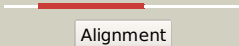
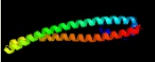

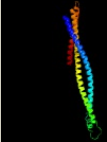
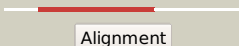

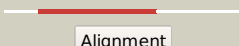
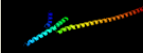


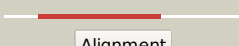
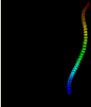
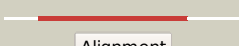
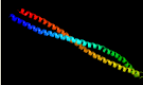

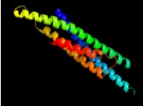



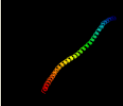

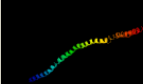
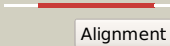

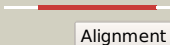

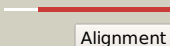
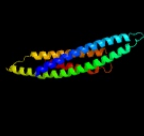

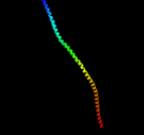



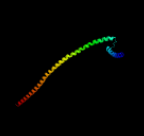
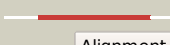
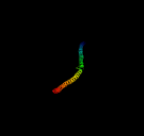

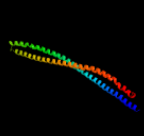

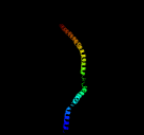
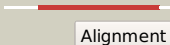
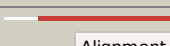
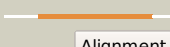
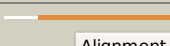
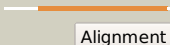

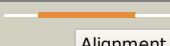



Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD2744c_(35kd_ag)_3057261_3058073
 Date Wed Aug 7 12:50:40 BST 2019
 Unique Job ID d7c6e3efb647fa2e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4wheA_	 Alignment		98.5	13	PDB header: signaling protein Chain: A; PDB Molecule: phage shock protein a; PDBTitle: crystal structure of e. coli phage shock protein a (pspa 1-144)
2	c4cgkA_	 Alignment		97.4	12	PDB header: cell cycle Chain: A; PDB Molecule: secreted 45 kda protein; PDBTitle: crystal structure of the essential protein pcsb from streptococcus pneumoniae
3	c6gapB_	 Alignment		96.8	10	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
4	c3ojaB_	 Alignment		96.2	9	PDB header: protein binding Chain: B; PDB Molecule: anopheles plasmodium-responsive leucine-rich repeat protein PDBTitle: crystal structure of lrim1/ap1c complex
5	c3ghgK_	 Alignment		95.6	8	PDB header: blood clotting Chain: K; PDB Molecule: fibrinogen beta chain; PDBTitle: crystal structure of human fibrinogen
6	c2efrB_	 Alignment		95.1	13	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- and 2 c-terminal extensions of the leucine zipper at 1.8 angstroms3 resolution
7	c3vkgA_	 Alignment		95.1	11	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
8	c1bf5A_	 Alignment		94.9	8	PDB header: gene regulation/dna Chain: A; PDB Molecule: signal transducer and activator of transcription 1- PDBTitle: tyrosine phosphorylated stat-1/dna complex
9	c6gaiA_	 Alignment		94.8	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)
10	c1ei3E_	 Alignment		94.7	4	PDB header: blood clotting Chain: E; PDB Molecule: fibrinogen; PDBTitle: crystal structure of native chicken fibrinogen
11	c1deqO_	 Alignment		94.1	9	PDB header: blood clotting Chain: O; PDB Molecule: fibrinogen (beta chain); PDBTitle: the crystal structure of modified bovine fibrinogen (at ~42 angstrom resolution)

12	c4gkwB_	 Alignment		93.8	12	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
13	c5ew5C_	 Alignment		93.8	10	PDB header: hydrolase Chain: C: PDB Molecule: colicin-e9; PDBTitle: crystal structure of colicin e9 in complex with its immunity protein2 im9
14	c1bg1A_	 Alignment		92.6	10	PDB header: transcription/dna Chain: A: PDB Molecule: protein (transcription factor stat3b); PDBTitle: transcription factor stat3b/dna complex
15	c4a7fB_	 Alignment		92.5	11	PDB header: structural protein/hydrolase Chain: B: PDB Molecule: tropomyosin 1 alpha; PDBTitle: structure of the actin-tropomyosin-myosin complex (rigor atm 3)
16	c1y4cA_	 Alignment		92.5	13	PDB header: de novo protein Chain: A: PDB Molecule: maltose binding protein fused with designed PDBTitle: designed helical protein fusion mbp
17	c5dfzD_	 Alignment		92.1	8	PDB header: transferase Chain: D: PDB Molecule: vacuolar protein sorting-associated protein 30; PDBTitle: structure of vps34 complex ii from s. cerevisiae.
18	c2d3eD_	 Alignment		92.0	12	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
19	c3vkgB_	 Alignment		91.5	10	PDB header: motor protein Chain: B: PDB Molecule: dynein heavy chain, cytoplasmic; PDBTitle: x-ray structure of an mtbd truncation mutant of dynein motor domain
20	c1deqF_	 Alignment		90.9	6	PDB header: blood clotting Chain: F: PDB Molecule: fibrinogen (gamma chain); PDBTitle: the crystal structure of modified bovine fibrinogen (at ~42 angstrom resolution)
21	c3na7A_	 Alignment	not modelled	90.8	5	PDB header: gene regulation, chaperone Chain: A: PDB Molecule: hp0958; PDBTitle: 2.2 angstrom structure of the hp0958 protein from helicobacter pylori2 ccug 17874
22	c1ciiA_	 Alignment	not modelled	90.2	11	PDB header: transmembrane protein Chain: A: PDB Molecule: colicin ia; PDBTitle: colicin ia
23	c4i1bB_	 Alignment	not modelled	89.1	13	PDB header: signaling protein/transferase/inhibitor Chain: B: PDB Molecule: phosphatidylinositol 3-kinase regulatory subunit alpha; PDBTitle: crystal structure of p110alpha complexed with nish2 of p85alpha
24	c6ewyA_	 Alignment	not modelled	89.0	10	PDB header: structural protein Chain: A: PDB Molecule: peptidoglycan endopeptidase ripa; PDBTitle: ripa peptidoglycan hydrolase (rv1477, mycobacterium tuberculosis) n-2 terminal domain
25	c4iloA_	 Alignment	not modelled	88.7	9	PDB header: unknown function Chain: A: PDB Molecule: ct398; PDBTitle: 2.12a resolution structure of ct398 from chlamydia trachomatis
26	c2rd0B_	 Alignment	not modelled	88.7	8	PDB header: transferase/oncoprotein Chain: B: PDB Molecule: phosphatidylinositol 3-kinase regulatory subunit alpha; PDBTitle: structure of a human p110alpha/p85alpha complex
27	c2fxmB_	 Alignment	not modelled	88.3	11	PDB header: contractile protein Chain: B: PDB Molecule: myosin heavy chain, cardiac muscle beta isoform; PDBTitle: structure of the human beta-myosin s2 fragment
28	c5y06A_	 Alignment	not modelled	88.0	10	PDB header: unknown function Chain: A: PDB Molecule: msmeg_4306; PDBTitle: structural characterization of msmeg_4306 from mycobacterium smegmatis

29	c5oenB	Alignment	not modelled	87.9	11	PDB header: transcription Chain: B: PDB Molecule: signal transducer and activator of transcription; PDBTitle: crystal structure of stat2 in complex with irf9
30	c4xa3A	Alignment	not modelled	87.8	6	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
31	c5cwsj	Alignment	not modelled	87.8	11	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
32	c3ghgl	Alignment	not modelled	87.5	12	PDB header: blood clotting Chain: I: PDB Molecule: fibrinogen gamma chain; PDBTitle: crystal structure of human fibrinogen
33	c5wjba	Alignment	not modelled	87.4	10	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
34	c1yvlB	Alignment	not modelled	85.0	9	PDB header: signaling protein Chain: B: PDB Molecule: signal transducer and activator of transcription PDBTitle: structure of unphosphorylated stat1
35	c5cwsC	Alignment	not modelled	83.3	11	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
36	c5goxB	Alignment	not modelled	83.1	8	PDB header: hydrolase Chain: B: PDB Molecule: dna repair protein rad50; PDBTitle: eukaryotic rad50 functions as a rod-shaped dimer
37	c2b9cA	Alignment	not modelled	82.4	11	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
38	c6flnE	Alignment	not modelled	82.1	13	PDB header: protein binding Chain: E: PDB Molecule: e3 ubiquitin/isg15 ligase trim25; PDBTitle: crystal structure of the human trim25 coiled-coil and pryspry domains
39	c6gaoC	Alignment	not modelled	82.1	9	PDB header: viral protein Chain: C: PDB Molecule: outer capsid protein sigma-1; PDBTitle: crystal structure of the t11 reovirus sigma1 coiled coil tail and body
40	c2v71A	Alignment	not modelled	81.9	8	PDB header: nuclear protein Chain: A: PDB Molecule: nuclear distribution protein nude-like 1; PDBTitle: coiled-coil region of nudel
41	c3hizB	Alignment	not modelled	81.7	5	PDB header: transferase/oncoprotein Chain: B: PDB Molecule: phosphatidylinositol 3-kinase regulatory subunit alpha; PDBTitle: crystal structure of p110alpha h1047r mutant in complex with nish2 of2 p85alpha
42	c4a55B	Alignment	not modelled	81.7	5	PDB header: transferase Chain: B: PDB Molecule: phosphatidylinositol 3-kinase regulatory subunit alpha; PDBTitle: crystal structure of p110alpha in complex with ish2 of p85alpha and2 the inhibitor pik-108
43	c6djlE	Alignment	not modelled	81.2	11	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
44	c5nmoA	Alignment	not modelled	80.8	6	PDB header: cell cycle Chain: A: PDB Molecule: chromosome partition protein smc,chromosome partition PDBTitle: structure of the bacillus subtilis smc joint domain
45	c2gl2B	Alignment	not modelled	80.6	9	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
46	c5xq2A	Alignment	not modelled	80.5	9	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 yanosii smc
47	c1l8dB	Alignment	not modelled	79.5	7	PDB header: replication Chain: B: PDB Molecule: dna double-strand break repair rad50 atpase; PDBTitle: rad50 coiled-coil zn hook
48	c3cwgA	Alignment	not modelled	79.1	8	PDB header: transcription Chain: A: PDB Molecule: signal transducer and activator of transcription PDBTitle: unphosphorylated mouse stat3 core fragment
49	c2ocyB	Alignment	not modelled	78.4	8	PDB header: endocytosis/exocytosis Chain: B: PDB Molecule: rab guanine nucleotide exchange factor sec2; PDBTitle: complex of the guanine exchange factor sec2p and the rab gtpase sec4p
50	c5nugB	Alignment	not modelled	77.5	8	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
51	c6a9pD	Alignment	not modelled	77.2	12	PDB header: structural protein Chain: D: PDB Molecule: glial fibrillary acidic protein; PDBTitle: crystal structure of the human glial fibrillary acidic protein 1b2 domain
52	c6mi3A	Alignment	not modelled	77.1	15	PDB header: transcription Chain: A: PDB Molecule: nf-kb essential modulator,nf-kappa-b essential modulator, PDBTitle: structure of nemo(51-112) with n- and c-terminal coiled-coil adaptors.

53	c3o0zD	Alignment	not modelled	75.9	12	PDB header: transferase Chain: D: PDB Molecule: rho-associated protein kinase 1; PDBTitle: crystal structure of a coiled-coil domain from human rock i
54	c6e2jB	Alignment	not modelled	74.3	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
55	c3u59C	Alignment	not modelled	72.4	12	PDB header: contractile protein Chain: C: PDB Molecule: tropomyosin beta chain; PDBTitle: n-terminal 98-aa fragment of smooth muscle tropomyosin beta
56	c5j1iA	Alignment	not modelled	72.1	11	PDB header: structural protein Chain: A: PDB Molecule: plectin; PDBTitle: structure of the spectrin repeats 7, 8, and 9 of the plakin domain of 2 plectin
57	c3q8tB	Alignment	not modelled	70.7	9	PDB header: apoptosis Chain: B: PDB Molecule: beclin-1; PDBTitle: crystal structure of the coiled coil domain of beclin 1, an essential 2 autophagy protein
58	c6ec0A	Alignment	not modelled	69.8	12	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) and 3 keratin 10 (krt10)
59	c4cg4D	Alignment	not modelled	69.3	10	PDB header: actin-binding protein Chain: D: PDB Molecule: pyrin; PDBTitle: crystal structure of the chs-b30.2 domains of trim20
60	c2qa7C	Alignment	not modelled	65.1	12	PDB header: actin binding Chain: C: PDB Molecule: huntingtin-interacting protein 1; PDBTitle: crystal structure of huntingtin-interacting protein 12 (hip1) coiled-coil domain with a basic surface suitable 3 for hip-protein interactor (hippi)
61	c3o1iA	Alignment	not modelled	64.1	10	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
62	c2y3aB	Alignment	not modelled	62.8	4	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 the 2 drug gdc-0941
63	c1c1gA	Alignment	not modelled	61.2	12	PDB header: contractile protein Chain: A: PDB Molecule: tropomyosin; PDBTitle: crystal structure of tropomyosin at 7 angstroms resolution in the 2 spermine-induced crystal form
64	c3dtpA	Alignment	not modelled	60.6	9	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 tarantula 2 muscle thick filament cryo-em 3d-map
65	c4zryA	Alignment	not modelled	60.0	15	PDB header: protein fibril Chain: A: PDB Molecule: keratin, type i cytoskeletal 10; PDBTitle: crystal structure of the heterocomplex between coil 2b domains of 2 human intermediate filament proteins keratin 1 (krt1) and keratin 103 (krt10)
66	c5tvbB	Alignment	not modelled	56.6	8	PDB header: transferase Chain: B: PDB Molecule: nucleoprotein tpr; PDBTitle: structure of the tpr oligomerization domain
67	c4k1pG	Alignment	not modelled	55.1	5	PDB header: toxin Chain: G: PDB Molecule: nhea; PDBTitle: structure of the nhea component of the nhe toxin from bacillus cereus
68	c5ijnT	Alignment	not modelled	53.8	15	PDB header: transport protein Chain: T: PDB Molecule: nuclear pore glycoprotein p62; PDBTitle: composite structure of the inner ring of the human nuclear pore 2 complex (32 copies of nup205)
69	c4i18E	Alignment	not modelled	51.7	12	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
70	c5lm2B	Alignment	not modelled	50.4	14	PDB header: hydrolase Chain: B: PDB Molecule: tyrosine-protein phosphatase non-receptor type 23; PDBTitle: crystal structure of hd-ptp phosphatase
71	c1jchC	Alignment	not modelled	50.2	11	PDB header: ribosome inhibitor, hydrolase Chain: C: PDB Molecule: colicin e3; PDBTitle: crystal structure of colicin e3 in complex with its immunity protein
72	c1deqD	Alignment	not modelled	46.0	13	PDB header: blood clotting Chain: D: PDB Molecule: fibrinogen (alpha chain); PDBTitle: the crystal structure of modified bovine fibrinogen (at ~42 angstrom resolution)
73	c6f1tX	Alignment	not modelled	41.7	8	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 and 2 bicdr1
74	c5oi7A	Alignment	not modelled	41.5	5	PDB header: protein binding Chain: A: PDB Molecule: centrosomal protein of 85 kda; PDBTitle: human cep85 - coiled coil domain 4
75	c6h2xA	Alignment	not modelled	40.8	11	PDB header: dna binding protein Chain: A: PDB Molecule: chromosome partition protein mukb, chromosome partition PDBTitle: mukb coiled-coil elbow from e. coli
76	c1ei3C	Alignment	not modelled	39.7	10	PDB header: blood clotting Chain: C: PDB Molecule: fibrinogen; PDBTitle: crystal structure of native chicken fibrinogen

77	c3ipkA_	Alignment	not modelled	39.3	12	PDB header: cell adhesion Chain: A: PDB Molecule: agi/ii; PDBTitle: crystal structure of a3vp1 of agi/ii of streptococcus mutans
78	c6gv8A_	Alignment	not modelled	39.2	10	PDB header: cell adhesion Chain: A: PDB Molecule: hyperosmolarity resistance protein emb; PDBTitle: characterization of extracellular matrix binding protein-(embp)-2 mediated staphylococcus epidermidis adherence to fibronectin
79	c3swkB_	Alignment	not modelled	37.5	11	PDB header: structural protein Chain: B: PDB Molecule: vimentin; PDBTitle: crystal structure of vimentin coil1b fragment
80	c6f1tx_	Alignment	not modelled	37.4	8	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
81	c4rfxA_	Alignment	not modelled	37.2	13	PDB header: protein transport Chain: A: PDB Molecule: dynactin subunit 1; PDBTitle: crystal structure of the dynactin dctn1 fragment involved in dynein2 interaction
82	c2v1yB_	Alignment	not modelled	35.9	13	PDB header: transferase Chain: B: PDB Molecule: phosphatidylinositol 3-kinase regulatory subunit alpha; PDBTitle: structure of a phosphoinositide 3-kinase alpha adaptor-2 binding domain (abd) in a complex with the ish2 domain3 from p85 alpha
83	c3ojaA_	Alignment	not modelled	35.1	11	PDB header: protein binding Chain: A: PDB Molecule: leucine-rich immune molecule 1; PDBTitle: crystal structure of Irim1/apl1c complex
84	c5mg8B_	Alignment	not modelled	34.3	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
85	c6o7xa_	Alignment	not modelled	31.2	10	PDB header: membrane protein Chain: A: PDB Molecule: vacuolar atp synthase catalytic subunit a; PDBTitle: saccharomyces cerevisiae v-atpase stv1-v1vo state 3
86	c5bu8A_	Alignment	not modelled	30.2	6	PDB header: viral protein Chain: A: PDB Molecule: dna stabilization protein; PDBTitle: hk620 tail needle crystallized at ph 7.5 and derivatized with xenon
87	c3vkhA_	Alignment	not modelled	30.0	13	PDB header: motor protein Chain: A: PDB Molecule: dynein heavy chain, cytoplasmic; PDBTitle: x-ray structure of a functional full-length dynein motor domain
88	c4fmyE_	Alignment	not modelled	29.4	7	PDB header: viral protein Chain: E: PDB Molecule: dna stabilization protein; PDBTitle: hk620 tail needle crystal form i
89	c4jioA_	Alignment	not modelled	28.8	12	PDB header: protein binding Chain: A: PDB Molecule: bro1; PDBTitle: bro1 v domain and ubiquitin
90	c4xa1D_	Alignment	not modelled	28.2	9	PDB header: motor protein Chain: D: PDB Molecule: gp7-myh7(1173-1238)-eb1 chimera protein; PDBTitle: crystal structure of the coiled-coil surrounding skip 1 of myh7
91	c5cj1B_	Alignment	not modelled	27.8	13	PDB header: motor protein Chain: B: PDB Molecule: gp7-myh7-(1526-1571) chimera protein; PDBTitle: crystal structure of the coiled coil of myh7 residues 1526 to 15712 fused to gp7
92	c5nenB_	Alignment	not modelled	26.9	9	PDB header: hydrolase Chain: B: PDB Molecule: lipase c; PDBTitle: crystal structure of the soluble domain of lipc, a membrane fusion2 protein of a type i secretion system
93	c3tnuB_	Alignment	not modelled	26.2	10	PDB header: cytosolic protein Chain: B: PDB Molecule: keratin, type ii cytoskeletal 5; PDBTitle: heterocomplex of coil 2b domains of human intermediate filament2 proteins, keratin 5 (krt5) and keratin 14 (krt14)
94	c3u1aC_	Alignment	not modelled	25.8	16	PDB header: contractile protein Chain: C: PDB Molecule: smooth muscle tropomyosin alpha; PDBTitle: n-terminal 81-aa fragment of smooth muscle tropomyosin alpha
95	c3jbhA_	Alignment	not modelled	25.2	9	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
96	c6ianA_	Alignment	not modelled	22.8	7	PDB header: cytosolic protein Chain: A: PDB Molecule: intraflagellar transport protein 74; PDBTitle: t. brucei ift22/74/81 gtp-bound crystal structure
97	c1p0oA_	Alignment	not modelled	22.7	38	PDB header: ribosome Chain: A: PDB Molecule: 19-mer peptide from 50s ribosomal protein l1; PDBTitle: hp (2-20) substitution of trp for gln and asp at position2 17 and 19 modification in sds-d25 micelles
98	c3g67A_	Alignment	not modelled	21.5	10	PDB header: signaling protein Chain: A: PDB Molecule: methyl-accepting chemotaxis protein; PDBTitle: crystal structure of a soluble chemoreceptor from thermotoga2 maritima
99	c5yz0C_	Alignment	not modelled	21.0	11	PDB header: cell cycle Chain: C: PDB Molecule: atr-interacting protein; PDBTitle: cryo-em structure of human atr-atrrip complex
100	c3n4xB_	Alignment	not modelled	20.8	13	PDB header: replication Chain: B: PDB Molecule: monopolin complex subunit csm1; PDBTitle: structure of csm1 full-length
101	c5ia1B_	Alignment	not modelled	20.8	50	PDB header: ligase Chain: B: PDB Molecule: enterobactin biosynthesis protein ybdz;

101	c2j01B_	Alignment	not modelled	20.8	90	PDBTitle: entf, a terminal nonribosomal peptide synthetase module bound to the2 mbth-like protein ybdz
102	c4nqjB_	Alignment	not modelled	20.4	9	PDB header: ligase Chain: B: PDB Molecule: e3 ubiquitin-protein ligase trim69; PDBTitle: structure of coiled-coil domain