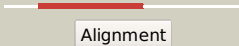
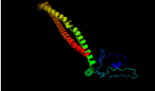

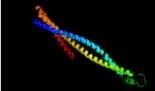
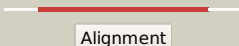
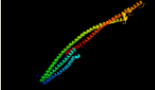
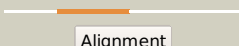
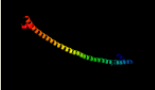
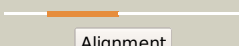
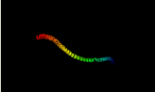
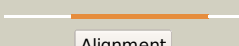
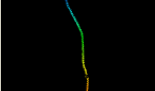
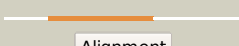
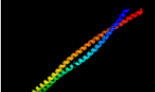
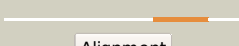
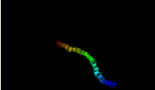





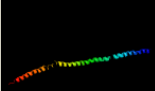


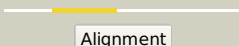

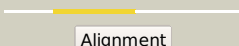
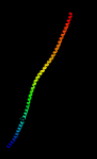
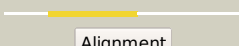
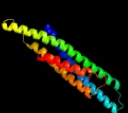
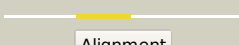

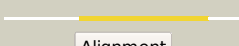

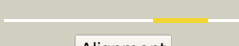





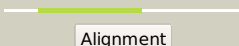
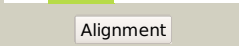

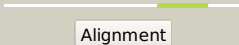
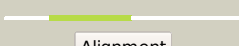
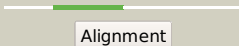
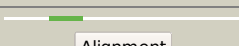
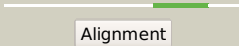


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2731 (-)_3043036_3044388
Date	Wed Aug 7 12:50:38 BST 2019
Unique Job ID	6c1a63ac67253657

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5ew5C_	 Alignment		96.1	9	PDB header: hydrolase Chain: C: PDB Molecule: colicin-e9; PDBTitle: crystal structure of colicin e9 in complex with its immunity protein2 im9
2	c4cgkA_	 Alignment		95.8	8	PDB header: cell cycle Chain: A: PDB Molecule: secreted 45 kda protein; PDBTitle: crystal structure of the essential protein pcsb from streptococcus2 pneumoniae
3	c1ciiA_	 Alignment		95.1	11	PDB header: transmembrane protein Chain: A: PDB Molecule: colicin ia; PDBTitle: colicin ia
4	c4xa3A_	 Alignment		88.5	9	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
5	c6gapB_	 Alignment		87.4	7	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
6	c1c1gA_	 Alignment		86.5	11	PDB header: contractile protein Chain: A: PDB Molecule: tropomyosin; PDBTitle: crystal structure of tropomyosin at 7 angstroms resolution in the2 spermine-induced crystal form
7	c6ewyA_	 Alignment		84.3	10	PDB header: structural protein Chain: A: PDB Molecule: peptidoglycan endopeptidase ripa; PDBTitle: ripa peptidoglycan hydrolase (rv1477, mycobacterium tuberculosis) n-2 terminal domain
8	c3ghgK_	 Alignment		83.2	5	PDB header: blood clotting Chain: K: PDB Molecule: fibrinogen beta chain; PDBTitle: crystal structure of human fibrinogen
9	c5yz0C_	 Alignment		81.2	15	PDB header: cell cycle Chain: C: PDB Molecule: atr-interacting protein; PDBTitle: cryo-em structure of human atr-atrip complex
10	c1bg1A_	 Alignment		79.3	10	PDB header: transcription/dna Chain: A: PDB Molecule: protein (transcription factor stat3b); PDBTitle: transcription factor stat3b/dna complex
11	c1deqO_	 Alignment		77.6	3	PDB header: blood clotting Chain: O: PDB Molecule: fibrinogen (beta chain); PDBTitle: the crystal structure of modified bovine fibrinogen (at ~42 angstrom resolution)

12	c5yz0D_	 Alignment		77.0	20	PDB header: cell cycle Chain: D: PDB Molecule: atr-interacting protein; PDBTitle: cryo-em structure of human atr-atrip complex
13	c3ojaB_	 Alignment		76.2	10	PDB header: protein binding Chain: B: PDB Molecule: anopheles plasmodium-responsive leucine-rich repeat protein PDBTitle: crystal structure of lrim1/apl1c complex
14	c2v71A_	 Alignment		76.2	8	PDB header: nuclear protein Chain: A: PDB Molecule: nuclear distribution protein nude-like 1; PDBTitle: coiled-coil region of nudel
15	c1bf5A_	 Alignment		75.7	10	PDB header: gene regulation/dna Chain: A: PDB Molecule: signal transducer and activator of transcription 1- PDBTitle: tyrosine phosphorylated stat-1/dna complex
16	c1degF_	 Alignment		74.8	9	PDB header: blood clotting Chain: F: PDB Molecule: fibrinogen (gamma chain); PDBTitle: the crystal structure of modified bovine fibrinogen (at ~42 angstrom resolution)
17	c3wuqA_	 Alignment		74.8	6	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
18	c1ei3E_	 Alignment		74.4	8	PDB header: blood clotting Chain: E: PDB Molecule: fibrinogen; PDBTitle: crystal structure of native chicken fibrinogen
19	c6gaoC_	 Alignment		72.5	7	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
20	c2d3eD_	 Alignment		71.1	13	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
21	c1jchC_	 Alignment	not modelled	68.0	9	PDB header: ribosome inhibitor, hydrolase Chain: C: PDB Molecule: colicin e3; PDBTitle: crystal structure of colicin e3 in complex with its immunity protein
22	c1y4cA_	 Alignment	not modelled	67.7	14	PDB header: de novo protein Chain: A: PDB Molecule: maltose binding protein fused with designed PDBTitle: designed helical protein fusion mbp
23	c5xg2A_	 Alignment	not modelled	65.3	11	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
24	c2fxmB_	 Alignment	not modelled	62.1	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
25	c2efrB_	 Alignment	not modelled	60.0	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- and 2 c-terminal extensions of the leucine zipper at 1.8 angstroms3 resolution
26	c6gajA_	 Alignment	not modelled	59.3	8	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)
27	c3cvfA_	 Alignment	not modelled	56.6	15	PDB header: signaling protein Chain: A: PDB Molecule: homer protein homolog 3; PDBTitle: crystal structure of the carboxy terminus of homer3
28	c4lI8E_	 Alignment	not modelled	54.9	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
29	c6djIE_	Alignment	not modelled	48.9	10	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
30	c3o0zD_	Alignment	not modelled	45.2	6	PDB header: transferase Chain: D: PDB Molecule: rho-associated protein kinase 1; PDBTitle: crystal structure of a coiled-coil domain from human rock i
31	c4xa1D_	Alignment	not modelled	44.7	11	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
32	c4nl6C_	Alignment	not modelled	43.7	19	PDB header: splicing Chain: C: PDB Molecule: survival motor neuron protein; PDBTitle: structure of the full-length form of the protein smn found in healthy2 patients
33	c3cwgA_	Alignment	not modelled	43.7	11	PDB header: transcription Chain: A: PDB Molecule: signal transducer and activator of transcription PDBTitle: unphosphorylated mouse stat3 core fragment
34	c5wjba_	Alignment	not modelled	43.1	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
35	c6ec0A_	Alignment	not modelled	42.8	6	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)
36	c3dtpA_	Alignment	not modelled	41.8	10	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
37	dlwp1a_	Alignment	not modelled	41.8	17	Fold: Outer membrane efflux proteins (OEP) Superfamily: Outer membrane efflux proteins (OEP) Family: Outer membrane efflux proteins (OEP)
38	c5ijnF_	Alignment	not modelled	41.3	9	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)
39	c4zryA_	Alignment	not modelled	38.8	11	PDB header: protein fibril Chain: A: PDB Molecule: keratin, type i cytoskeletal 10; PDBTitle: crystal structure of the heterocomplex between coil 2b domains of2 human intermediate filament proteins keratin 1 (krt1) and keratin 103 (krt10)
40	c6mi3A_	Alignment	not modelled	37.1	9	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.
41	c3q8tB_	Alignment	not modelled	36.8	15	PDB header: apoptosis Chain: B: PDB Molecule: beclin-1; PDBTitle: crystal structure of the coiled coil domain of beclin 1, an essential2 autophagy protein
42	c3ghgl_	Alignment	not modelled	34.8	6	PDB header: blood clotting Chain: I: PDB Molecule: fibrinogen gamma chain; PDBTitle: crystal structure of human fibrinogen
43	c3u59C_	Alignment	not modelled	34.3	11	PDB header: contractile protein Chain: C: PDB Molecule: tropomyosin beta chain; PDBTitle: n-terminal 98-aa fragment of smooth muscle tropomyosin beta
44	c6e2jB_	Alignment	not modelled	31.4	5	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
45	c4a7fB_	Alignment	not modelled	30.7	9	PDB header: structural protein/hydrolase Chain: B: PDB Molecule: tropomyosin 1 alpha; PDBTitle: structure of the actin-tropomyosin-myosin complex (rigor atm 3)
46	c4gkwB_	Alignment	not modelled	28.8	13	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
47	c1ei3C_	Alignment	not modelled	28.4	6	PDB header: blood clotting Chain: C: PDB Molecule: fibrinogen; PDBTitle: crystal structure of native chicken fibrinogen
48	c2ocyB_	Alignment	not modelled	25.2	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
49	c6a9pD_	Alignment	not modelled	22.2	13	PDB header: structural protein Chain: D: PDB Molecule: glial fibrillary acidic protein; PDBTitle: crystal structure of the human glial fibrillary acidic protein 1b2 domain
50	c3cveC_	Alignment	not modelled	18.6	18	PDB header: signaling protein Chain: C: PDB Molecule: homer protein homolog 1; PDBTitle: crystal structure of the carboxy terminus of homer1
51	c5cwsj_	Alignment	not modelled	18.5	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
52	c6flnF_	Alignment	not modelled	18.0	8	PDB header: protein binding Chain: E: PDB Molecule: e3 ubiquitin/isg15 ligase trim25;

52	c3iitE_	Alignment	not modelled	18.0	0	PDBTitle: crystal structure of the human trim25 coiled-coil and pryspry domains
53	c3ojaA_	Alignment	not modelled	17.7	12	PDB header: protein binding Chain: A: PDB Molecule: leucine-rich immune molecule 1; PDBTitle: crystal structure of lrim1/apl1c complex
54	c3ipkA_	Alignment	not modelled	17.4	13	PDB header: cell adhesion Chain: A: PDB Molecule: agi/ii; PDBTitle: crystal structure of a3vp1 of agi/ii of streptococcus mutans
55	c5dfzD_	Alignment	not modelled	16.9	8	PDB header: transferase Chain: D: PDB Molecule: vacuolar protein sorting-associated protein 30; PDBTitle: structure of vps34 complex ii from s. cerevisiae.
56	c3oi1A_	Alignment	not modelled	16.3	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
57	c5nnvD_	Alignment	not modelled	16.0	6	PDB header: cell cycle Chain: D: PDB Molecule: chromosome partition protein smc,chromosome partition PDBTitle: structure of a bacillus subtilis smc coiled coil middle fragment
58	c6ianA_	Alignment	not modelled	15.7	9	PDB header: cytosolic protein Chain: A: PDB Molecule: intraflagellar transport protein 74; PDBTitle: t. brucei ift22/74/81 gtp-bound crystal structure
59	c5nenB_	Alignment	not modelled	14.4	10	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
60	c4cg4D_	Alignment	not modelled	14.0	9	PDB header: actin-binding protein Chain: D: PDB Molecule: pyrin; PDBTitle: crystal structure of the chs-b30.2 domains of trim20
61	c5nmoA_	Alignment	not modelled	13.7	13	PDB header: cell cycle Chain: A: PDB Molecule: chromosome partition protein smc,chromosome partition PDBTitle: structure of the bacillus subtilis smc joint domain
62	c5cwsC_	Alignment	not modelled	13.5	7	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
63	d1j8ca_	Alignment	not modelled	13.2	19	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
64	c4iloA_	Alignment	not modelled	12.8	3	PDB header: unknown function Chain: A: PDB Molecule: ct398; PDBTitle: 2.12a resolution structure of ct398 from chlamydia trachomatis
65	c2miiA_	Alignment	not modelled	12.0	20	PDB header: protein binding Chain: A: PDB Molecule: penicillin-binding protein activator lpob; PDBTitle: nmr structure of e. coli lpob
66	c3hnwB_	Alignment	not modelled	11.7	6	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
67	c2b9cA_	Alignment	not modelled	11.4	10	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
68	c5tbyA_	Alignment	not modelled	11.4	9	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-3jhb), rigidly fitted to human beta-4 cardiac negatively stained thick filament 3d-reconstruction (emd-5 2240)
69	c5oi7A_	Alignment	not modelled	10.8	10	PDB header: protein binding Chain: A: PDB Molecule: centrosomal protein of 85 kda; PDBTitle: human cep85 - coiled coil domain 4
70	c2kogA_	Alignment	not modelled	10.6	14	PDB header: membrane protein Chain: A: PDB Molecule: vesicle-associated membrane protein 2; PDBTitle: lipid-bound synaptobrevin solution nmr structure
71	c4wheA_	Alignment	not modelled	10.2	14	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)
72	c4rfxA_	Alignment	not modelled	10.0	10	PDB header: protein transport Chain: A: PDB Molecule: dynactin subunit 1; PDBTitle: crystal structure of the dynactin dctn1 fragment involved in dynein2 interaction
73	c1cagA_	Alignment	not modelled	9.9	58	PDB header: collagen Chain: A: PDB Molecule: collagen-like peptide; PDBTitle: crystal and molecular structure of a collagen-like peptide2 at 1.9 angstrom resolution
74	c2gl2B_	Alignment	not modelled	9.9	8	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
75	c1cagC_	Alignment	not modelled	9.9	58	PDB header: collagen Chain: C: PDB Molecule: collagen-like peptide; PDBTitle: crystal and molecular structure of a collagen-like peptide2 at 1.9 angstrom resolution
76	c5fv8B_	Alignment	not modelled	9.8	22	PDB header: structural protein Chain: B: PDB Molecule: fosw; PDBTitle: structure of cjun-fosw coiled coil complex.
						PDB header: gene regulation, chaperone

77	c3na7A_	Alignment	not modelled	9.7	11	Chain: A; PDB Molecule: hp0958; PDBTitle: 2.2 angstrom structure of the hp0958 protein from helicobacter pylori2 ccug 17874
78	c5fv8A_	Alignment	not modelled	9.7	22	PDB header: structural protein Chain: A; PDB Molecule: fosw; PDBTitle: structure of cjun-fosw coiled coil complex.
79	d2gqba1	Alignment	not modelled	9.6	24	Fold: RPA2825-like Superfamily: RPA2825-like Family: RPA2825-like
80	c2oevA_	Alignment	not modelled	9.5	9	PDB header: protein transport Chain: A; PDB Molecule: programmed cell death 6-interacting protein; PDBTitle: crystal structure of alix/aip1
81	c4pxjB_	Alignment	not modelled	9.2	21	PDB header: protein binding Chain: B; PDB Molecule: c-jun-amino-terminal kinase-interacting protein 3; PDBTitle: crystallographic structure of the lzii fragment (anti-parallel2 orientation) from jip3
82	c1cgdC_	Alignment	not modelled	9.2	55	PDB header: collagen Chain: C; PDB Molecule: collagen-like peptide; PDBTitle: hydration structure of a collagen peptide
83	c1cagB_	Alignment	not modelled	9.2	55	PDB header: collagen Chain: B; PDB Molecule: collagen-like peptide; PDBTitle: crystal and molecular structure of a collagen-like peptide2 at 1.9 angstrom resolution
84	c1cgdB_	Alignment	not modelled	9.2	55	PDB header: collagen Chain: B; PDB Molecule: collagen-like peptide; PDBTitle: hydration structure of a collagen peptide
85	c1cgdA_	Alignment	not modelled	9.2	55	PDB header: collagen Chain: A; PDB Molecule: collagen-like peptide; PDBTitle: hydration structure of a collagen peptide
86	c5cj1B_	Alignment	not modelled	9.1	10	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
87	c3jhbA_	Alignment	not modelled	9.0	8	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
88	c3iynQ_	Alignment	not modelled	9.0	8	PDB header: virus Chain: Q; PDB Molecule: hexon-associated protein; PDBTitle: 3.6-angstrom cryoem structure of human adenovirus type 5
89	c4a55B_	Alignment	not modelled	8.9	7	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
90	c1wt6B_	Alignment	not modelled	8.5	18	PDB header: transferase Chain: B; PDB Molecule: myotonin-protein kinase; PDBTitle: coiled-coil domain of dmpk
91	c3a1hF_	Alignment	not modelled	8.0	38	PDB header: structural protein Chain: F; PDB Molecule: collagen-like peptide; PDBTitle: crystal structure analysis of the collagen-like peptide, (ppg)4-otg-2 (ppg)4
92	c5sxpG_	Alignment	not modelled	7.9	26	PDB header: signaling protein/ligase Chain: G; PDB Molecule: e3 ubiquitin-protein ligase itchy homolog; PDBTitle: structural basis for the interaction between itch prr and beta-pix
93	c2eqbC_	Alignment	not modelled	7.6	11	PDB header: endocytosis/exocytosis Chain: C; PDB Molecule: rab guanine nucleotide exchange factor sec2; PDBTitle: crystal structure of the rab gtpase sec4p, the sec2p gef2 domain, and phosphate complex
94	c5sxpF_	Alignment	not modelled	7.5	26	PDB header: signaling protein/ligase Chain: F; PDB Molecule: e3 ubiquitin-protein ligase itchy homolog; PDBTitle: structural basis for the interaction between itch prr and beta-pix
95	c2zv4O_	Alignment	not modelled	7.4	16	PDB header: structural protein Chain: O; PDB Molecule: major vault protein; PDBTitle: the structure of rat liver vault at 3.5 angstrom resolution
96	c6h2xA_	Alignment	not modelled	7.3	9	PDB header: dna binding protein Chain: A; PDB Molecule: chromosome partition protein mukb,chromosome partition PDBTitle: mukb coiled-coil elbow from e. coli
97	c3a1hA_	Alignment	not modelled	7.2	40	PDB header: structural protein Chain: A; PDB Molecule: collagen-like peptide; PDBTitle: crystal structure analysis of the collagen-like peptide, (ppg)4-otg-2 (ppg)4
98	c5lm2B_	Alignment	not modelled	7.2	10	PDB header: hydrolase Chain: B; PDB Molecule: tyrosine-protein phosphatase non-receptor type 23; PDBTitle: crystal structure of hd-ptp phosphatase
99	c3vkhA_	Alignment	not modelled	7.0	14	PDB header: motor protein Chain: A; PDB Molecule: dynein heavy chain, cytoplasmic; PDBTitle: x-ray structure of a functional full-length dynein motor domain