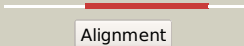

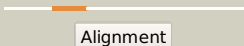

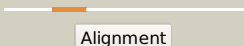
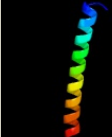
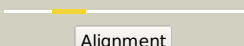
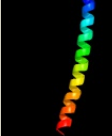
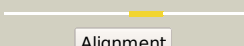

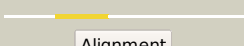

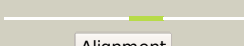


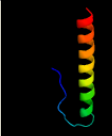

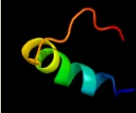
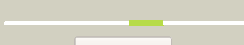


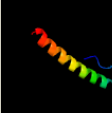

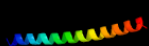

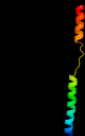
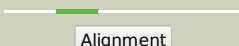

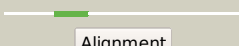

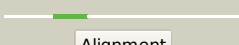

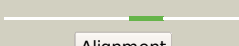

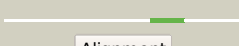




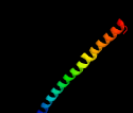

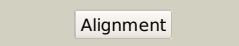




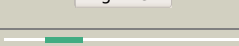
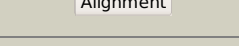


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0012 (-) _14089_14877
Date	Tue Jul 23 14:50:04 BST 2019
Unique Job ID	b2a85e0d306bdf7b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3gmgB_	 Alignment		100.0	31	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: uncharacterized protein rv1825/mt1873; PDBTitle: crystal structure of an uncharacterized conserved protein from2 mycobacterium tuberculosis
2	c5fv8A_	 Alignment		82.6	15	PDB header: structural protein Chain: A; PDB Molecule: fosw; PDBTitle: structure of cjun-fosw coiled coil complex.
3	c5fv8B_	 Alignment		81.9	15	PDB header: structural protein Chain: B; PDB Molecule: fosw; PDBTitle: structure of cjun-fosw coiled coil complex.
4	c1junB_	 Alignment		77.9	19	PDB header: transcription regulation Chain: B; PDB Molecule: c-jun homodimer; PDBTitle: nmr study of c-jun homodimer
5	d1nh8a2	 Alignment		74.0	29	Fold: Ferredoxin-like Superfamily: GlnB-like Family: ATP phosphoribosyltransferase (ATP-PRTase, HisG), regulatory C-terminal domain
6	c5xbjA_	 Alignment		70.0	13	PDB header: biosynthetic protein Chain: A; PDB Molecule: flagellar hook-associated protein flgk; PDBTitle: the structure of the flagellar hook junction protein hap1 (flgk) from2 campylobacter jejuni
7	c2vd3B_	 Alignment		69.9	29	PDB header: transferase Chain: B; PDB Molecule: atp phosphoribosyltransferase; PDBTitle: the structure of histidine inhibited hisg from2 methanobacterium thermoautotrophicum
8	c2x7IP_	 Alignment		69.2	24	PDB header: immune system Chain: P; PDB Molecule: protein rev; PDBTitle: implications of the hiv-1 rev dimer structure at 3.2a resolution for2 multimeric binding to the rev response element
9	c4yb5B_	 Alignment		68.0	25	PDB header: transferase Chain: B; PDB Molecule: atp phosphoribosyltransferase; PDBTitle: adenosine triphosphate phosphoribosyltransferase from campylobacter2 jejuni in complex with the allosteric inhibitor histidine
10	c1nh7A_	 Alignment		64.2	29	PDB header: transferase Chain: A; PDB Molecule: atp phosphoribosyltransferase; PDBTitle: atp phosphoribosyltransferase (atp-prtase) from mycobacterium2 tuberculosis
11	c3lphD_	 Alignment		57.6	21	PDB header: viral protein Chain: D; PDB Molecule: protein rev; PDBTitle: crystal structure of the hiv-1 rev dimer

12	c1ci6B_	 Alignment		56.8	14	PDB header: transcription Chain: B: PDB Molecule: transcription factor c/ebp beta; PDBTitle: transcription factor atf4-c/ebp beta bzip heterodimer
13	c3tnuA_	 Alignment		56.0	12	PDB header: cytosolic protein Chain: A: PDB Molecule: keratin, type i cytoskeletal 14; PDBTitle: heterocomplex of coil 2b domains of human intermediate filament2 proteins, keratin 5 (krt5) and keratin 14 (krt14)
14	c4cgkA_	 Alignment		55.8	12	PDB header: cell cycle Chain: A: PDB Molecule: secreted 45 kda protein; PDBTitle: crystal structure of the essential protein pcsb from streptococcus2 pneumoniae
15	c3m9bK_	 Alignment		55.7	9	PDB header: chaperone Chain: K: PDB Molecule: proteasome-associated atpase; PDBTitle: crystal structure of the amino terminal coiled coil domain and the2 inter domain of the mycobacterium tuberculosis proteasomal atpase mpa
16	c1fosF_	 Alignment		53.5	21	PDB header: transcription/dna Chain: F: PDB Molecule: c-jun proto-oncogene protein; PDBTitle: two human c-fos:c-jun:dna complexes
17	d1h3da2	 Alignment		51.5	21	Fold: Ferredoxin-like Superfamily: GlnB-like Family: ATP phosphoribosyltransferase (ATP-PRTase, HisG), regulatory C-terminal domain
18	d1vioa2	 Alignment		50.7	3	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Pseudouridine synthase RsuA N-terminal domain
19	c6czlA_	 Alignment		50.4	13	PDB header: transferase Chain: A: PDB Molecule: atp phosphoribosyltransferase catalytic subunit; PDBTitle: crystal structure of medicago truncatula atp-phosphoribosyltransferase2 in relaxed form
20	c3n4xB_	 Alignment		50.3	5	PDB header: replication Chain: B: PDB Molecule: monopolin complex subunit csm1; PDBTitle: structure of csm1 full-length
21	c6h9mA_	 Alignment	not modelled	49.1	9	PDB header: membrane protein Chain: A: PDB Molecule: coiled-coil domain-containing protein 90b, mitochondrial, PDBTitle: coiled-coil domain-containing protein 90b residues 43-125 from homo2 sapiens fused to a gcn4 adaptor
22	c2xdjC_	 Alignment	not modelled	48.4	14	PDB header: unknown function Chain: C: PDB Molecule: uncharacterized protein ybgf; PDBTitle: crystal structure of the n-terminal domain of e.coli ybgf
23	c1fosE_	 Alignment	not modelled	47.9	15	PDB header: transcription/dna Chain: E: PDB Molecule: p55-c-fos proto-oncogene protein; PDBTitle: two human c-fos:c-jun:dna complexes
24	c2xdjF_	 Alignment	not modelled	47.5	14	PDB header: unknown function Chain: F: PDB Molecule: uncharacterized protein ybgf; PDBTitle: crystal structure of the n-terminal domain of e.coli ybgf
25	c2e43A_	 Alignment	not modelled	44.8	18	PDB header: transcription/dna Chain: A: PDB Molecule: ccaat/enhancer-binding protein beta; PDBTitle: crystal structure of c/ebpbeta bzip homodimer k269a mutant2 bound to a high affinity dna fragment
26	c6o7xa_	 Alignment	not modelled	43.2	7	PDB header: membrane protein Chain: A: PDB Molecule: vacuolar atp synthase catalytic subunit a; PDBTitle: saccharomyces cerevisiae v-atpase stv1-v1vo state 3
27	c3kinB_	 Alignment	not modelled	43.1	7	PDB header: motor protein Chain: B: PDB Molecule: kinesin heavy chain; PDBTitle: kinesin (dimeric) from rattus norvegicus
28	c3s4rB_	 Alignment	not modelled	42.5	14	PDB header: structural protein Chain: B: PDB Molecule: vimentin; PDBTitle: crystal structure of vimentin coil1a/1b fragment with a stabilizing2 mutation PDB header: transcription

29	c2yy0D_	Alignment	not modelled	42.3	10	Chain: D: PDB Molecule: c-myc-binding protein; PDBTitle: crystal structure of ms0802, c-myc-1 binding protein domain2 from homo sapiens
30	c4u4pA_	Alignment	not modelled	42.3	15	PDB header: protein binding Chain: A: PDB Molecule: structural maintenance of chromosomes protein 2; PDBTitle: crystal structure of the human condensin smc hinge domain heterodimer2 with short coiled coils
31	d1qfha1	Alignment	not modelled	40.8	22	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Filamin repeat (rod domain)
32	c1hf9B_	Alignment	not modelled	40.6	17	PDB header: atpase inhibitor Chain: B: PDB Molecule: atpase inhibitor (mitochondrial); PDBTitle: c-terminal coiled-coil domain from bovine if1
33	c2xzaA_	Alignment	not modelled	40.0	3	PDB header: cell adhesion Chain: A: PDB Molecule: immunoglobulin-binding protein eibd; PDBTitle: escherichia coli immunoglobulin-binding protein eibd 391-438 fused2 to gcn4 adaptors
34	c3lynR_	Alignment	not modelled	39.8	11	PDB header: virus Chain: R: PDB Molecule: hexon-associated protein; PDBTitle: 3.6-angstrom cryoem structure of human adenovirus type 5
35	c5wwiN_	Alignment	not modelled	39.3	10	PDB header: cell cycle Chain: N: PDB Molecule: kinetochore protein nnf1; PDBTitle: crystal structure of the schizogenesis pombe kinetochore mis12c2 subcomplex
36	c3ra3D_	Alignment	not modelled	39.2	30	PDB header: de novo protein Chain: D: PDB Molecule: p2f; PDBTitle: crystal structure of a section of a de novo design gigadalton protein2 fibre
37	c1t2kD_	Alignment	not modelled	38.9	12	PDB header: transcription/dna Chain: D: PDB Molecule: cyclic-amp-dependent transcription factor atf-2; PDBTitle: structure of the dna binding domains of irf3, atf-2 and jun2 bound to dna
38	c4u8us_	Alignment	not modelled	38.2	13	PDB header: oxygen storage/transport Chain: S: PDB Molecule: globin d chain; PDBTitle: the crystallographic structure of the giant hemoglobin from2 glossoscolex paulistus at 3.2 a resolution.
39	c1ci6A_	Alignment	not modelled	37.2	12	PDB header: transcription Chain: A: PDB Molecule: transcription factor atf-4; PDBTitle: transcription factor atf4-c/ebp beta bzip heterodimer
40	c6r8fD_	Alignment	not modelled	36.6	16	PDB header: signaling protein Chain: D: PDB Molecule: brisc complex subunit abraxas 2; PDBTitle: cryo-em structure of the human brisc-shmt2 complex
41	c6e1rA_	Alignment	not modelled	35.6	35	PDB header: hydrolase Chain: A: PDB Molecule: tailspike protein; PDBTitle: crystal structure of the acinetobacter phage vb_apip_p1 tailspike2 protein
42	c1u2uA_	Alignment	not modelled	35.2	19	PDB header: transcription Chain: A: PDB Molecule: general control protein gcn4; PDBTitle: nmr solution structure of a designed heterodimeric leucine2 zipper
43	c2pnvA_	Alignment	not modelled	34.4	13	PDB header: membrane protein Chain: A: PDB Molecule: small conductance calcium-activated potassium PDBTitle: crystal structure of the leucine zipper domain of small-2 conductance ca2+-activated k+ (skca) channel from rattus3 norvegicus
44	c2l5gB_	Alignment	not modelled	34.0	9	PDB header: transcription regulator Chain: B: PDB Molecule: putative uncharacterized protein ncor2; PDBTitle: co-ordinates and 1h, 13c and 15n chemical shift assignments for the2 complex of gps2 53-90 and smrt 167-207
45	c4pxjB_	Alignment	not modelled	33.8	18	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
46	c1ij2C_	Alignment	not modelled	32.4	20	PDB header: transcription Chain: C: PDB Molecule: general control protein gcn4; PDBTitle: gcn4-pvtl coiled-coil trimer with threonine at the a(16)2 position
47	c2oqqB_	Alignment	not modelled	32.3	12	PDB header: transcription Chain: B: PDB Molecule: transcription factor hy5; PDBTitle: crystal structure of hy5 leucine zipper homodimer from arabidopsis2 thaliana
48	c3k7zB_	Alignment	not modelled	32.1	20	PDB header: dna binding protein Chain: B: PDB Molecule: general control protein gcn4; PDBTitle: gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
49	c3k7za_	Alignment	not modelled	32.1	20	PDB header: dna binding protein Chain: A: PDB Molecule: general control protein gcn4; PDBTitle: gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
50	c1rb1B_	Alignment	not modelled	32.1	20	PDB header: dna binding protein Chain: B: PDB Molecule: general control protein gcn4; PDBTitle: gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
51	c1rb1A_	Alignment	not modelled	32.1	20	PDB header: dna binding protein Chain: A: PDB Molecule: general control protein gcn4; PDBTitle: gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
52	c2w83C_	Alignment	not modelled	32.0	17	PDB header: protein transport Chain: C: PDB Molecule: c-jun-amino-terminal kinase-interacting protein PDBTitle: crystal structure of the arf6 gtpase in complex with a2 specific effector, jip4
53	c4p6vC_	Alignment	not modelled	31.9	9	PDB header: oxidoreductase Chain: C: PDB Molecule: na(+)-translocating nadh-quinone reductase subunit c;

						PDBTitle: crystal structure of the na ⁺ -translocating nadh: ubiquinone2 oxidoreductase from vibrio cholerae
54	c3swkB_	Alignment	not modelled	31.9	16	PDB header: structural protein Chain: B: PDB Molecule: vimentin; PDBTitle: crystal structure of vimentin coil1b fragment
55	c1ij3C_	Alignment	not modelled	31.8	20	PDB header: transcription Chain: C: PDB Molecule: general control protein gcn4; PDBTitle: gcn4-pvsl coiled-coil trimer with serine at the a(16)2 position
56	c1q1kA_	Alignment	not modelled	31.2	21	PDB header: transferase Chain: A: PDB Molecule: atp phosphoribosyltransferase; PDBTitle: structure of atp-phosphoribosyltransferase from e. coli complexed with2 pr-atp
57	c1deqO_	Alignment	not modelled	31.1	4	PDB header: blood clotting Chain: O: PDB Molecule: fibrinogen (beta chain); PDBTitle: the crystal structure of modified bovine fibrinogen (at ~42 angstrom resolution)
58	c2o7hF_	Alignment	not modelled	31.1	18	PDB header: transcription Chain: F: PDB Molecule: general control protein gcn4; PDBTitle: crystal structure of trimeric coiled coil gcn4 leucine zipper
59	d1ryba_	Alignment	not modelled	31.0	15	Fold: Phosphorylase/hydrolase-like Superfamily: Peptidyl-tRNA hydrolase-like Family: Peptidyl-tRNA hydrolase-like
60	c6e2jB_	Alignment	not modelled	31.0	8	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 s231l mutation and wild-type human keratin 10 coil 1b
61	c3a5tB_	Alignment	not modelled	30.9	21	PDB header: transcription regulator/dna Chain: B: PDB Molecule: transcription factor mafg; PDBTitle: crystal structure of mafg-dna complex
62	c1rb6C_	Alignment	not modelled	30.7	21	PDB header: dna binding protein Chain: C: PDB Molecule: general control protein gcn4; PDBTitle: antiparallel trimer of gcn4-leucine zipper core mutant as n16a2 tetragonal form
63	c1swiA_	Alignment	not modelled	30.7	21	PDB header: leucine zipper Chain: A: PDB Molecule: gcn4p1; PDBTitle: gcn4-leucine zipper core mutant as n16a complexed with benzene
64	c3iynQ_	Alignment	not modelled	30.6	12	PDB header: virus Chain: Q: PDB Molecule: hexon-associated protein; PDBTitle: 3.6-angstrom cryoem structure of human adenovirus type 5
65	c5h6sB_	Alignment	not modelled	30.6	16	PDB header: hydrolase Chain: B: PDB Molecule: amidase; PDBTitle: crystal structure of hydrazidase s179a mutant complexed with a2 substrate
66	c1ij3B_	Alignment	not modelled	30.4	21	PDB header: transcription Chain: B: PDB Molecule: general control protein gcn4; PDBTitle: gcn4-pvsl coiled-coil trimer with serine at the a(16)2 position
67	c6a9pD_	Alignment	not modelled	30.2	22	PDB header: structural protein Chain: D: PDB Molecule: glial fibrillary acidic protein; PDBTitle: crystal structure of the human glial fibrillary acidic protein 1b2 domain
68	c1ij2B_	Alignment	not modelled	29.7	20	PDB header: transcription Chain: B: PDB Molecule: general control protein gcn4; PDBTitle: gcn4-pvtl coiled-coil trimer with threonine at the a(16)2 position
69	c1ztaA_	Alignment	not modelled	29.6	19	PDB header: dna-binding motif Chain: A: PDB Molecule: leucine zipper monomer; PDBTitle: the solution structure of a leucine-zipper motif peptide
70	c3ra3A_	Alignment	not modelled	29.3	23	PDB header: de novo protein Chain: A: PDB Molecule: p1c; PDBTitle: crystal structure of a section of a de novo design gigadalton protein2 fibre
71	c5lskB_	Alignment	not modelled	29.1	18	PDB header: cell cycle Chain: B: PDB Molecule: polyamine-modulated factor 1; PDBTitle: crystal structure of the human kinetochore mis12-cenp-c complex
72	d1r05a_	Alignment	not modelled	29.0	14	Fold: HLH-like Superfamily: HLH, helix-loop-helix DNA-binding domain Family: HLH, helix-loop-helix DNA-binding domain
73	c4clvB_	Alignment	not modelled	28.7	10	PDB header: metal binding protein Chain: B: PDB Molecule: nickel-cobalt-cadmium resistance protein nccx; PDBTitle: crystal structure of dodecylphosphocholine-solubilized nccx2 from cupriavidus metallidurans 31a
74	c1cz7C_	Alignment	not modelled	28.3	10	PDB header: contractile protein Chain: C: PDB Molecule: microtubule motor protein ncd; PDBTitle: the crystal structure of a minus-end directed microtubule2 motor protein ncd reveals variable dimer conformations
75	c1ce0B_	Alignment	not modelled	27.1	10	PDB header: hiv-1 envelope protein Chain: B: PDB Molecule: protein (leucine zipper model h38-p1); PDBTitle: trimerization specificity in hiv-1 gp41: analysis with a2 gcn4 leucine zipper model
76	c2cqjA_	Alignment	not modelled	27.1	6	PDB header: rna binding protein Chain: A: PDB Molecule: u3 small nucleolar ribonucleoprotein protein PDBTitle: solution structure of the s4 domain of u3 small nucleolar2 ribonucleoprotein protein imp3 homolog
77	c2wt7B_	Alignment	not modelled	26.9	18	PDB header: transcription Chain: B: PDB Molecule: transcription factor mafb; PDBTitle: crystal structure of the bzip heterodimeric complex mafb:cfos bound to2 dna
78	c3ol1A_	Alignment	not modelled	26.8	14	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
79	c2wg6L	Alignment	not modelled	26.8	11	PDB header: transcription,hydrolase Chain: L: PDB Molecule: general control protein gcn4, proteasome-activating PDBTitle: proteasome-activating nucleotidase (pan) n-domain (57-134) from2 archaeoglobus fulgidus fused to gcn4, p61a mutant
80	c1dipA	Alignment	not modelled	26.6	29	PDB header: acetylation Chain: A: PDB Molecule: delta-sleep-inducing peptide immunoreactive PDBTitle: the solution structure of porcine delta-sleep-inducing2 peptide immunoreactive peptide, nmr, 10 structures
81	c1u0iA	Alignment	not modelled	26.2	24	PDB header: de novo protein Chain: A: PDB Molecule: iaal-e3; PDBTitle: iaal-e3/k3 heterodimer
82	d1nkpa	Alignment	not modelled	26.0	16	Fold: HLH-like Superfamily: HLH, helix-loop-helix DNA-binding domain Family: HLH, helix-loop-helix DNA-binding domain
83	c5cw5D	Alignment	not modelled	25.8	21	PDB header: metal binding protein Chain: D: PDB Molecule: protein fam175b; PDBTitle: structure of cfbrcc36-cfkiaa0157 complex (qsq mutant)
84	c4y66D	Alignment	not modelled	25.5	10	PDB header: cell cycle Chain: D: PDB Molecule: putative tbpip family protein; PDBTitle: crystal structure of giardia lamblia hop2-mnd1 complex
85	c3cvfA	Alignment	not modelled	25.3	9	PDB header: signaling protein Chain: A: PDB Molecule: homer protein homolog 3; PDBTitle: crystal structure of the carboxy terminus of homer3
86	c2zvfG	Alignment	not modelled	25.3	22	PDB header: ligase Chain: G: PDB Molecule: alanyl-trna synthetase; PDBTitle: crystal structure of archaeoglobus fulgidus alanyl-trna2 synthetase c-terminal dimerization domain
87	c5lskA	Alignment	not modelled	25.3	7	PDB header: cell cycle Chain: A: PDB Molecule: protein mis12 homolog; PDBTitle: crystal structure of the human kinetochore mis12-cenp-c complex
88	d1h3fa2	Alignment	not modelled	24.7	4	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Tyrosyl-tRNA synthetase (TyrRS), C-terminal domain
89	c5hytC	Alignment	not modelled	24.7	20	PDB header: immune system Chain: C: PDB Molecule: precursor to protein sir22; PDBTitle: structure of human c4b-binding protein alpha chain ccp domains 1 and 22 in complex with the hypervariable region of group a streptococcus m223 protein
90	c5hytE	Alignment	not modelled	24.7	20	PDB header: immune system Chain: E: PDB Molecule: precursor to protein sir22; PDBTitle: structure of human c4b-binding protein alpha chain ccp domains 1 and 22 in complex with the hypervariable region of group a streptococcus m223 protein
91	c4e61A	Alignment	not modelled	24.3	13	PDB header: cell cycle Chain: A: PDB Molecule: protein bim1; PDBTitle: crystal structure of the eb1-like motif of bim1p
92	c5hytG	Alignment	not modelled	24.0	20	PDB header: immune system Chain: G: PDB Molecule: precursor to protein sir22; PDBTitle: structure of human c4b-binding protein alpha chain ccp domains 1 and 22 in complex with the hypervariable region of group a streptococcus m223 protein
93	c5hytA	Alignment	not modelled	24.0	20	PDB header: immune system Chain: A: PDB Molecule: precursor to protein sir22; PDBTitle: structure of human c4b-binding protein alpha chain ccp domains 1 and 22 in complex with the hypervariable region of group a streptococcus m223 protein
94	c5t76A	Alignment	not modelled	23.7	9	PDB header: translation Chain: A: PDB Molecule: alanine--trna ligase, cytoplasmic; PDBTitle: a fragment of a human trna synthetase
95	c5h6tB	Alignment	not modelled	23.3	16	PDB header: hydrolase Chain: B: PDB Molecule: amidase; PDBTitle: crystal structure of hydrazidase from microbacterium sp. strain hm58-2
96	c2gd7B	Alignment	not modelled	23.3	10	PDB header: transcription Chain: B: PDB Molecule: hexim1 protein; PDBTitle: the structure of the cyclin t-binding domain of hexim12 reveals the molecular basis for regulation of3 transcription elongation
97	c5mg8B	Alignment	not modelled	23.2	13	PDB header: recombination Chain: B: PDB Molecule: structural maintenance of chromosomes protein 6; PDBTitle: crystal structure of the s.pombe smc5/6 hinge domain
98	c4ug1A	Alignment	not modelled	23.2	10	PDB header: cell cycle Chain: A: PDB Molecule: cell cycle protein gpsb; PDBTitle: gpsb n-terminal domain
99	c5zk1A	Alignment	not modelled	23.0	14	PDB header: transcription/dna Chain: A: PDB Molecule: cyclic amp-responsive element-binding protein 1; PDBTitle: crystal structure of the crtc2(semet)-creb-cre complex
100	c5vgzC	Alignment	not modelled	22.7	18	PDB header: hydrolase Chain: C: PDB Molecule: 26s proteasome regulatory subunit 8; PDBTitle: conformational landscape of the p28-bound human proteasome regulatory2 particle
101	c1kskA	Alignment	not modelled	22.7	3	PDB header: lyase Chain: A: PDB Molecule: ribosomal small subunit pseudouridine synthase a; PDBTitle: structure of rsua
102	c6ec0A	Alignment	not modelled	22.6	10	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)

103	c2wl2B_	Alignment	not modelled	22.6	13	PDB header: isomerase Chain: B: PDB Molecule: dna gyrase subunit a; PDBTitle: crystal structure of n-terminal domain of gyra with the2 antibiotic simocyclinone d8
104	c3ojaB_	Alignment	not modelled	22.1	14	PDB header: protein binding Chain: B: PDB Molecule: anopheles plasmodium-responsive leucine-rich repeat protein PDBTitle: crystal structure of Irim1/apl1c complex
105	d2f9ha1	Alignment	not modelled	21.5	30	Fold: PTSIIA/GutA-like Superfamily: PTSIIA/GutA-like Family: PTSIIA/GutA-like
106	c5t58B_	Alignment	not modelled	21.4	18	PDB header: cell cycle Chain: B: PDB Molecule: klla0e05809p; PDBTitle: structure of the mind complex shows a regulatory focus of yeast2 kinetochore assembly
107	c4c47B_	Alignment	not modelled	21.3	8	PDB header: cell adhesion Chain: B: PDB Molecule: inner membrane lipoprotein; PDBTitle: salmonella enterica trimeric lipoprotein sadb
108	c6gqaD_	Alignment	not modelled	21.2	8	PDB header: cell cycle Chain: D: PDB Molecule: cell cycle protein gpsb; PDBTitle: cell division regulator s. pneumoniae gpsb
109	c4etpA_	Alignment	not modelled	21.1	8	PDB header: motor protein Chain: A: PDB Molecule: kinesin-like protein kar3; PDBTitle: c-terminal motor and motor homology domain of kar3vik1 fused to a2 synthetic heterodimeric coiled coil
110	d1an2a_	Alignment	not modelled	20.7	8	Fold: HLH-like Superfamily: HLH, helix-loop-helix DNA-binding domain Family: HLH, helix-loop-helix DNA-binding domain
111	c4u8uc_	Alignment	not modelled	20.3	11	PDB header: oxygen storage/transport Chain: C: PDB Molecule: globin c chain; PDBTitle: the crystallographic structure of the giant hemoglobin from2 glossoscolex paulistus at 3.2 a resolution.
112	c1p9iA_	Alignment	not modelled	20.2	22	PDB header: unknown function Chain: A: PDB Molecule: cortexillin i/gcn4 hybrid peptide; PDBTitle: coiled-coil x-ray structure at 1.17 a resolution
113	c6n6sB_	Alignment	not modelled	20.1	16	PDB header: signaling protein Chain: B: PDB Molecule: tnfaip3-interacting protein 1; PDBTitle: crystal structure of abin-1 uban
114	c2w6aB_	Alignment	not modelled	20.1	28	PDB header: signaling protein Chain: B: PDB Molecule: arf gtpase-activating protein git1; PDBTitle: x-ray structure of the dimeric git1 coiled-coil domain
115	c6nrb5_	Alignment	not modelled	20.1	21	PDB header: chaperone Chain: 5: PDB Molecule: prefoldin subunit 5; PDBTitle: htric-hpfd class2