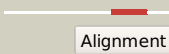
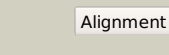
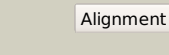
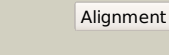
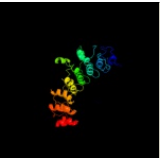
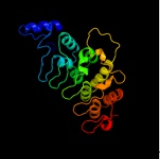
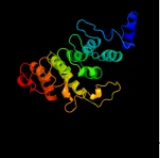
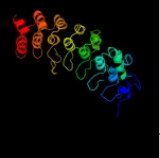
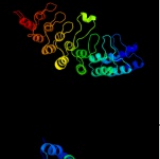
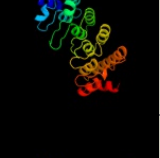
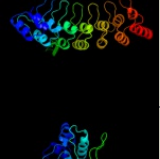
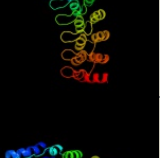
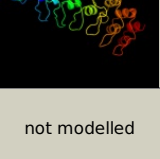


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1n11a_	 Alignment		100.0	34	Fold: beta-hairpin-alpha-hairpin repeat Superfamily: Ankyrin repeat Family: Ankyrin repeat
2	c1n11A_	 Alignment		100.0	34	PDB header: structural protein Chain: A: PDB Molecule: ankyrin; PDBTitle: d34 region of human ankyrin-r and linker
3	c3keaB_	 Alignment		100.0	16	PDB header: viral protein Chain: B: PDB Molecule: k1l; PDBTitle: structure function studies of vaccinia virus host-range protein k12 reveal a novel ankyrin repeat interaction surface for k1s function
4	d2ajaa1	 Alignment		100.0	19	Fold: alpha-alpha superhelix Superfamily: Pseudo ankyrin repeat-like Family: Pseudo ankyrin repeat
5	c4bepB_	 Alignment		100.0	14	PDB header: transferase Chain: B: PDB Molecule: phosphocholine transferase ankx; PDBTitle: crystal structure of the legionella pneumophila fic domain-2 containing effector ankx protein (apo-form)
6	d1s70b_	 Alignment		100.0	20	Fold: beta-hairpin-alpha-hairpin repeat Superfamily: Ankyrin repeat Family: Ankyrin repeat
7	c3utmA_	 Alignment		100.0	25	PDB header: transferase/signaling protein Chain: A: PDB Molecule: tankyrase-1; PDBTitle: crystal structure of a mouse tankyrase-axin complex
8	c3ljnA_	 Alignment		100.0	18	PDB header: unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: ankyrin repeat protein from leishmania major
9	c2ajaA_	 Alignment		100.0	17	PDB header: protein binding Chain: A: PDB Molecule: ankyrin repeat family protein; PDBTitle: x-ray structure of an ankyrin repeat family protein q5zsv02 from legionella pneumophila. northeast structural genomics3 consortium target lgr21.
10	c4g8kA_	 Alignment		100.0	29	PDB header: hydrolase Chain: A: PDB Molecule: 2-5a-dependent ribonuclease; PDBTitle: intact sensor domain of human rnase I in the inactive signaling state
11	c2xaiD_	 Alignment		100.0	19	PDB header: transcription Chain: D: PDB Molecule: ankyrin repeat and socs box protein 9; PDBTitle: crystal structure of ankyrin repeat and socs box-containing2 protein 9 (asb9) in complex with elonginb and elonginc

12	c2fo1E_	Alignment		100.0	22	PDB header: gene regulation/signalling protein/dna Chain: E: PDB Molecule: lin-12 protein; PDBTitle: crystal structure of the csl-notch-mastermind ternary2 complex bound to dna
13	c1sw6A_	Alignment		100.0	19	PDB header: transcription regulation Chain: A: PDB Molecule: regulatory protein swi6; PDBTitle: s. cerevisiae swi6 ankyrin-repeat fragment
14	d1sw6a_	Alignment		100.0	19	Fold: beta-hairpin-alpha-hairpin repeat Superfamily: Ankyrin repeat Family: Ankyrin repeat
15	d2fo1e1	Alignment		100.0	22	Fold: beta-hairpin-alpha-hairpin repeat Superfamily: Ankyrin repeat Family: Ankyrin repeat
16	d1wdya_	Alignment		100.0	29	Fold: beta-hairpin-alpha-hairpin repeat Superfamily: Ankyrin repeat Family: Ankyrin repeat
17	c3jxiA_	Alignment		100.0	24	PDB header: membrane protein Chain: A: PDB Molecule: vanilloid receptor-related osmotically activated channel PDBTitle: crystal structure of the chicken trpv4 ankyrin repeat domain
18	c3b7bB_	Alignment		100.0	28	PDB header: transferase Chain: B: PDB Molecule: euchromatic histone-lysine n-methyltransferase 1; PDBTitle: euhmt1 (glp) ankyrin repeat domain (structure 1)
19	d1uoha_	Alignment		100.0	30	Fold: beta-hairpin-alpha-hairpin repeat Superfamily: Ankyrin repeat Family: Ankyrin repeat
20	c3eu9B_	Alignment		100.0	25	PDB header: protein binding, methyl-lysine-binding p Chain: B: PDB Molecule: huntingtin-interacting protein 14; PDBTitle: the ankyrin repeat domain of huntingtin interacting protein 14
21	c2f8xK_	Alignment	not modelled	100.0	24	PDB header: transcription/dna Chain: K: PDB Molecule: neurogenic locus notch homolog protein 1; PDBTitle: crystal structure of activated notch, csl and mam1 on hes-12 promoter dna sequence
22	c2f37B_	Alignment	not modelled	100.0	23	PDB header: membrane protein Chain: B: PDB Molecule: transient receptor potential cation channel PDBTitle: crystal structure of the ankyrin repeat domain of human2 trpv2
23	c4hbdA_	Alignment	not modelled	100.0	29	PDB header: protein binding Chain: A: PDB Molecule: kn motif and ankyrin repeat domain-containing protein 2; PDBTitle: crystal structure of kank2 ankyrin repeats
24	d1k1aa_	Alignment	not modelled	100.0	25	Fold: beta-hairpin-alpha-hairpin repeat Superfamily: Ankyrin repeat Family: Ankyrin repeat
25	c2vgeA_	Alignment	not modelled	100.0	23	PDB header: transcription Chain: A: PDB Molecule: rela-associated inhibitor; PDBTitle: crystal structure of the c-terminal region of human iaspp
26	c1ycsB_	Alignment	not modelled	100.0	22	PDB header: complex (anti-oncogene/ankyrin repeats) Chain: B: PDB Molecule: 53bp2; PDBTitle: p53-53bp2 complex
27	c3d9hA_	Alignment	not modelled	100.0	18	PDB header: structural protein, protein binding Chain: A: PDB Molecule: cdna flj77766, highly similar to homo sapiens PDBTitle: crystal structure of the splice variant of human asb92 (hasb9-2), an ankyrin repeat protein
28	d1lixva_	Alignment	not modelled	100.0	27	Fold: beta-hairpin-alpha-hairpin repeat Superfamily: Ankyrin repeat Family: Ankyrin repeat

29	c3t8kB	Alignment	not modelled	99.9	17	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: the crystal structure of a functionally unknown protein lebu_0176 from2 leptotrichia buccalis c-1013-b
30	d1iknd	Alignment	not modelled	99.9	22	Fold: beta-hairpin-alpha-hairpin repeat Superfamily: Ankyrin repeat Family: Ankyrin repeat
31	c2kbxA	Alignment	not modelled	99.9	28	PDB header: cell adhesion Chain: A: PDB Molecule: integrin-linked protein kinase; PDBTitle: solution structure of ilk-pinch complex
32	d1ot8a	Alignment	not modelled	99.9	31	Fold: beta-hairpin-alpha-hairpin repeat Superfamily: Ankyrin repeat Family: Ankyrin repeat
33	c3ui2A	Alignment	not modelled	99.9	23	PDB header: transport protein Chain: A: PDB Molecule: signal recognition particle 43 kda protein, chloroplastic; PDBTitle: crystal structure of the cpsrp54 tail bound to cpsrp43
34	c2nyiA	Alignment	not modelled	99.9	22	PDB header: transport protein Chain: A: PDB Molecule: transient receptor potential cation channel PDBTitle: crystal structure of the ankyrin repeat domain of trpv1
35	c3t9kA	Alignment	not modelled	99.9	22	PDB header: protein transport Chain: A: PDB Molecule: arf-gap with coiled-coil, ank repeat and ph domain- PDBTitle: crystal structure of acap1 c-portion mutant s554d fused with integrin2 beta1 peptide
36	c3ehrB	Alignment	not modelled	99.9	24	PDB header: signaling protein Chain: B: PDB Molecule: osteoclast-stimulating factor 1; PDBTitle: crystal structure of human osteoclast stimulating factor
37	c1oy3D	Alignment	not modelled	99.9	25	PDB header: dna binding protein Chain: D: PDB Molecule: transcription factor inhibitor i-kappa-b-beta; PDBTitle: crystal structure of an ikbbeta/nf-kb p65 homodimer complex
38	d1oy3d	Alignment	not modelled	99.9	25	Fold: beta-hairpin-alpha-hairpin repeat Superfamily: Ankyrin repeat Family: Ankyrin repeat
39	c3deoA	Alignment	not modelled	99.9	26	PDB header: protein transport, membrane protein Chain: A: PDB Molecule: signal recognition particle 43 kda protein; PDBTitle: structural basis for specific substrate recognition by the2 chloroplast signal recognition particle protein cpsrp43
40	c3jueA	Alignment	not modelled	99.9	26	PDB header: protein transport/endocytosis Chain: A: PDB Molecule: arfgap with coiled-coil, ank repeat and ph domain- PDBTitle: crystal structure of arfgap and ank repeat domain of acap1
41	c2rfaA	Alignment	not modelled	99.9	23	PDB header: membrane protein Chain: A: PDB Molecule: transient receptor potential cation channel subfamily v PDBTitle: crystal structure of the mouse trpv6 ankyrin repeat domain
42	c3v31A	Alignment	not modelled	99.9	25	PDB header: protein binding Chain: A: PDB Molecule: ankyrin repeat family a protein 2; PDBTitle: crystal structure of the peptide bound complex of the ankyrin repeat2 domains of human ankra2
43	c3hraA	Alignment	not modelled	99.9	25	PDB header: structural protein Chain: A: PDB Molecule: ankyrin repeat family protein; PDBTitle: crystal structure of ef0377 an ankyrin repeat protein
44	c2b0oF	Alignment	not modelled	99.9	21	PDB header: metal binding protein Chain: F: PDB Molecule: uplc1; PDBTitle: crystal structure of uplc1 gap domain
45	c3lvrE	Alignment	not modelled	99.9	22	PDB header: protein transport Chain: E: PDB Molecule: arf-gap with sh3 domain, ank repeat and ph domain- PDBTitle: the crystal structure of asap3 in complex with arf6 in transition2 state soaked with calcium
46	d1dcqa1	Alignment	not modelled	99.9	24	Fold: beta-hairpin-alpha-hairpin repeat Superfamily: Ankyrin repeat Family: Ankyrin repeat
47	c4b93B	Alignment	not modelled	99.9	29	PDB header: exocytosis Chain: B: PDB Molecule: ankyrin repeat domain-containing protein 27; PDBTitle: complex of vamp7 cytoplasmic domain with 2nd ankyrin repeat2 domain of varp
48	c1dcqA	Alignment	not modelled	99.9	24	PDB header: metal binding protein Chain: A: PDB Molecule: pyk2-associated protein beta; PDBTitle: crystal structure of the arf-gap domain and ankyrin repeats2 of papbeta.
49	c4gmrA	Alignment	not modelled	99.9	42	PDB header: de novo protein Chain: A: PDB Molecule: or266 de novo protein; PDBTitle: crystal structure of engineered protein. northeast structural genomics2 consortium target or266.
50	c1ympB	Alignment	not modelled	99.9	25	PDB header: transcription Chain: B: PDB Molecule: notch 1 protein; PDBTitle: the crystal structure of a partial mouse notch-1 ankyrin2 domain: repeats 4 through 7 preserve an ankyrin fold
51	d1ycsb1	Alignment	not modelled	99.9	25	Fold: beta-hairpin-alpha-hairpin repeat Superfamily: Ankyrin repeat Family: Ankyrin repeat
52	c1ympA	Alignment	not modelled	99.9	25	PDB header: transcription Chain: A: PDB Molecule: notch 1 protein; PDBTitle: the crystal structure of a partial mouse notch-1 ankyrin2 domain: repeats 4 through 7 preserve an ankyrin fold
53	c2rfmB	Alignment	not modelled	99.9	24	PDB header: protein binding Chain: B: PDB Molecule: putative ankyrin repeat protein tv1425; PDBTitle: structure of a thermophilic ankyrin repeat protein

54	c3twtd	Alignment	not modelled	99.9	32	PDB header: signaling protein/peptide Chain: D: PDB Molecule: tankyrase-2; PDBTitle: crystal structure of arc4 from human tankyrase 2 in complex with2 peptide from human mcl1 (chimeric peptide)
55	d2a5ea	Alignment	not modelled	99.9	26	Fold: beta-hairpin-alpha-hairpin repeat Superfamily: Ankyrin repeat Family: Ankyrin repeat
56	c1mj0A	Alignment	not modelled	99.9	37	PDB header: de novo protein Chain: A: PDB Molecule: sank e3_5 protein; PDBTitle: sank e3_5: an artificial ankyrin repeat protein
57	c3v30A	Alignment	not modelled	99.8	30	PDB header: protein binding Chain: A: PDB Molecule: dna-binding protein rfxank; PDBTitle: crystal structure of the peptide bound complex of the ankyrin repeat2 domains of human rfxank
58	d1blxb	Alignment	not modelled	99.8	31	Fold: beta-hairpin-alpha-hairpin repeat Superfamily: Ankyrin repeat Family: Ankyrin repeat
59	d1awcb	Alignment	not modelled	99.8	32	Fold: beta-hairpin-alpha-hairpin repeat Superfamily: Ankyrin repeat Family: Ankyrin repeat
60	d1ihba	Alignment	not modelled	99.8	35	Fold: beta-hairpin-alpha-hairpin repeat Superfamily: Ankyrin repeat Family: Ankyrin repeat
61	d1myoa	Alignment	not modelled	99.8	31	Fold: beta-hairpin-alpha-hairpin repeat Superfamily: Ankyrin repeat Family: Ankyrin repeat
62	c3c5rB	Alignment	not modelled	99.8	29	PDB header: protein binding Chain: B: PDB Molecule: brca1-associated ring domain protein 1; PDBTitle: crystal structure of the bard1 ankyrin repeat domain and its2 functional consequences
63	c2v5qC	Alignment	not modelled	99.8	40	PDB header: transferase Chain: C: PDB Molecule: design ankyrin repeat protein; PDBTitle: crystal structure of wild-type plk-1 kinase domain in2 complex with a selective darpin
64	c2jabC	Alignment	not modelled	99.8	34	PDB header: de novo protein Chain: C: PDB Molecule: h10-2-g3; PDBTitle: a designed ankyrin repeat protein evolved to picomolar2 affinity to her2
65	d1bd8a	Alignment	not modelled	99.8	30	Fold: beta-hairpin-alpha-hairpin repeat Superfamily: Ankyrin repeat Family: Ankyrin repeat
66	d1bi7b	Alignment	not modelled	99.8	25	Fold: beta-hairpin-alpha-hairpin repeat Superfamily: Ankyrin repeat Family: Ankyrin repeat
67	c2l6bA	Alignment	not modelled	99.8	37	PDB header: de novo protein Chain: A: PDB Molecule: nrc1c; PDBTitle: nrc consensus ankyrin repeat protein solution structure
68	c2zgdA	Alignment	not modelled	99.8	35	PDB header: de novo protein Chain: A: PDB Molecule: 3 repeat synthetic ankyrin; PDBTitle: asn-hydroxylation stabilises the ankyrin repeat domain fold
69	c2xenA	Alignment	not modelled	99.7	38	PDB header: de novo protein Chain: A: PDB Molecule: ni1c mut4; PDBTitle: structural determinants for improved thermal stability of2 designed ankyrin repeat proteins with a redesigned c-3 capping module.
70	c3iytG	Alignment		99.7	17	PDB header: apoptosis Chain: G: PDB Molecule: apoptotic protease-activating factor 1; PDBTitle: structure of an apoptosome-procaspase-9 card complex
71	c1n0qB	Alignment	not modelled	99.7	50	PDB header: structural protein Chain: B: PDB Molecule: 3 ankyrin repeats; PDBTitle: 3ank: a designed ankyrin repeat protein with three identical consensus2 repeats
72	c1n0rA	Alignment	not modelled	99.6	51	PDB header: structural protein Chain: A: PDB Molecule: 4 ankyrin repeats; PDBTitle: 4ank: a designed ankyrin repeat protein with four identical2 consensus repeats
73	c2qenA	Alignment	not modelled	99.4	14	PDB header: unknown function Chain: A: PDB Molecule: walker-type atpase; PDBTitle: the walker-type atpase paby2304 of pyrococcus abyssi
74	c4kxfF	Alignment	not modelled	99.3	17	PDB header: immune system Chain: F: PDB Molecule: nlr family card domain-containing protein 4; PDBTitle: crystal structure of nlrc4 reveals its autoinhibition mechanism
75	c2fnaA	Alignment	not modelled	99.2	13	PDB header: atp-binding protein Chain: A: PDB Molecule: conserved hypothetical protein; PDBTitle: crystal structure of an archaeal aaa+ atpase (ssol1545) from sulfobolbus2 solfataricus p2 at 2.00 a resolution
76	c2v1uA	Alignment	not modelled	99.1	16	PDB header: replication Chain: A: PDB Molecule: cell division control protein 6 homolog; PDBTitle: structure of the aeropyrum pernix orc1 protein in complex2 with dna
77	c4kxfP	Alignment	not modelled	99.0	18	PDB header: immune system Chain: P: PDB Molecule: nlr family card domain-containing protein 4; PDBTitle: crystal structure of nlrc4 reveals its autoinhibition mechanism
78	d2fnaa2	Alignment	not modelled	99.0	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain

79	c1w5sB_	Alignment	not modelled	98.8	9	PDB header: replication Chain: B: PDB Molecule: origin recognition complex subunit 2 orc2; PDBTitle: structure of the aeropyrum pernix orc2 protein (adp form)
80	c2qbyB_	Alignment	not modelled	98.7	14	PDB header: replication/dna Chain: B: PDB Molecule: cell division control protein 6 homolog 3; PDBTitle: crystal structure of a heterodimer of cdc6/orc1 initiators2 bound to origin dna (from s. solfataricus)
81	c3iz8A_	Alignment	not modelled	98.6	14	PDB header: apoptosis Chain: A: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
82	c3iz8F_	Alignment	not modelled	98.6	14	PDB header: apoptosis Chain: F: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
83	c3iz8D_	Alignment	not modelled	98.6	14	PDB header: apoptosis Chain: D: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
84	c1vt4M_	Alignment	not modelled	98.6	14	PDB header: apoptosis Chain: M: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
85	c1vt4I_	Alignment	not modelled	98.6	14	PDB header: apoptosis Chain: I: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
86	c3iz8B_	Alignment	not modelled	98.6	14	PDB header: apoptosis Chain: B: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
87	c3iz8E_	Alignment	not modelled	98.6	14	PDB header: apoptosis Chain: E: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
88	c1vt4P_	Alignment	not modelled	98.6	14	PDB header: apoptosis Chain: P: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
89	c1vt4N_	Alignment	not modelled	98.6	14	PDB header: apoptosis Chain: N: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
90	c1vt4O_	Alignment	not modelled	98.6	14	PDB header: apoptosis Chain: O: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
91	c1vt4K_	Alignment	not modelled	98.6	14	PDB header: apoptosis Chain: K: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
92	c1vt4J_	Alignment	not modelled	98.6	14	PDB header: apoptosis Chain: J: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
93	c3iz8H_	Alignment	not modelled	98.6	14	PDB header: apoptosis Chain: H: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
94	c3iz8G_	Alignment	not modelled	98.6	14	PDB header: apoptosis Chain: G: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
95	c1vt4L_	Alignment	not modelled	98.6	14	PDB header: apoptosis Chain: L: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
96	c3iz8C_	Alignment	not modelled	98.6	14	PDB header: apoptosis Chain: C: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
97	c2qbyA_	Alignment	not modelled	98.5	17	PDB header: replication/dna Chain: A: PDB Molecule: cell division control protein 6 homolog 1; PDBTitle: crystal structure of a heterodimer of cdc6/orc1 initiators2 bound to origin dna (from s. solfataricus)
98	c1z6tC_	Alignment	not modelled	98.5	15	PDB header: apoptosis Chain: C: PDB Molecule: apoptotic protease activating factor 1; PDBTitle: structure of the apoptotic protease-activating factor 12 bound to adp
99	c1fnnB_	Alignment	not modelled	98.3	15	PDB header: cell cycle Chain: B: PDB Molecule: cell division control protein 6; PDBTitle: crystal structure of cdc6p from pyrobaculum aerophilum
100	c3te6A_	Alignment	not modelled	98.2	21	PDB header: gene regulation Chain: A: PDB Molecule: regulatory protein sir3; PDBTitle: crystal structure of the s. cerevisiae sir3 aaa+ domain
101	d1w5sa2	Alignment	not modelled	97.8	11	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
102	c2zamA_	Alignment	not modelled	97.4	22	PDB header: protein transport Chain: A: PDB Molecule: vacuolar protein sorting-associating protein 4b; PDBTitle: crystal structure of mouse skd1/vps4b apo-form
103	d1a5ta2	Alignment	not modelled	97.3	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
104	d1fnna2	Alignment	not modelled	97.3	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
105	c3b9pA_	Alignment	not modelled	97.3	21	PDB header: hydrolase Chain: A: PDB Molecule: cg5977-pa, isoform a; PDBTitle: spastin
						Fold: P-loop containing nucleoside triphosphate hydrolases

106	d1sxb2	Alignment	not modelled	97.2	18	Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
107	c4b4tj	Alignment	not modelled	97.1	24	PDB header: hydrolase Chain: J; PDB Molecule: 26s protease regulatory subunit 8 homolog; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
108	d1szpa2	Alignment	not modelled	97.0	12	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
109	d1jbka	Alignment	not modelled	97.0	30	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
110	c2chvE	Alignment	not modelled	96.9	17	PDB header: dna-binding protein Chain: E; PDB Molecule: replication factor c small subunit; PDBTitle: replication factor c adnpn complex
111	c2chgB	Alignment	not modelled	96.9	16	PDB header: dna-binding protein Chain: B; PDB Molecule: replication factor c small subunit; PDBTitle: replication factor c domains 1 and 2
112	c1xxhB	Alignment	not modelled	96.9	16	PDB header: transferase Chain: B; PDB Molecule: dna polymerase iii subunit gamma; PDBTitle: atpgs bound e. coli clamp loader complex
113	c3pvsA	Alignment	not modelled	96.9	15	PDB header: recombination Chain: A; PDB Molecule: replication-associated recombination protein a; PDBTitle: structure and biochemical activities of escherichia coli mgsa
114	c4b4tK	Alignment	not modelled	96.8	23	PDB header: hydrolase Chain: K; PDB Molecule: 26s protease regulatory subunit 6b homolog; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
115	c1jr3E	Alignment	not modelled	96.8	16	PDB header: transferase Chain: E; PDB Molecule: dna polymerase iii, delta' subunit; PDBTitle: crystal structure of the processivity clamp loader gamma2 complex of e. coli dna polymerase iii
116	c1sxE	Alignment	not modelled	96.8	15	PDB header: replication Chain: E; PDB Molecule: activator 1 40 kda subunit; PDBTitle: crystal structure of the eukaryotic clamp loader (replication factor2 c, rfc) bound to the dna sliding clamp (proliferating cell nuclear3 antigen, pcna)
117	d1r6bx2	Alignment	not modelled	96.8	27	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
118	c2p65A	Alignment	not modelled	96.8	26	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: hypothetical protein pf08_0063; PDBTitle: crystal structure of the first nucleotide binding domain of2 chaperone clpb1, putative, (pv089580) from plasmodium vivax
119	c4b4tL	Alignment	not modelled	96.7	22	PDB header: hydrolase Chain: L; PDB Molecule: 26s protease subunit rpt4; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
120	d1n0wa	Alignment	not modelled	96.7	12	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)