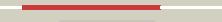
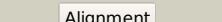
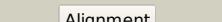
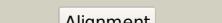
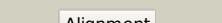


Phyre²

Email	mdejesus@rockefeller.edu
Description	RVBD2008c_(-)_2256625_2257950
Date	Mon Aug 5 13:25:11 BST 2019
Unique Job ID	59af98a18b32d80f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2fnaA_			99.6	20	PDB header: atp-binding protein Chain: A: PDB Molecule: conserved hypothetical protein; PDBTitle: crystal structure of an archaeal aaa+ atpase (sso1545) from sulfolobus2 solfataricus p2 at 2.00 a resolution
2	c2genA_			99.4	18	PDB header: unknown function Chain: A: PDB Molecule: walker-type atpase; PDBTitle: the walker-type atpase paby2304 of pyrococcus abyssi
3	d2fnna2			99.2	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
4	c3pfB_			99.0	16	PDB header: hydrolase Chain: B: PDB Molecule: holliday junction atp-dependent dna helicase ruvb; PDBTitle: 2.7 angstrom resolution crystal structure of a probable holliday2 junction dna helicase (ruvb) from campylobacter jejuni subsp. jejuni3 nctc 11168 in complex with adenosine-5'-diphosphate
5	c1in8A_			98.9	19	PDB header: dna binding protein Chain: A: PDB Molecule: holliday junction dna helicase ruvb; PDBTitle: thermotoga maritima ruvb t158v
6	c2v1uA_			98.8	19	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
7	c4xgcA_			98.8	10	PDB header: dna binding protein Chain: A: PDB Molecule: origin recognition complex subunit 1; PDBTitle: crystal structure of the eukaryotic origin recognition complex
8	c4uxjB_			98.7	21	PDB header: transferase Chain: B: PDB Molecule: thymidine kinase; PDBTitle: leishmania major thymidine kinase in complex with dttp
9	c6blbA_			98.7	17	PDB header: hydrolase Chain: A: PDB Molecule: holliday junction atp-dependent dna helicase ruvb; PDBTitle: 1.88 angstrom resolution crystal structure holliday junction atp-2 dependent dna helicase (ruvb) from pseudomonas aeruginosa in complex3 with adp
10	c5ujmE_			98.7	17	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
11	d1xbta1			98.7	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Type II thymidine kinase

12	c3pvsA		Alignment		98.7	18	PDB header: recombination Chain: A; PDB Molecule: replication-associated recombination protein a; PDBTitle: structure and biochemical activities of escherichia coli mgsa
13	c2qbyA		Alignment		98.7	12	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)
14	c3iz8B		Alignment		98.6	18	PDB header: apoptosis Chain: B; PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
15	c3iz8E		Alignment		98.6	18	PDB header: apoptosis Chain: E; PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
16	c1vt4N		Alignment		98.6	18	PDB header: apoptosis Chain: N; PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
17	c3iz8H		Alignment		98.6	18	PDB header: apoptosis Chain: H; PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
18	c1vt4J		Alignment		98.6	18	PDB header: apoptosis Chain: J; PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
19	c1vt4M		Alignment		98.6	18	PDB header: apoptosis Chain: M; PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
20	c1vt4O		Alignment		98.6	18	PDB header: apoptosis Chain: O; PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
21	c3iz8D		Alignment	not modelled	98.6	18	PDB header: apoptosis Chain: D; PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
22	c1vt4K		Alignment	not modelled	98.6	18	PDB header: apoptosis Chain: K; PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
23	c3iz8G		Alignment	not modelled	98.6	18	PDB header: apoptosis Chain: G; PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
24	c3iz8F		Alignment	not modelled	98.6	18	PDB header: apoptosis Chain: F; PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
25	c3iz8C		Alignment	not modelled	98.6	18	PDB header: apoptosis Chain: C; PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
26	c1vt4P		Alignment	not modelled	98.6	18	PDB header: apoptosis Chain: P; PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
27	c1vt4I		Alignment	not modelled	98.6	18	PDB header: apoptosis Chain: I; PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
28	c3iz8A		Alignment	not modelled	98.6	18	PDB header: apoptosis Chain: A; PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
29	c1vt4L		Alignment	not modelled	98.6	18	PDB header: apoptosis Chain: L; PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome

30	c2qbyB	Alignment	not modelled	98.6	13	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)
31	c1ojID	Alignment	not modelled	98.6	16	PDB header: response regulator Chain: D: PDB Molecule: transcriptional regulatory protein zrar; PDBTitle: crystal structure of a sigma54-activator suggests the mechanism for the conformational switch necessary for sigma54 binding
32	c4xgcE	Alignment	not modelled	98.5	21	PDB header: dna binding protein Chain: E: PDB Molecule: origin recognition complex subunit 5; PDBTitle: crystal structure of the eukaryotic origin recognition complex
33	c5udb9	Alignment	not modelled	98.5	10	PDB header: replication Chain: 9: PDB Molecule: cell division control protein 6; PDBTitle: structural basis of mcm2-7 replicative helicase loading by orc-cdc62 and cdt1
34	c6mfvC	Alignment	not modelled	98.5	20	PDB header: signaling protein Chain: C: PDB Molecule: tetratricopeptide repeat sensor ph0952; PDBTitle: crystal structure of the signal transduction atpase with numerous2 domains (stand) protein with a tetratricopeptide repeat sensor ph09523 from pyrococcus horikoshii
35	c1sxjC	Alignment	not modelled	98.5	19	PDB header: replication Chain: C: 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)
36	d1jbka	Alignment	not modelled	98.4	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
37	c1xxhB	Alignment	not modelled	98.4	22	PDB header: transferase Chain: B: PDB Molecule: dna polymerase iii subunit gamma; PDBTitle: atpgs bound e. coli clamp loader complex
38	c1sxjE	Alignment	not modelled	98.4	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)
39	c1sxjA	Alignment	not modelled	98.4	16	PDB header: replication Chain: A: PDB Molecule: activator 1 95 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)
40	c4xgcD	Alignment	not modelled	98.4	25	PDB header: dna binding protein Chain: D: PDB Molecule: origin recognition complex subunit 4; PDBTitle: crystal structure of the eukaryotic origin recognition complex
41	c2chgB	Alignment	not modelled	98.3	16	PDB header: dna-binding protein Chain: B: PDB Molecule: replication factor c small subunit; PDBTitle: replication factor c domains 1 and 2
42	c5kneA	Alignment	not modelled	98.3	18	PDB header: chaperone Chain: A: PDB Molecule: heat shock protein 104; PDBTitle: cryoem reconstruction of hsp104 hexamer
43	d1qvra2	Alignment	not modelled	98.3	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
44	c1sxjB	Alignment	not modelled	98.3	19	PDB header: replication Chain: B: PDB Molecule: activator 1 37 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)
45	c5e7pA	Alignment	not modelled	98.3	17	PDB header: hydrolase Chain: A: PDB Molecule: cell division control protein cdc48; PDBTitle: crystal structure of msmeg_0858 (uniprot a0qq54), a aaa atpase.
46	c6djua	Alignment	not modelled	98.3	16	PDB header: chaperone Chain: A: PDB Molecule: chaperone protein clpb; PDBTitle: mtb clpb in complex with atpgammas and casein, conformer 1
47	c4b4tl	Alignment	not modelled	98.3	16	PDB header: hydrolase Chain: I: PDB Molecule: 26s protease regulatory subunit 4 homolog; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
48	c5uj7B	Alignment	not modelled	98.3	14	PDB header: dna binding protein Chain: B: PDB Molecule: origin recognition complex subunit 1; PDBTitle: structure of the active form of human origin recognition complex2 atpase motor module, complex subunits 1, 4, 5
49	c1fnnB	Alignment	not modelled	98.3	21	PDB header: cell cycle Chain: B: PDB Molecule: cell division control protein 6; PDBTitle: crystal structure of cdc6p from pyrobaculum aerophilum
50	c5m7nA	Alignment	not modelled	98.3	20	PDB header: signaling protein Chain: A: PDB Molecule: nitrogen assimilation regulatory protein; PDBTitle: crystal structure of ntrx from brucella abortus in complex with atp2 processed with the crystallidirect automated mounting and cryo-cooling3 technology
51	c1jr3E	Alignment	not modelled	98.2	15	PDB header: transferase Chain: E: PDB Molecule: dna polymerase iii, delta' subunit; PDBTitle: crystal structure of the processivity clamp loader gamma complex of e.2 coli dna polymerase iii
52	c3nbX	Alignment	not modelled	98.2	17	PDB header: hydrolase Chain: X: PDB Molecule: atpase rava; PDBTitle: crystal structure of e. coli rava (regulatory atpase variant a) in2 complex with adp
53	d1qvra3	Alignment	not modelled	98.2	23	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
						PDB header: hydrolase

54	c1hqcB	Alignment	not modelled	98.2	20	Chain: B: PDB Molecule: ruvb; PDBTitle: structure of ruvb from thermus thermophilus hb8
55	c5w0tA	Alignment	not modelled	98.2	18	PDB header: hydrolase Chain: A: PDB Molecule: protein msp1; PDBTitle: crystal structure of monomeric msp1 from s. cerevisiae
56	c4z8xC	Alignment	not modelled	98.2	21	PDB header: hydrolase Chain: C: PDB Molecule: atp-dependent zinc metalloprotease ftsh; PDBTitle: truncated ftsh from a. aeolicus
57	d1r6bx2	Alignment	not modelled	98.2	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
58	c2x8aA	Alignment	not modelled	98.2	17	PDB header: nuclear protein Chain: A: PDB Molecule: nuclear valosin-containing protein-like; PDBTitle: human nuclear valosin containing protein like (nvl), c-2 terminal aaa-atpase domain
59	c4ciuA	Alignment	not modelled	98.2	22	PDB header: chaperone Chain: A: PDB Molecule: chaperone protein clpb; PDBTitle: crystal structure of e. coli clpb
60	c5uj7C	Alignment	not modelled	98.2	18	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
61	c3hu2C	Alignment	not modelled	98.2	21	PDB header: transport protein Chain: C: PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: structure of p97 n-d1 r86a mutant in complex with atpgs
62	c2chvE	Alignment	not modelled	98.2	17	PDB header: dna-binding protein Chain: E: PDB Molecule: replication factor c small subunit; PDBTitle: replication factor c adpnp complex
63	c1qvrB	Alignment	not modelled	98.2	21	PDB header: chaperone Chain: B: PDB Molecule: clpb protein; PDBTitle: crystal structure analysis of clpb
64	c1s3sA	Alignment	not modelled	98.1	23	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
65	d1sxjc2	Alignment	not modelled	98.1	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
66	c2dhrC	Alignment	not modelled	98.1	24	PDB header: hydrolase Chain: C: PDB Molecule: ftsh; PDBTitle: whole cytosolic region of atp-dependent metalloprotease2 ftsh (g399i)
67	c6azyA	Alignment	not modelled	98.1	16	PDB header: chaperone Chain: A: PDB Molecule: heat shock protein hsp104; PDBTitle: crystal structure of hsp104 r328m/r757m mutant from calcarisporiella2 thermophila
68	d1sxje2	Alignment	not modelled	98.1	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
69	c2hcbC	Alignment	not modelled	98.1	18	PDB header: replication Chain: C: PDB Molecule: chromosomal replication initiator protein dnaa; PDBTitle: structure of amppcp-bound dnaa from aquifex aeolicus
70	d1ny5a2	Alignment	not modelled	98.1	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
71	c5vy9C	Alignment	not modelled	98.1	18	PDB header: chaperone Chain: C: PDB Molecule: heat shock protein 104; PDBTitle: s. cerevisiae hsp104:casein complex, middle domain conformation
72	c3zw6B	Alignment	not modelled	98.1	17	PDB header: photosynthesis Chain: B: PDB Molecule: ribulose bisphosphate carboxylase/oxygenase activase 1, PDBTitle: model of hexameric aaa domain arrangement of green-type rubisco2 activase from tobacco.
73	c4ypnA	Alignment	not modelled	98.1	24	PDB header: hydrolase Chain: A: PDB Molecule: ion protease; PDBTitle: crystal structure of a lona fragment containing the 3-helix bundle and2 the aaa-alpha/beta domain
74	c4d2qC	Alignment	not modelled	98.1	22	PDB header: chaperone Chain: C: PDB Molecule: clpb; PDBTitle: negative-stain electron microscopy of e. coli clpb mutant e432a (bap2 form bound to clpb)
75	c6b5cA	Alignment	not modelled	98.1	14	PDB header: cell cycle Chain: A: PDB Molecule: katanin p60 atpase-containing subunit a-like 1; PDBTitle: structural basis for katanin self-assembly
76	c5x06G	Alignment	not modelled	98.1	20	PDB header: replication Chain: G: PDB Molecule: dnaa regulatory inactivator hda; PDBTitle: dna replication regulation protein
77	c2p65A	Alignment	not modelled	98.1	18	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
78	c3b9pA	Alignment	not modelled	98.1	20	PDB header: hydrolase Chain: A: PDB Molecule: cg5977-pa, isoform a; PDBTitle: spastin
79	c2qz4A	Alignment	not modelled	98.1	21	PDB header: hydrolase Chain: A: PDB Molecule: paraplegin; PDBTitle: human paraplegin, aaa domain in complex with adp
80	c6az0A	Alignment	not modelled	98.1	22	PDB header: hydrolase Chain: A: PDB Molecule: mitochondrial inner membrane i-aaa protease supercomplex

					PDBTitle: mitochondrial atpase protease yme1
81	c3cf2B	Alignment	not modelled	98.1	PDB header: transport protein Chain: B: PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: structure of p97/vcp in complex with adp/amp-pnp
82	c5d4wB	Alignment	not modelled	98.1	PDB header: chaperone Chain: B: PDB Molecule: putative heat shock protein; PDBTitle: crystal structure of hsp104
83	c3u5zM	Alignment	not modelled	98.1	PDB header: dna binding protein/dna Chain: M: PDB Molecule: dna polymerase accessory protein 44; PDBTitle: structure of t4 bacteriophage clamp loader bound to the t4 clamp,2 primer-template dna, and atp analog
84	c5udbA	Alignment	not modelled	98.1	PDB header: replication Chain: A: PDB Molecule: origin recognition complex subunit 1; PDBTitle: structural basis of mcm2-7 replicative helicase loading by orc-cdc62 and cdt1
85	d1iqpa2	Alignment	not modelled	98.1	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
86	c5ifwB	Alignment	not modelled	98.1	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
87	d1l8qa2	Alignment	not modelled	98.1	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
88	c5oafB	Alignment	not modelled	98.1	PDB header: gene regulation Chain: B: PDB Molecule: rvvb-like 2; PDBTitle: human rvb1/rvb2 heterohexamer in ino80 complex
89	c1r6bx	Alignment	not modelled	98.0	PDB header: hydrolase Chain: X: PDB Molecule: cipa protein; PDBTitle: high resolution crystal structure of cipa
90	c5lkmB	Alignment	not modelled	98.0	PDB header: dna binding protein Chain: B: PDB Molecule: dna repair protein rada; PDBTitle: rada bound to dtdp
91	d1lin4a2	Alignment	not modelled	98.0	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
92	c6nyyC	Alignment	not modelled	98.0	PDB header: translocase Chain: C: PDB Molecule: afg3-like protein 2; PDBTitle: human m-aaa protease afg3l2, substrate-bound
93	d1nifa	Alignment	not modelled	98.0	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
94	d1g41a	Alignment	not modelled	98.0	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
95	d1ixza	Alignment	not modelled	98.0	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
96	c1iqpF	Alignment	not modelled	98.0	PDB header: replication Chain: F: PDB Molecule: rfc5; PDBTitle: crystal structure of the clamp loader small subunit from2 pyrococcus furiosus
97	c5SudbE	Alignment	not modelled	98.0	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
98	c6djvE	Alignment	not modelled	98.0	PDB header: chaperone Chain: E: PDB Molecule: chaperone protein clpb; PDBTitle: mtb clpb in complex with atpgamma and casein, conformer 2
99	c5kneF	Alignment	not modelled	98.0	PDB header: chaperone Chain: F: PDB Molecule: heat shock protein 104; PDBTitle: cryoem reconstruction of hsp104 hexamer
100	d1sxja2	Alignment	not modelled	98.0	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
101	c3cf1C	Alignment	not modelled	98.0	PDB header: transport protein Chain: C: PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: structure of p97/vcp in complex with adp/adp.alfx
102	c6em8F	Alignment	not modelled	98.0	PDB header: chaperone Chain: F: PDB Molecule: atp-dependent clp protease atp-binding subunit clpc; PDBTitle: s.aureus clpc resting state, c2 symmetrised
103	d1sxjb2	Alignment	not modelled	98.0	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
104	c5mpaL	Alignment	not modelled	98.0	PDB header: hydrolase Chain: L: PDB Molecule: 26s protease subunit rpt4; PDBTitle: 26s proteasome in presence of atp (s2)
105	c2z4rb	Alignment	not modelled	98.0	PDB header: dna binding protein Chain: B: PDB Molecule: chromosomal replication initiator protein dnaa; PDBTitle: crystal structure of domain iii from the thermotoga2 maritima replication initiation protein dnaa
106	c3pxiB	Alignment	not modelled	98.0	PDB header: protein binding Chain: B: PDB Molecule: negative regulator of genetic competence clpc/meccb; PDBTitle: structure of meca108:clpc
					Fold: P-loop containing nucleoside triphosphate hydrolases

107	d1e32a2	Alignment	not modelled	98.0	21	Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
108	c1nsfA	Alignment	not modelled	98.0	18	PDB header: protein transport Chain: A: PDB Molecule: n-ethylmaleimide sensitive factor; PDBTitle: d2 hexamerization domain of n-ethylmaleimide sensitive factor (nsf)
109	c6s2pN	Alignment	not modelled	97.9	17	PDB header: plant protein Chain: N: PDB Molecule: rc1; PDBTitle: structure of the nb-arc domain from the tomato immune receptor nrc1
110	d1fnna2	Alignment	not modelled	97.9	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
111	c4b4tj	Alignment	not modelled	97.9	17	PDB header: hydrolase Chain: J: PDB Molecule: 26s protease regulatory subunit 8 homolog; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
112	c3hteC	Alignment	not modelled	97.9	24	PDB header: motor protein Chain: C: PDB Molecule: atp-dependent clp protease atp-binding subunit clpx; PDBTitle: crystal structure of nucleotide-free hexameric clpx
113	c4b4tH	Alignment	not modelled	97.9	22	PDB header: hydrolase Chain: H: PDB Molecule: 26s protease regulatory subunit 7 homolog; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
114	c4l16A	Alignment	not modelled	97.9	22	PDB header: hydrolase Chain: A: PDB Molecule: fidgetin-like protein 1; PDBTitle: crystal structure of figl-1 aaa domain in complex with adp
115	c5j1sA	Alignment	not modelled	97.9	22	PDB header: hydrolase Chain: A: PDB Molecule: torsin-1a; PDBTitle: torsina-lull1 complex, h. sapiens, bound to vhh-bs2
116	c6e111	Alignment	not modelled	97.9	23	PDB header: protein transport Chain: 1: PDB Molecule: heat shock protein 101; PDBTitle: ptx core complex in the resetting (compact) state
117	c4b4tl	Alignment	not modelled	97.9	17	PDB header: hydrolase Chain: L: PDB Molecule: 26s protease subunit rpt4; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
118	c2r44A	Alignment	not modelled	97.9	16	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative atpase (chu_0153) from cytophaga2 hutchinsonii atcc 33406 at 2.00 a resolution
119	d1d2na	Alignment	not modelled	97.9	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
120	c1w4rC	Alignment	not modelled	97.9	18	PDB header: transferase Chain: C: PDB Molecule: thymidine kinase; PDBTitle: structure of a type ii thymidine kinase with bound dttp