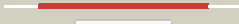
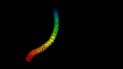

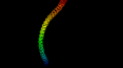
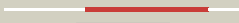
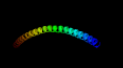

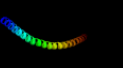

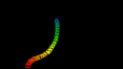

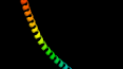

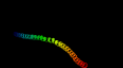

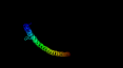

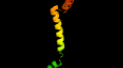

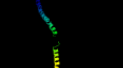

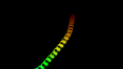
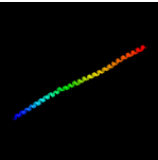
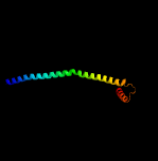
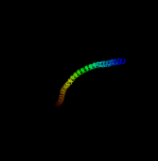

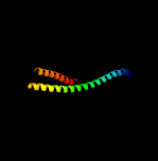

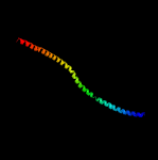
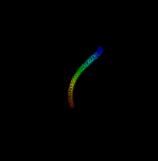
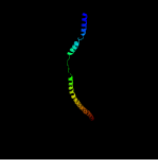


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1444c_(-)_1623293_1623703
Date	Fri Aug 2 13:30:02 BST 2019
Unique Job ID	d8c1167ac23dbaa2

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6gajA_	 Alignment		98.9	12	PDB header: viral protein Chain: A; PDB Molecule: outer capsid protein sigma-1; PDBTitle: crystal structure of the t1l reovirus sigma1 coiled coil tail (iodide)
2	c6gapB_	 Alignment		98.1	13	PDB header: viral protein Chain: B; PDB Molecule: outer capsid protein sigma-1; PDBTitle: crystal structure of the t3d reovirus sigma1 coiled coil tail and body
3	c4fmyE_	 Alignment		97.8	17	PDB header: viral protein Chain: E; PDB Molecule: dna stabilization protein; PDBTitle: hk620 tail needle crystal form i
4	c5bu8A_	 Alignment		96.5	14	PDB header: viral protein Chain: A; PDB Molecule: dna stabilization protein; PDBTitle: hk620 tail needle crystallized at ph 7.5 and derivatized with xenon
5	c6gaoC_	 Alignment		96.3	11	PDB header: viral protein Chain: C; PDB Molecule: outer capsid protein sigma-1; PDBTitle: crystal structure of the t1l reovirus sigma1 coiled coil tail and body
6	c3u1aC_	 Alignment		96.2	12	PDB header: contractile protein Chain: C; PDB Molecule: smooth muscle tropomyosin alpha; PDBTitle: n-terminal 81-aa fragment of smooth muscle tropomyosin alpha
7	c2d3eD_	 Alignment		96.1	11	PDB header: contractile protein Chain: D; PDB Molecule: general control protein gcn4 and tropomyosin 1 alpha chain; PDBTitle: crystal structure of the c-terminal fragment of rabbit skeletal alpha-2 tropomyosin
8	c2fxmB_	 Alignment		96.1	13	PDB header: contractile protein Chain: B; PDB Molecule: myosin heavy chain, cardiac muscle beta isoform; PDBTitle: structure of the human beta-myosin s2 fragment
9	c4abxB_	 Alignment		95.6	11	PDB header: dna binding protein Chain: B; PDB Molecule: dna repair protein recn; PDBTitle: crystal structure of deinococcus radiodurans recn coiled-2 coil domain
10	c3ghgl_	 Alignment		95.5	9	PDB header: blood clotting Chain: I; PDB Molecule: fibrinogen gamma chain; PDBTitle: crystal structure of human fibrinogen
11	c5wjba_	 Alignment		95.4	11	PDB header: actin/dna binding protein Chain: A; PDB Molecule: capsid assembly scaffolding protein,myosin-7; PDBTitle: crystal structure of amino acids 1733-1797 of human beta cardiac2 myosin fused to gp7

12	c3u59C_	Alignment		94.9	11	PDB header: contractile protein Chain: C; PDB Molecule: tropomyosin beta chain; PDBTitle: n-terminal 98-aa fragment of smooth muscle tropomyosin beta
13	c5cwsE_	Alignment		94.8	12	PDB header: protein transport Chain: E; PDB Molecule: nucleoporin nup57; PDBTitle: crystal structure of the intact chaetomium thermophilum nsp1-nup49-2 nup57 channel nucleoporin heterotrimer bound to its nic96 nuclear3 pore complex attachment site
14	c2pohA_	Alignment		94.5	8	PDB header: viral protein Chain: A; PDB Molecule: head completion protein; PDBTitle: structure of phage p22 tail needle gp26
15	c2b9cA_	Alignment		94.4	16	PDB header: contractile protein Chain: A; PDB Molecule: striated-muscle alpha tropomyosin; PDBTitle: structure of tropomyosin's mid-region: bending and binding sites for2 actin
16	c5nmoA_	Alignment		94.4	14	PDB header: cell cycle Chain: A; PDB Molecule: chromosome partition protein smc,chromosome partition PDBTitle: structure of the bacillus subtilis smc joint domain
17	c2gl2B_	Alignment		94.2	14	PDB header: cell adhesion Chain: B; PDB Molecule: adhesion a; PDBTitle: crystal structure of the tetra mutant (t66g,r67g,f68g,y69g) of2 bacterial adhesin fada
18	c1ei3C_	Alignment		94.1	7	PDB header: blood clotting Chain: C; PDB Molecule: fibrinogen; PDBTitle: crystal structure of native chicken fibrinogen
19	c2efrB_	Alignment		93.8	11	PDB header: contractile protein Chain: B; PDB Molecule: general control protein gcn4 and tropomyosin 1 alpha chain; PDBTitle: crystal structure of the c-terminal tropomyosin fragment with n- and2 c-terminal extensions of the leucine zipper at 1.8 angstroms3 resolution
20	c1deqF_	Alignment		93.5	10	PDB header: blood clotting Chain: F; PDB Molecule: fibrinogen (gamma chain); PDBTitle: the crystal structure of modified bovine fibrinogen (at ~42 angstrom resolution)
21	c5c31C_	Alignment	not modelled	93.4	17	PDB header: transport protein Chain: C; PDB Molecule: nucleoporin nup62; PDBTitle: structure of the metazoan nup62.nup58.nup54 nucleoporin complex.
22	c3ojaB_	Alignment	not modelled	92.5	6	PDB header: protein binding Chain: B; PDB Molecule: anopheles plasmodium-responsive leucine-rich repeat protein PDBTitle: crystal structure of Irim1/ap1c complex
23	c4rh7A_	Alignment	not modelled	92.4	10	PDB header: motor protein Chain: A; PDB Molecule: green fluorescent protein/cytoplasmic dynein 2 heavy chain PDBTitle: crystal structure of human cytoplasmic dynein 2 motor domain in2 complex with adp.vi
24	c6ewyA_	Alignment	not modelled	92.3	12	PDB header: structural protein Chain: A; PDB Molecule: peptidoglycan endopeptidase ripa; PDBTitle: ripa peptidoglycan hydrolase (rv1477, mycobacterium tuberculosis) n-2 terminal domain
25	c4a7fB_	Alignment	not modelled	92.3	12	PDB header: structural protein/hydrolase Chain: B; PDB Molecule: tropomyosin 1 alpha; PDBTitle: structure of the actin-tropomyosin-myosin complex (rigor atm 3)
26	c1c1gA_	Alignment	not modelled	92.1	10	PDB header: contractile protein Chain: A; PDB Molecule: tropomyosin; PDBTitle: crystal structure of tropomyosin at 7 angstroms resolution in the2 spermine-induced crystal form
27	c5ijnF_	Alignment	not modelled	91.6	11	PDB header: transport protein Chain: F; PDB Molecule: nuclear pore complex protein nup54; PDBTitle: composite structure of the inner ring of the human nuclear pore2 complex (32 copies of nup205)
28	c3cwgA_	Alignment	not modelled	91.5	9	PDB header: transcription Chain: A; PDB Molecule: signal transducer and activator of transcription

						PDBTitle: unphosphorylated mouse stat3 core fragment PDB header: hydrolase Chain: M: PDB Molecule: synaptosomal-associated protein 25; PDBTitle: structure of 20s supercomplex determined by single particle2 cryoelectron microscopy (state iib)
29	c3j99M_	Alignment	not modelled	91.4	11	
30	c5nugB_	Alignment	not modelled	90.8	10	PDB header: motor protein Chain: B: PDB Molecule: cytoplasmic dynein 1 heavy chain 1; PDBTitle: motor domains from human cytoplasmic dynein-1 in the phi-particle2 conformation
31	c1deqO_	Alignment	not modelled	90.7	13	PDB header: blood clotting Chain: O: PDB Molecule: fibrinogen (beta chain); PDBTitle: the crystal structure of modified bovine fibrinogen (at ~42 angstrom resolution)
32	c5gnaB_	Alignment	not modelled	90.5	19	PDB header: gene regulation Chain: B: PDB Molecule: flagellar hook-associated protein 2; PDBTitle: crystal structure of flagellin assembly related protein
33	c2ba2A_	Alignment	not modelled	90.5	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical upf0134 protein mpn010; PDBTitle: crystal structure of the duf16 domain of mpn010 from2 mycoplasma pneumoniae
34	c5ijnT_	Alignment	not modelled	90.1	14	PDB header: transport protein Chain: T: PDB Molecule: nuclear pore glycoprotein p62; PDBTitle: composite structure of the inner ring of the human nuclear pore2 complex (32 copies of nup205)
35	c5xauB_	Alignment	not modelled	89.2	12	PDB header: cell adhesion Chain: B: PDB Molecule: laminin subunit beta-1; PDBTitle: crystal structure of integrin binding fragment of laminin-511
36	c3q8tB_	Alignment	not modelled	88.3	12	PDB header: apoptosis Chain: B: PDB Molecule: beclin-1; PDBTitle: crystal structure of the coiled coil domain of beclin 1, an essential2 autophagy protein
37	c1ei3E_	Alignment	not modelled	87.8	12	PDB header: blood clotting Chain: E: PDB Molecule: fibrinogen; PDBTitle: crystal structure of native chicken fibrinogen
38	c6o7xa_	Alignment	not modelled	87.7	9	PDB header: membrane protein Chain: A: PDB Molecule: vacuolar atp synthase catalytic subunit a; PDBTitle: saccharomyces cerevisiae v-atpase stv1-v1vo state 3
39	c2ykqC_	Alignment	not modelled	87.4	5	PDB header: rna binding protein Chain: C: PDB Molecule: line-1 orf1p; PDBTitle: structure of the human line-1 orf1p trimer
40	c3swfA_	Alignment	not modelled	87.1	16	PDB header: transport protein Chain: A: PDB Molecule: cgmp-gated cation channel alpha-1; PDBTitle: cnga1 621-690 containing clz domain
41	c3dtpA_	Alignment	not modelled	87.1	11	PDB header: contractile protein Chain: A: PDB Molecule: myosin 2 heavy chain chimera of smooth and cardiac muscle; PDBTitle: tarantula heavy meromyosin obtained by flexible docking to tarantula2 muscle thick filament cryo-em 3d-map
42	c1ic2B_	Alignment	not modelled	87.0	16	PDB header: contractile protein Chain: B: PDB Molecule: tropomyosin alpha chain, skeletal muscle; PDBTitle: deciphering the design of the tropomyosin molecule
43	c6ec0A_	Alignment	not modelled	87.0	9	PDB header: protein fibril Chain: A: PDB Molecule: keratin 1; PDBTitle: crystal structure of the wild-type heterocomplex between coil 1b2 domains of human intermediate filament proteins keratin 1 (krt1) and3 keratin 10 (krt10)
44	c5j1gA_	Alignment	not modelled	86.8	16	PDB header: structural protein Chain: A: PDB Molecule: plectin; PDBTitle: structure of the spectrin repeats 7 and 8 of the plakin domain of2 plectin
45	c5tvbB_	Alignment	not modelled	85.7	10	PDB header: transferase Chain: B: PDB Molecule: nucleoprotein tpr; PDBTitle: structure of the tpr oligomerization domain
46	c5mg8B_	Alignment	not modelled	85.5	10	PDB header: recombination Chain: B: PDB Molecule: structural maintenance of chromosomes protein 6; PDBTitle: crystal structure of the s.pombe smc5/6 hinge domain
47	c5lm2B_	Alignment	not modelled	85.5	8	PDB header: hydrolase Chain: B: PDB Molecule: tyrosine-protein phosphatase non-receptor type 23; PDBTitle: crystal structure of hd-ptp phosphatase
48	c5gasN_	Alignment	not modelled	85.1	15	PDB header: hydrolase Chain: N: PDB Molecule: archaeal/vacuolar-type h+-atpase subunit i; PDBTitle: thermus thermophilus v/a-atpase, conformation 2
49	c6o7ua_	Alignment	not modelled	84.6	20	PDB header: membrane protein Chain: A: PDB Molecule: PDBTitle: saccharomyces cerevisiae v-atpase stv1-vo
50	c5yfpE_	Alignment	not modelled	84.0	10	PDB header: exocytosis Chain: E: PDB Molecule: exocyst complex component sec10; PDBTitle: cryo-em structure of the exocyst complex
51	c4xa3A_	Alignment	not modelled	83.9	12	PDB header: motor protein Chain: A: PDB Molecule: gp7-myh7(1361-1425)-eb1 chimera protein; PDBTitle: crystal structure of the coiled-coil surrounding skip 2 of myh7
52	c3g67A_	Alignment	not modelled	82.5	9	PDB header: signaling protein Chain: A: PDB Molecule: methyl-accepting chemotaxis protein; PDBTitle: crystal structure of a soluble chemoreceptor from thermotoga2 maritima
53	c1l4aD_	Alignment	not modelled	82.3	8	PDB header: endocytosis/exocytosis Chain: D: PDB Molecule: s-snap25 fusion protein; PDBTitle: x-ray structure of the neuronal complex/snare complex2 from the squid loligo pealei
						PDB header: viral protein Chain: B: PDB Molecule: 2

54	c1wyyB_	Alignment	not modelled	82.1	16	Chain: B; PDB Molecule: ez glycoprotein; PDBTitle: post-fusion hairpin conformation of the sars coronavirus spike2 glycoprotein
55	c5xg2A_	Alignment	not modelled	81.9	12	PDB header: dna binding protein Chain: A; PDB Molecule: chromosome partition protein smc; PDBTitle: crystal structure of a coiled-coil segment (residues 345-468 and 694-2 814) of pyrococcus yayanosii smc
56	c1sfcD_	Alignment	not modelled	81.7	14	PDB header: transport protein Chain: D; PDB Molecule: protein (snap-25b); PDBTitle: neuronal synaptic fusion complex
57	c1qu7A_	Alignment	not modelled	81.7	13	PDB header: signaling protein Chain: A; PDB Molecule: methyl-accepting chemotaxis protein i; PDBTitle: four helical-bundle structure of the cytoplasmic domain of a serine2 chemotaxis receptor
58	c3ghgK_	Alignment	not modelled	81.4	11	PDB header: blood clotting Chain: K; PDB Molecule: fibrinogen beta chain; PDBTitle: crystal structure of human fibrinogen
59	c3b5nL_	Alignment	not modelled	80.8	19	PDB header: membrane protein Chain: L; PDB Molecule: protein transport protein sec9; PDBTitle: structure of the yeast plasma membrane snare complex
60	c5c3IA_	Alignment	not modelled	80.4	11	PDB header: transport protein Chain: A; PDB Molecule: nup54; PDBTitle: structure of the metazoan nup62.nup58.nup54 nucleoporin complex.
61	c6a9pD_	Alignment	not modelled	79.1	8	PDB header: structural protein Chain: D; PDB Molecule: glial fibrillary acidic protein; PDBTitle: crystal structure of the human glial fibrillary acidic protein 1b2 domain
62	c3vkgA_	Alignment	not modelled	78.6	9	PDB header: motor protein Chain: A; PDB Molecule: dynein heavy chain, cytoplasmic; PDBTitle: x-ray structure of an mtbd truncation mutant of dynein motor domain
63	c2wpqA_	Alignment	not modelled	78.4	8	PDB header: membrane protein Chain: A; PDB Molecule: trimeric autotransporter adhesin fragment; PDBTitle: salmonella enterica sada 479-519 fused to gcn4 adaptors (sada3, in-2 register fusion)
64	c3o1IA_	Alignment	not modelled	78.1	7	PDB header: structural protein Chain: A; PDB Molecule: vimentin; PDBTitle: crystal structure of vimentin (fragment 144-251) from homo sapiens,2 northeast structural genomics consortium target hr4796b
65	c5yixA_	Alignment	not modelled	76.7	13	PDB header: dna binding protein Chain: A; PDB Molecule: rna polymerase sigma factor rpod; PDBTitle: caulobacter crescentus gcra sigma-interacting domain (sid) in complex2 with domain 2 of sigma 70
66	c6e2jB_	Alignment	not modelled	75.5	11	PDB header: protein fibril Chain: B; PDB Molecule: keratin, type i cytoskeletal 10; PDBTitle: crystal structure of the heterocomplex between human keratin 1 coil 1b2 containing s233l mutation and wild-type human keratin 10 coil 1b
67	c2ch7A_	Alignment	not modelled	75.0	9	PDB header: chemotaxis Chain: A; PDB Molecule: methyl-accepting chemotaxis protein; PDBTitle: crystal structure of the cytoplasmic domain of a bacterial2 chemoreceptor from thermotoga maritima
68	c1degD_	Alignment	not modelled	74.9	8	PDB header: blood clotting Chain: D; PDB Molecule: fibrinogen (alpha chain); PDBTitle: the crystal structure of modified bovine fibrinogen (at ~42 angstrom resolution)
69	c3o0zD_	Alignment	not modelled	74.5	9	PDB header: transferase Chain: D; PDB Molecule: rho-associated protein kinase 1; PDBTitle: crystal structure of a coiled-coil domain from human rock i
70	d1i6za_	Alignment	not modelled	74.2	16	Fold: Spectrin repeat-like Superfamily: BAG domain Family: BAG domain
71	c4cgbA_	Alignment	not modelled	73.5	12	PDB header: cell cycle Chain: A; PDB Molecule: echinoderm microtubule-associated protein-like 2; PDBTitle: crystal structure of the trimerization domain of eml2
72	c4l18E_	Alignment	not modelled	71.9	7	PDB header: motor protein/transport protein Chain: E; PDB Molecule: swi5-dependent ho expression protein 3; PDBTitle: complex of carboxy terminal domain of myo4p and she3p middle fragment
73	c2npsD_	Alignment	not modelled	71.6	25	PDB header: transport protein Chain: D; PDB Molecule: syntaxin-6; PDBTitle: crystal structure of the early endosomal snare complex
74	c3pltB_	Alignment	not modelled	70.9	19	PDB header: structural protein Chain: B; PDB Molecule: sphingolipid long chain base-responsive protein lsp1; PDBTitle: crystal structure of lsp1 from saccharomyces cerevisiae
75	c2y3aB_	Alignment	not modelled	70.8	7	PDB header: transferase Chain: B; PDB Molecule: phosphatidylinositol 3-kinase regulatory subunit beta; PDBTitle: crystal structure of p110beta in complex with icsh2 of p85beta and the2 drug gdc-0941
76	c4rsiB_	Alignment	not modelled	70.6	5	PDB header: cell cycle Chain: B; PDB Molecule: structural maintenance of chromosomes protein 4; PDBTitle: yeast smc2-smc4 hinge domain with extended coiled coils
77	c3wuqA_	Alignment	not modelled	70.5	9	PDB header: motor protein Chain: A; PDB Molecule: cytoplasmic dynein 1 heavy chain 1; PDBTitle: structure of the entire stalk region of the dynein motor domain
78	c4gkwB_	Alignment	not modelled	70.4	8	PDB header: structural protein Chain: B; PDB Molecule: spindle assembly abnormal protein 6; PDBTitle: crystal structure of the coiled-coil domain of c. elegans sas-6
						PDB header: transcription

79	c5u0pU_	Alignment	not modelled	70.0	9	Chain: U: PDB Molecule: mediator complex subunit 21; PDBTitle: cryo-em structure of the transcriptional mediator
80	c4cgbE_	Alignment	not modelled	69.8	13	PDB header: cell cycle Chain: E: PDB Molecule: echinoderm microtubule-associated protein-like 2; PDBTitle: crystal structure of the trimerization domain of eml2
81	c3hnbB_	Alignment	not modelled	69.7	13	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a basic coiled-coil protein of unknown function2 from eubacterium eligens atcc 27750
82	c6f1tX_	Alignment	not modelled	69.5	10	PDB header: motor protein Chain: X: PDB Molecule: bicd family-like cargo adapter 1,bicd family-like cargo PDBTitle: cryo-em structure of two dynein tail domains bound to dynactin and2 bicdr1
83	c6bwfB_	Alignment	not modelled	68.4	16	PDB header: membrane protein Chain: B: PDB Molecule: trpm7; PDBTitle: 4.1 angstrom mg2+-unbound structure of mouse trpm7
84	c6bwfD_	Alignment	not modelled	68.4	16	PDB header: membrane protein Chain: D: PDB Molecule: trpm7; PDBTitle: 4.1 angstrom mg2+-unbound structure of mouse trpm7
85	c6bwfC_	Alignment	not modelled	68.4	16	PDB header: membrane protein Chain: C: PDB Molecule: trpm7; PDBTitle: 4.1 angstrom mg2+-unbound structure of mouse trpm7
86	c6bwfA_	Alignment	not modelled	68.4	16	PDB header: membrane protein Chain: A: PDB Molecule: trpm7; PDBTitle: 4.1 angstrom mg2+-unbound structure of mouse trpm7
87	c6f1tx_	Alignment	not modelled	68.1	10	PDB header: motor protein Chain: X: PDB Molecule: bicd family-like cargo adapter 1,bicd family-like cargo PDBTitle: cryo-em structure of two dynein tail domains bound to dynactin and2 bicdr1
88	c6nzkB_	Alignment	not modelled	66.6	16	PDB header: viral protein Chain: B: PDB Molecule: spike surface glycoprotein; PDBTitle: structural basis for human coronavirus attachment to sialic acid2 receptors
89	c4qkvB_	Alignment	not modelled	65.8	5	PDB header: transcription Chain: B: PDB Molecule: polymerase i and transcript release factor; PDBTitle: crystal structure of the mouse cavin1 hr1 domain
90	c4iloA_	Alignment	not modelled	65.6	10	PDB header: unknown function Chain: A: PDB Molecule: ct398; PDBTitle: 2.12a resolution structure of ct398 from chlamydia trachomatis
91	c3ci9B_	Alignment	not modelled	65.1	7	PDB header: transcription Chain: B: PDB Molecule: heat shock factor-binding protein 1; PDBTitle: crystal structure of the human hsbp1
92	c4qkwB_	Alignment	not modelled	64.5	11	PDB header: signaling protein Chain: B: PDB Molecule: muscle-related coiled-coil protein; PDBTitle: crystal structure of the zebrafish cavin4a hr1 domain
93	c4rfxA_	Alignment	not modelled	64.1	11	PDB header: protein transport Chain: A: PDB Molecule: dynactin subunit 1; PDBTitle: crystal structure of the dynactin dctn1 fragment involved in dynein2 interaction
94	c4wy4D_	Alignment	not modelled	63.9	20	PDB header: membrane protein Chain: D: PDB Molecule: synaptosomal-associated protein 29; PDBTitle: crystal structure of autophagic snare complex
95	c6b3oB_	Alignment	not modelled	62.6	18	PDB header: viral protein Chain: B: PDB Molecule: spike glycoprotein; PDBTitle: tectonic conformational changes of a coronavirus spike glycoprotein2 promote membrane fusion
96	c5cwsJ_	Alignment	not modelled	62.6	13	PDB header: protein transport Chain: J: PDB Molecule: nucleoporin nup49; PDBTitle: crystal structure of the intact chaetomium thermophilum nsp1-nup49-2 nup57 channel nucleoporin heterotrimer bound to its nic96 nuclear3 pore complex attachment site
97	c3jhbA_	Alignment	not modelled	62.1	12	PDB header: contractile protein Chain: A: PDB Molecule: myosin 2 heavy chain striated muscle; PDBTitle: two heavy meromyosin interacting-heads motifs flexible docked into2 tarantula thick filament 3d-map allows in depth study of intra- and3 intermolecular interactions
98	c6fiaB_	Alignment	not modelled	61.9	11	PDB header: rna binding protein Chain: B: PDB Molecule: line-1 retrotransposable element orf1 protein; PDBTitle: structure of the human line-1 orf1p coiled coil domain
99	c3oa7A_	Alignment	not modelled	61.0	13	PDB header: structural protein Chain: A: PDB Molecule: head morphogenesis protein, chaotic nuclear migration PDBTitle: structure of the c-terminal domain of cnm67, a core component of the2 spindle pole body of saccharomyces cerevisiae
100	c5yfpG_	Alignment	not modelled	60.4	15	PDB header: exocytosis Chain: G: PDB Molecule: exocyst complex component exo70; PDBTitle: cryo-em structure of the exocyst complex
101	c5y06A_	Alignment	not modelled	60.3	16	PDB header: unknown function Chain: A: PDB Molecule: msmeg_4306; PDBTitle: structural characterization of msmeg_4306 from mycobacterium smegmatis
102	c51iaA_	Alignment	not modelled	59.7	11	PDB header: structural protein Chain: A: PDB Molecule: plectin; PDBTitle: structure of the spectrin repeats 7, 8, and 9 of the plakin domain of2 plectin
103	c3vkhD_	Alignment	not modelled	58.6	12	PDB header: motor protein Chain: D: PDB Molecule: PDBTitle: x-ray structure of a functional full-length dynein motor domain
104	c5vxyh_	Alignment	not modelled	58.4	9	PDB header: hydrolase Chain: B: PDB Molecule: v-type proton atpase subunit b;

104	c3v6xU_	Alignment	not modelled	58.4	9	PDBTitle: yeast v-atpase in complex with legionella pneumophila effector sidk2 (rotational state 1)
105	c5frgA_	Alignment	not modelled	58.3	16	PDB header: protein binding Chain: A: PDB Molecule: formin-binding protein 1-like; PDBTitle: the nmr structure of the cdc42-interacting region of toca1
106	d1eq1a_	Alignment	not modelled	58.0	14	Fold: Apolipophorin-III Superfamily: Apolipophorin-III Family: Apolipophorin-III
107	c5oenB_	Alignment	not modelled	57.4	15	PDB header: transcription Chain: B: PDB Molecule: signal transducer and activator of transcription; PDBTitle: crystal structure of stat2 in complex with irf9
108	c1gl2D_	Alignment	not modelled	57.1	19	PDB header: membrane protein Chain: D: PDB Molecule: syntaxin 8; PDBTitle: crystal structure of an endosomal snare core complex
109	c6djlE_	Alignment	not modelled	56.8	7	PDB header: signaling protein/protein transport Chain: E: PDB Molecule: sh3 domain-binding protein 5; PDBTitle: crystal structure of the rab11 gef sh3bp5 bound to nucleotide free2 rab11a
110	c5lobG_	Alignment	not modelled	56.4	18	PDB header: exocytosis Chain: G: PDB Molecule: synaptosomal-associated protein 25; PDBTitle: structure of the ca2+-bound rabphilin3a c2b- snap25 complex (c2 space2 group)
111	d1t7sa_	Alignment	not modelled	56.3	12	Fold: Spectrin repeat-like Superfamily: BAG domain Family: BAG domain
112	c3zx6A_	Alignment	not modelled	56.2	13	PDB header: signaling Chain: A: PDB Molecule: hamp, methyl-accepting chemotaxis protein i; PDBTitle: structure of hamp(af1503)-tsr fusion - hamp (a291v) mutant
113	c3vkhA_	Alignment	not modelled	55.7	9	PDB header: motor protein Chain: A: PDB Molecule: dynein heavy chain, cytoplasmic; PDBTitle: x-ray structure of a functional full-length dynein motor domain
114	c4ll7C_	Alignment	not modelled	55.6	13	PDB header: transport protein Chain: C: PDB Molecule: swi5-dependent ho expression protein 3; PDBTitle: structure of she3p amino terminus.
115	c5tbyA_	Alignment	not modelled	55.5	14	PDB header: contractile protein Chain: A: PDB Molecule: myosin-7; PDBTitle: 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)
116	c3uulB_	Alignment	not modelled	55.4	14	PDB header: structural protein Chain: B: PDB Molecule: utrophin; PDBTitle: crystal structure of first n-terminal utrophin spectrin repeat
117	c3na7A_	Alignment	not modelled	54.5	6	PDB header: gene regulation, chaperone Chain: A: PDB Molecule: hp0958; PDBTitle: 2.2 angstrom structure of the hp0958 protein from helicobacter pylori2 ccug 17874
118	c2ke4A_	Alignment	not modelled	53.9	15	PDB header: membrane protein Chain: A: PDB Molecule: cdc42-interacting protein 4; PDBTitle: the nmr structure of the tc10 and cdc42 interacting domain2 of cjp4
119	c5cwsC_	Alignment	not modelled	53.2	9	PDB header: protein transport Chain: C: PDB Molecule: nucleoporin nsp1; PDBTitle: crystal structure of the intact chaetomium thermophilum nsp1-nup49-2 nup57 channel nucleoporin heterotrimer bound to its nic96 nuclear3 pore complex attachment site
120	c2ieqC_	Alignment	not modelled	53.1	17	PDB header: viral protein Chain: C: PDB Molecule: spike glycoprotein; PDBTitle: core structure of s2 from the human coronavirus nl63 spike2 glycoprotein