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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4nh0A_	 Alignment		100.0	40	PDB header: cell cycle Chain: A: PDB Molecule: cell divisionftsks/poiiii; PDBTitle: cytoplasmic domain of the thermomonospora curvata type vii secretion2 atpase eccc
2	c4n1aE_	 Alignment		100.0	37	PDB header: protein binding/protein binding Chain: E: PDB Molecule: cell divisionftsks/poiiii; PDBTitle: thermomonospora curvata eccc (atpases 2 and 3) in complex with a2 signal sequence peptide
3	c4lyaA_	 Alignment		100.0	18	PDB header: cell cycle Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: essc (atpases 2 and 3) from geobacillus thermodenitrificans (semet)
4	c2iuuE_	 Alignment		100.0	24	PDB header: membrane protein Chain: E: PDB Molecule: dna translocase ftsk; PDBTitle: p. aeruginosa ftsk motor domain, hexamer
5	c2iutA_	 Alignment		100.0	24	PDB header: membrane protein Chain: A: PDB Molecule: dna translocase ftsk; PDBTitle: p. aeruginosa ftsk motor domain, dimeric
6	c2iusB_	 Alignment		100.0	26	PDB header: membrane protein Chain: B: PDB Molecule: dna translocase ftsk; PDBTitle: e. coli ftsk motor domain
7	c4kfuC_	 Alignment		99.9	14	PDB header: hydrolase Chain: C: PDB Molecule: genome packaging ntpase b204; PDBTitle: structure of the genome packaging ntpase b204 from sulfolobus turreted2 icosahedral virus 2 in complex with amppcp
8	c4d2iB_	 Alignment		99.9	18	PDB header: hydrolase Chain: B: PDB Molecule: hera; PDBTitle: crystal structure of the hera hexameric dna translocase2 from sulfolobus solfataricus bound to amp-ppn
9	c4ag5A_	 Alignment		99.8	18	PDB header: hydrolase Chain: A: PDB Molecule: type iv secretory pathway virb4 components-like protein; PDBTitle: structure of virb4 of thermoanaerobacter pseudethanolicus
10	d1e9ra_	 Alignment		99.5	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
11	c6matE_	 Alignment		99.1	15	PDB header: ribosomal protein Chain: E: PDB Molecule: rix7 mutant; PDBTitle: cryo-em structure of the essential ribosome assembly aaa-atpase rix7

12	c5g4gF_	Alignment		99.1	15	PDB header: hydrolase Chain: F: PDB Molecule: vcp-like atpase; PDBTitle: structure of the atpgs-bound vat complex
13	c4ag5D_	Alignment		99.1	14	PDB header: hydrolase Chain: D: PDB Molecule: type iv secretory pathway virb4 components-like protein; PDBTitle: structure of virb4 of thermoanaerobacter pseudethanolicus
14	c3cf2B_	Alignment		98.9	15	PDB header: transport protein Chain: B: PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: structure of p97/vcp in complex with adp/amp-pnp
15	c3cf1C_	Alignment		98.9	15	PDB header: transport protein Chain: C: PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: structure of p97/vcp in complex with adp/adp.alfx
16	c5ifwB_	Alignment		98.8	16	PDB header: signaling protein Chain: B: PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: quantitative interaction mapping reveals an extended ubiquitin2 regulatory domain in aspl that disrupts functional p97 hexamers and3 induces cell death
17	c1u9iA_	Alignment		98.7	15	PDB header: circadian clock protein Chain: A: PDB Molecule: kaic; PDBTitle: crystal structure of circadian clock protein kaic with phosphorylation2 sites
18	c5jwqA_	Alignment		98.6	14	PDB header: transcription regulator Chain: A: PDB Molecule: circadian clock protein kinase kaic; PDBTitle: crystal structure of kaic s431e in complex with foldswitch-stabilized2 kaib from thermosynechococcus elongatus
19	c6b5cA_	Alignment		98.2	15	PDB header: cell cycle Chain: A: PDB Molecule: katanin p60 atpase-containing subunit a-like 1; PDBTitle: structural basis for katanin self-assembly
20	c1xwiA_	Alignment		98.1	16	PDB header: protein transport Chain: A: PDB Molecule: skd1 protein; PDBTitle: crystal structure of vps4b
21	c5vq9D_	Alignment	not modelled	98.1	15	PDB header: protein binding Chain: D: PDB Molecule: pachytene checkpoint protein 2 homolog; PDBTitle: structure of human trip13, apo form
22	c1yqtA_	Alignment	not modelled	98.0	14	PDB header: hydrolyase/translation Chain: A: PDB Molecule: rnase I inhibitor; PDBTitle: rnase-I inhibitor
23	c6opcF_	Alignment	not modelled	98.0	17	PDB header: motor protein Chain: F: PDB Molecule: cell division control protein 48; PDBTitle: cdc48 hexamer in a complex with substrate and shp1(ubx domain)
24	c4b4tj_	Alignment	not modelled	98.0	15	PDB header: hydrolase Chain: J: PDB Molecule: 26s protease regulatory subunit 8 homolog; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
25	c5udbD_	Alignment	not modelled	97.9	14	PDB header: replication Chain: D: PDB Molecule: origin recognition complex subunit 4; PDBTitle: structural basis of mcm2-7 replicative helicase loading by orc-cdc62 and cdt1
26	c4xgcE_	Alignment	not modelled	97.9	10	PDB header: dna binding protein Chain: E: PDB Molecule: origin recognition complex subunit 5; PDBTitle: crystal structure of the eukaryotic origin recognition complex
27	c3l0oA_	Alignment	not modelled	97.9	17	PDB header: hydrolase Chain: A: PDB Molecule: transcription termination factor rho; PDBTitle: structure of rna-free rho transcription termination factor from2 thermotoga maritima
28	d1nlfa_	Alignment	not modelled	97.9	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)

29	c4xguB_	Alignment	not modelled	97.9	13	PDB header: atp-binding protein Chain: B: PDB Molecule: putative pachytene checkpoint protein 2; PDBTitle: structure of c. elegans pch-2
30	c6epcJ_	Alignment	not modelled	97.9	13	PDB header: hydrolase Chain: J: PDB Molecule: 26s proteasome regulatory subunit 8; PDBTitle: ground state 26s proteasome (gs2)
31	c3b9pA_	Alignment	not modelled	97.8	16	PDB header: hydrolase Chain: A: PDB Molecule: cg5977-pa, isoform a; PDBTitle: spastin
32	c3d8bB_	Alignment	not modelled	97.8	21	PDB header: hydrolase Chain: B: PDB Molecule: fidgetin-like protein 1; PDBTitle: crystal structure of human fidgetin-like protein 1 in complex with adp
33	c4xgcD_	Alignment	not modelled	97.8	15	PDB header: dna binding protein Chain: D: PDB Molecule: origin recognition complex subunit 4; PDBTitle: crystal structure of the eukaryotic origin recognition complex
34	c4b4tK_	Alignment	not modelled	97.8	17	PDB header: hydrolase Chain: K: PDB Molecule: 26s protease regulatory subunit 6b homolog; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
35	c3j16B_	Alignment	not modelled	97.8	17	PDB header: ribosome Chain: B: PDB Molecule: rli1p; PDBTitle: models of ribosome-bound dom34p and rli1p and their ribosomal binding2 partners
36	c4z8xC_	Alignment	not modelled	97.8	22	PDB header: hydrolase Chain: C: PDB Molecule: atp-dependent zinc metalloprotease ftsh; PDBTitle: truncated ftsh from a. aeolicus
37	c2r2aB_	Alignment	not modelled	97.8	14	PDB header: toxin Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of n-terminal domain of zonular occludens toxin from2 neisseria meningitidis
38	c4b4tH_	Alignment	not modelled	97.8	18	PDB header: hydrolase Chain: H: PDB Molecule: 26s protease regulatory subunit 7 homolog; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
39	c3l0oB_	Alignment	not modelled	97.8	14	PDB header: hydrolase Chain: B: PDB Molecule: transcription termination factor rho; PDBTitle: structure of rna-free rho transcription termination factor from2 thermotoga maritima
40	c3bk7A_	Alignment	not modelled	97.8	18	PDB header: hydrolyase/translation Chain: A: PDB Molecule: abc transporter atp-binding protein; PDBTitle: structure of the complete abc1/rnaase-i inhibitor protein from2 pyrococcus abyssi
41	c6nyyC_	Alignment	not modelled	97.7	17	PDB header: translocase Chain: C: PDB Molecule: afg3-like protein 2; PDBTitle: human m-aaa protease afg3l2, substrate-bound
42	c5e7pA_	Alignment	not modelled	97.7	23	PDB header: hydrolase Chain: A: PDB Molecule: cell division control protein cdc48; PDBTitle: crystal structure of msmeq_0858 (uniprot a0qqs4), a aaa atpase.
43	c1s3sA_	Alignment	not modelled	97.7	17	PDB header: protein binding Chain: A: PDB Molecule: transitional endoplasmic reticulum atpase (ter) PDBTitle: crystal structure of aaa atpase p97/vcp nd1 in complex with2 p47 c
44	c2zamA_	Alignment	not modelled	97.7	19	PDB header: protein transport Chain: A: PDB Molecule: vacuolar protein sorting-associated protein 4b; PDBTitle: crystal structure of mouse skd1/vps4b apo-form
45	c4l16A_	Alignment	not modelled	97.7	16	PDB header: hydrolase Chain: A: PDB Molecule: fidgetin-like protein 1; PDBTitle: crystal structure of figl-1 aaa domain in complex with adp
46	c4b4tM_	Alignment	not modelled	97.7	16	PDB header: hydrolase Chain: M: PDB Molecule: 26s protease regulatory subunit 6a; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
47	c2dhrC_	Alignment	not modelled	97.7	23	PDB header: hydrolase Chain: C: PDB Molecule: ftsh; PDBTitle: whole cytosolic region of atp-dependent metalloprotease2 ftsh (g399l)
48	c5mpaL_	Alignment	not modelled	97.7	16	PDB header: hydrolase Chain: L: PDB Molecule: 26s protease subunit rpt4; PDBTitle: 26s proteasome in presence of atp (s2)
49	c5w0tA_	Alignment	not modelled	97.7	15	PDB header: hydrolase Chain: A: PDB Molecule: protein msp1; PDBTitle: crystal structure of monomeric msp1 from s. cerevisiae
50	c6hecH_	Alignment	not modelled	97.7	17	PDB header: hydrolase Chain: H: PDB Molecule: proteasome-activating nucleotidase; PDBTitle: pan-proteasome in state 4
51	c4kxfF_	Alignment	not modelled	97.7	23	PDB header: immune system Chain: F: PDB Molecule: nlr family card domain-containing protein 4; PDBTitle: crystal structure of nlrc4 reveals its autoinhibition mechanism
52	c3eihB_	Alignment	not modelled	97.7	16	PDB header: protein transport Chain: B: PDB Molecule: vacuolar protein sorting-associated protein 4; PDBTitle: crystal structure of s.cerevisiae vps4 in the presence of atpgammas
53	c2vyeA_	Alignment	not modelled	97.6	16	PDB header: hydrolase/dna Chain: A: PDB Molecule: replicative dna helicase; PDBTitle: crystal structure of the dna-c-ssdna complex
						PDB header: transport protein

54	c3hu2C_	Alignment	not modelled	97.6	17	Chain: C: PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: structure of p97 n-d1 r86a mutant in complex with atpgs
55	c5l3rC_	Alignment	not modelled	97.6	11	PDB header: protein transport Chain: C: PDB Molecule: signal recognition particle 54 kda protein, chloroplastic; PDBTitle: structure of the gtpase heterodimer of chloroplast srp54 and ftsy from2 arabidopsis thaliana
56	d1w5sa2	Alignment	not modelled	97.6	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
57	c3bh0A_	Alignment	not modelled	97.6	16	PDB header: replication Chain: A: PDB Molecule: dnab-like replicative helicase; PDBTitle: atpase domain of g40p
58	c5gjql_	Alignment	not modelled	97.6	15	PDB header: hydrolase Chain: L: PDB Molecule: 26s protease regulatory subunit 10b; PDBTitle: structure of the human 26s proteasome bound to usp14-ubal
59	c4b4tl_	Alignment	not modelled	97.6	15	PDB header: hydrolase Chain: L: PDB Molecule: 26s protease subunit rpt4; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
60	c4phtC_	Alignment	not modelled	97.5	30	PDB header: protein transport Chain: C: PDB Molecule: general secretory pathway protein e; PDBTitle: atpase gspe in complex with the cytoplasmic domain of gspl from the2 vibrio vulnificus type ii secretion system
61	d1p9ra_	Alignment	not modelled	97.5	29	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
62	c2ja1A_	Alignment	not modelled	97.5	17	PDB header: transferase Chain: A: PDB Molecule: thymidine kinase; PDBTitle: thymidine kinase from b. cereus with ttp bound as phosphate2 donor.
63	d1n0wa_	Alignment	not modelled	97.5	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
64	c1szpC_	Alignment	not modelled	97.5	19	PDB header: dna binding protein Chain: C: PDB Molecule: dna repair protein rad51; PDBTitle: a crystal structure of the rad51 filament
65	c1nsfA_	Alignment	not modelled	97.5	16	PDB header: protein transport Chain: A: PDB Molecule: n-ethylmaleimide sensitive factor; PDBTitle: d2 hexamerization domain of n-ethylmaleimide sensitive factor (nsf)
66	c5t0gA_	Alignment	not modelled	97.5	16	PDB header: hydrolase Chain: A: PDB Molecule: 26s protease regulatory subunit 7; PDBTitle: structural basis for dynamic regulation of the human 26s proteasome
67	c2v1uA_	Alignment	not modelled	97.5	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
68	c2ce7B_	Alignment	not modelled	97.5	20	PDB header: cell division protein Chain: B: PDB Molecule: cell division protein ftsh; PDBTitle: edta treated
69	c5kzfl_	Alignment	not modelled	97.5	16	PDB header: hydrolase Chain: J: PDB Molecule: proteasome-associated atpase; PDBTitle: crystal structure of near full-length hexameric mycobacterium2 tuberculosis proteasomal atpase mpa in apo form
70	c1xpuB_	Alignment	not modelled	97.5	17	PDB header: transcription/rna Chain: B: PDB Molecule: rho transcription termination factor; PDBTitle: structural mechanism of inhibition of the rho transcription2 termination factor by the antibiotic 5a-(3-formylphenylsulfanyl)-3 dihydrobicyclomyacin (fpdb)
71	c3bgwD_	Alignment	not modelled	97.5	17	PDB header: replication Chain: D: PDB Molecule: dnab-like replicative helicase; PDBTitle: the structure of a dnab-like replicative helicase and its interactions2 with primase
72	c1r6bX_	Alignment	not modelled	97.4	19	PDB header: hydrolase Chain: X: PDB Molecule: clpa protein; PDBTitle: high resolution crystal structure of clpa
73	d1d2na_	Alignment	not modelled	97.4	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
74	c3ldaA_	Alignment	not modelled	97.4	16	PDB header: dna binding protein Chain: A: PDB Molecule: dna repair protein rad51; PDBTitle: yeast rad51 h352y filament interface mutant
75	c3vfdA_	Alignment	not modelled	97.4	21	PDB header: hydrolase Chain: A: PDB Molecule: spastin; PDBTitle: human spastin aaa domain
76	c6epdM_	Alignment	not modelled	97.4	17	PDB header: hydrolase Chain: M: PDB Molecule: 26s proteasome regulatory subunit 6a; PDBTitle: substrate processing state 26s proteasome (sps1)
77	c5wc0D_	Alignment	not modelled	97.4	19	PDB header: motor protein Chain: D: PDB Molecule: meiotic spindle formation protein mei-1; PDBTitle: katanin hexamer in spiral conformation
78	c3cmvG_	Alignment	not modelled	97.4	17	PDB header: recombination Chain: G: PDB Molecule: protein reca; PDBTitle: mechanism of homologous recombination from the reca-ssdna/dsdna2 structures
79	c5ujmE_	Alignment	not modelled	97.4	14	PDB header: replication Chain: E: PDB Molecule: origin recognition complex subunit 5; PDBTitle: structure of the active form of human origin recognition complex and2 its atpase motor module
80	c4nnpA_	Alignment	not modelled	97.4	22	PDB header: replication Chain: A: PDB Molecule: replicative dna helicase;

80	c9mm7A	Alignment	not modelled	97.4	22	PDBTitle: aquifex aeolicus replicative helicase (dnab) complexed with adp, at2 3.3 resolution
81	c6qe1B	Alignment	not modelled	97.3	20	PDB header: replication Chain: B: PDB Molecule: replicative dna helicase; PDBTitle: e. coli dnabc apo complex
82	c1iy2A	Alignment	not modelled	97.3	17	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent metalloprotease ftsh; PDBTitle: crystal structure of the ftsh atpase domain from thermus2 thermophilus
83	c5uj7C	Alignment	not modelled	97.3	14	PDB header: dna binding protein Chain: C: PDB Molecule: origin recognition complex subunit 4; PDBTitle: structure of the active form of human origin recognition complex2 atpase motor module, complex subunits 1, 4, 5
84	d1u94a1	Alignment	not modelled	97.3	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
85	c2q6tB	Alignment	not modelled	97.3	17	PDB header: hydrolase Chain: B: PDB Molecule: dnab replication fork helicase; PDBTitle: crystal structure of the thermus aquaticus dnab monomer
86	c5udbE	Alignment	not modelled	97.3	12	PDB header: replication Chain: E: PDB Molecule: origin recognition complex subunit 5; PDBTitle: structural basis of mcm2-7 replicative helicase loading by orc-cdc62 and cdt1
87	c2eyuA	Alignment	not modelled	97.3	26	PDB header: protein transport Chain: A: PDB Molecule: twitching motility protein pilt; PDBTitle: the crystal structure of the c-terminal domain of aquifex2 aeolicus pilt
88	d2i1qa2	Alignment	not modelled	97.3	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
89	d1xpua3	Alignment	not modelled	97.3	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
90	d1w36d1	Alignment	not modelled	97.3	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
91	d1tf7a2	Alignment	not modelled	97.3	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
92	c4ydsA	Alignment	not modelled	97.2	15	PDB header: hydrolase Chain: A: PDB Molecule: flagella-related protein h; PDBTitle: flah from sulfobolbus acidocaldarius with atp and mg-ion
93	d2ce7a2	Alignment	not modelled	97.2	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
94	c5vy9C	Alignment	not modelled	97.2	16	PDB header: chaperone Chain: C: PDB Molecule: heat shock protein 104; PDBTitle: s. cerevisiae hsp104:casein complex, middle domain conformation
95	c4b4tl	Alignment	not modelled	97.2	17	PDB header: hydrolase Chain: I: PDB Molecule: 26s protease regulatory subunit 4 homolog; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
96	c2r65A	Alignment	not modelled	97.2	16	PDB header: hydrolase Chain: A: PDB Molecule: cell division protease ftsh homolog; PDBTitle: crystal structure of helicobacter pylori atp dependent protease, ftsh2 adp complex
97	c5tshF	Alignment	not modelled	97.2	27	PDB header: atp-binding protein Chain: F: PDB Molecule: type iv pilus biogenesis atpase pilb; PDBTitle: pilb from geobacter metallireducens bound to amp-pnp
98	c5l3qB	Alignment	not modelled	97.2	17	PDB header: protein transport Chain: B: PDB Molecule: signal recognition particle receptor subunit alpha; PDBTitle: structure of the gtpase heterodimer of human srp54 and sralpha
99	c4lcbA	Alignment	not modelled	97.2	14	PDB header: protein transport Chain: A: PDB Molecule: cell division protein cdvc, vps4; PDBTitle: structure of vps4 homolog from acidianus hospitalis
100	c2j7pA	Alignment	not modelled	97.2	14	PDB header: signal recognition Chain: A: PDB Molecule: signal recognition particle protein; PDBTitle: gmppnp-stabilized ng domain complex of the srp gtpases ffh2 and ftsy
101	d1fnna2	Alignment	not modelled	97.2	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
102	c1q57G	Alignment	not modelled	97.2	14	PDB header: transferase Chain: G: PDB Molecule: dna primase/helicase; PDBTitle: the crystal structure of the bifunctional primase-helicase of2 bacteriophage t7
103	c4ypnA	Alignment	not modelled	97.2	18	PDB header: hydrolase Chain: A: PDB Molecule: lon protease; PDBTitle: crystal structure of a lon fragment containing the 3-helix bundle and2 the aaa-alpha/beta domain
104	c3sylB	Alignment	not modelled	97.1	15	PDB header: chaperone Chain: B: PDB Molecule: protein cbbx; PDBTitle: crystal structure of the aaa+ protein cbbx, native structure
105	c2hcbC	Alignment	not modelled	97.1	15	PDB header: replication Chain: C: PDB Molecule: chromosomal replication initiator protein dnaa; PDBTitle: structure of amppcc-bound dnaa from aquifex aeolicus
106	d2qy9a2	Alignment	not modelled	97.1	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases

						Family: Nitrogenase iron protein-like
107	c3pvsA_	Alignment	not modelled	97.1	24	PDB header: recombination Chain: A: PDB Molecule: replication-associated recombination protein a; PDBTitle: structure and biochemical activities of escherichia coli mgsa
108	d1skyb3	Alignment	not modelled	97.1	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
109	c2kjqA_	Alignment	not modelled	97.1	23	PDB header: replication Chain: A: PDB Molecule: dnaa-related protein; PDBTitle: solution structure of protein nmb1076 from neisseria meningitidis.2 northeast structural genomics consortium target mr101b.
110	c6gefB_	Alignment	not modelled	97.1	20	PDB header: hydrolase Chain: B: PDB Molecule: type iv secretion system protein dotb; PDBTitle: x-ray structure of the yersinia pseudotuberculosis atpase dotb
111	c6az0A_	Alignment	not modelled	97.1	19	PDB header: hydrolase Chain: A: PDB Molecule: mitochondrial inner membrane i-aaa protease supercomplex PDBTitle: mitochondrial atpase protease yme1
112	c4kxfP_	Alignment	not modelled	97.1	17	PDB header: immune system Chain: P: PDB Molecule: nlr family card domain-containing protein 4; PDBTitle: crystal structure of nlr4 reveals its autoinhibition mechanism
113	c4a1fB_	Alignment	not modelled	97.0	23	PDB header: hydrolase Chain: B: PDB Molecule: replicative dna helicase; PDBTitle: crystal structure of c-terminal domain of helicobacter2 pylori dnab helicase
114	c6bbmA_	Alignment	not modelled	97.0	21	PDB header: replication Chain: A: PDB Molecule: replicative dna helicase; PDBTitle: mechanisms of opening and closing of the bacterial replicative2 helicase: the dnab helicase and lambda p helicase loader complex
115	c5x06G_	Alignment	not modelled	97.0	17	PDB header: replication Chain: G: PDB Molecule: dnaa regulatory inactivator hda; PDBTitle: dna replication regulation protein
116	d1mo6a1	Alignment	not modelled	97.0	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
117	d2jdia3	Alignment	not modelled	97.0	11	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
118	c4wiaA_	Alignment	not modelled	97.0	15	PDB header: atp-binding protein Chain: A: PDB Molecule: putative flagella-related protein h; PDBTitle: crystal structure of flagellar accessory protein flah from2 methanocaldococcus jannaschii
119	c3te6A_	Alignment	not modelled	97.0	11	PDB header: gene regulation Chain: A: PDB Molecule: regulatory protein sir3; PDBTitle: crystal structure of the s. cerevisiae sir3 aaa+ domain
120	d1xp8a1	Alignment	not modelled	97.0	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)