3A</a>	Alignment	not modelled	16.5	6	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> nf-kb essential modulator,nf-kappa-b essential modulator, <b>PDBTitle:</b> structure of nemo(51-112) with n- and c-terminal coiled-coil adaptors.
93	<a href="#">d1pd3a</a>	Alignment	not modelled	16.5	14	<b>Fold:</b> ROP-like <b>Superfamily:</b> Nonstructural protein ns2, Nep, M1-binding domain <b>Family:</b> Nonstructural protein ns2, Nep, M1-binding domain
94	<a href="#">c5xyiG</a>	Alignment	not modelled	15.0	20	<b>PDB header:</b> ribosome <b>Chain:</b> G: <b>PDB Molecule:</b> 40s ribosomal protein s6; <b>PDBTitle:</b> small subunit of trichomonas vaginalis ribosome
95	<a href="#">c4nqjB</a>	Alignment	not modelled	14.8	8	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> e3 ubiquitin-protein ligase trim69; <b>PDBTitle:</b> structure of coiled-coil domain
96	<a href="#">c5td8B</a>	Alignment	not modelled	14.7	15	<b>PDB header:</b> replication <b>Chain:</b> B: <b>PDB Molecule:</b> kinetochore protein nuf2; <b>PDBTitle:</b> crystal structure of an extended dwarf ndc80 complex
97	<a href="#">c3tweA</a>	Alignment	not modelled	14.5	28	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> alpha4h; <b>PDBTitle:</b> crystal structure of the de novo designed peptide alpha4h
98	<a href="#">c5y06A</a>	Alignment	not modelled	14.5	15	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> msmeg_4306; <b>PDBTitle:</b> structural characterization of msmeq_4306 from mycobacterium smegmatis
99	<a href="#">c1ytzl</a>	Alignment	not modelled	14.4	17	<b>PDB header:</b> contractile protein <b>Chain:</b> I: <b>PDB Molecule:</b> troponin i; <b>PDBTitle:</b> crystal structure of skeletal muscle troponin in the ca2+-activated state