





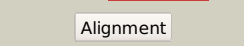

















Phyre2

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Description	RVBD3868 (-) _4343492_4345213
Date	Sat Aug 10 22:05:05 BST 2019
Unique Job ID	1a8651670af6f876

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3sylB_	 Alignment		100.0	37	PDB header: chaperone Chain: B; PDB Molecule: protein cbbx; PDBTitle: crystal structure of the aaa+ protein cbbx, native structure
2	c5e7pA_	 Alignment		100.0	20	PDB header: hydrolase Chain: A; PDB Molecule: cell division control protein cdc48; PDBTitle: crystal structure of msmeg_0858 (uniprot a0qqs4), a aaa atpase.
3	c6matE_	 Alignment		100.0	24	PDB header: ribosomal protein Chain: E; PDB Molecule: rix7 mutant; PDBTitle: cryo-em structure of the essential ribosome assembly aaa-atpase rix7
4	c5g4gF_	 Alignment		100.0	20	PDB header: hydrolase Chain: F; PDB Molecule: vcvp-like atpase; PDBTitle: structure of the atpgs-bound vat complex
5	c3cf1C_	 Alignment		100.0	19	PDB header: transport protein Chain: C; PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: structure of p97/vcp in complex with adp/adp.alfx
6	c4f3vB_	 Alignment		100.0	100	PDB header: protein transport Chain: B; PDB Molecule: esx-1 secretion system protein eccA1; PDBTitle: crystal structure of n-terminal domain of eccA1 atpase from esx-12 secretion system of mycobacterium tuberculosis
7	c3hu2C_	 Alignment		100.0	22	PDB header: transport protein Chain: C; PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: structure of p97 n-d1 r86a mutant in complex with atpgs
8	c6nyyC_	 Alignment		100.0	23	PDB header: translocase Chain: C; PDB Molecule: afg3-like protein 2; PDBTitle: human m-aaa protease afg3l2, substrate-bound
9	c6epdM_	 Alignment		100.0	24	PDB header: hydrolase Chain: M; PDB Molecule: 26s proteasome regulatory subunit 6a; PDBTitle: substrate processing state 26s proteasome (sps1)
10	c6genX_	 Alignment		100.0	30	PDB header: nuclear protein Chain: X; PDB Molecule: ruvb-like protein 1; PDBTitle: chromatin remodeller-nucleosome complex at 4.5 a resolution.
11	c5kzfj_	 Alignment		100.0	19	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

12	c2dhrC_	Alignment		100.0	25	PDB header: hydrolase Chain: C: PDB Molecule: ftsh; PDBTitle: whole cytosolic region of atp-dependent metalloprotease2 ftsh (g399l)
13	c1s3sA_	Alignment		100.0	22	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
14	c1xwiA_	Alignment		100.0	21	PDB header: protein transport Chain: A: PDB Molecule: skd1 protein; PDBTitle: crystal structure of vps4b
15	c4b4tH_	Alignment		100.0	20	PDB header: hydrolase Chain: H: PDB Molecule: 26s protease regulatory subunit 7 homolog; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
16	c3eihB_	Alignment		100.0	21	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
17	c4l16A_	Alignment		100.0	26	PDB header: hydrolase Chain: A: PDB Molecule: figletin-like protein 1; PDBTitle: crystal structure of figl-1 aaa domain in complex with adp
18	c6epcJ_	Alignment		100.0	21	PDB header: hydrolase Chain: J: PDB Molecule: 26s proteasome regulatory subunit 8; PDBTitle: ground state 26s proteasome (gs2)
19	c4b4tI_	Alignment		100.0	20	PDB header: hydrolase Chain: I: PDB Molecule: 26s protease regulatory subunit 4 homolog; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
20	c5ifwB_	Alignment		100.0	21	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
21	c3b9pA_	Alignment	not modelled	100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: cg5977-pa, isoform a; PDBTitle: spastin
22	c6az0A_	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: mitochondrial inner membrane i-aaa protease supercomplex PDBTitle: mitochondrial atpase protease yme1
23	c4b4tJ_	Alignment	not modelled	100.0	22	PDB header: hydrolase Chain: J: PDB Molecule: 26s protease regulatory subunit 8 homolog; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
24	c4b4tL_	Alignment	not modelled	100.0	23	PDB header: hydrolase Chain: L: PDB Molecule: 26s protease subunit rpt4; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
25	c6hecH_	Alignment	not modelled	100.0	24	PDB header: hydrolase Chain: H: PDB Molecule: proteasome-activating nucleotidase; PDBTitle: pan-proteasome in state 4
26	c6nyyA_	Alignment	not modelled	100.0	21	PDB header: translocase Chain: A: PDB Molecule: afg3-like protein 2; PDBTitle: human m-aaa protease afg3l2, substrate-bound
27	c4b4tM_	Alignment	not modelled	100.0	23	PDB header: hydrolase Chain: M: PDB Molecule: 26s protease regulatory subunit 6a; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
28	c4b4tK_	Alignment	not modelled	100.0	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
29	c5w0tA	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: A: PDB Molecule: protein msp1; PDBTitle: crystal structure of monomeric msp1 from s. cerevisiae
30	c4z8xC	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: C: PDB Molecule: atp-dependent zinc metalloprotease ftsh; PDBTitle: truncated ftsh from a. aeolicus
31	c5gjqL	Alignment	not modelled	100.0	22	PDB header: hydrolase Chain: L: PDB Molecule: 26s protease regulatory subunit 10b; PDBTitle: structure of the human 26s proteasome bound to usp14-ubal
32	c5mpaL	Alignment	not modelled	100.0	24	PDB header: hydrolase Chain: L: PDB Molecule: 26s protease subunit rpt4; PDBTitle: 26s proteasome in presence of atp (s2)
33	c5t0gA	Alignment	not modelled	100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: 26s protease regulatory subunit 7; PDBTitle: structural basis for dynamic regulation of the human 26s proteasome
34	c3cf2B	Alignment	not modelled	100.0	22	PDB header: transport protein Chain: B: PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: structure of p97/vcp in complex with adp/amp-pnp
35	c2ce7B	Alignment	not modelled	100.0	25	PDB header: cell division protein Chain: B: PDB Molecule: cell division protein ftsh; PDBTitle: edta treated
36	c2zamA	Alignment	not modelled	100.0	19	PDB header: protein transport Chain: A: PDB Molecule: vacuolar protein sorting-associated protein 4b; PDBTitle: crystal structure of mouse skd1/vps4b apo-form
37	c3d8bB	Alignment	not modelled	100.0	23	PDB header: hydrolase Chain: B: PDB Molecule: fidgetin-like protein 1; PDBTitle: crystal structure of human fidgetin-like protein 1 in complex with adp
38	c6b5cA	Alignment	not modelled	99.9	17	PDB header: cell cycle Chain: A: PDB Molecule: katanin p60 atpase-containing subunit a-like 1; PDBTitle: structural basis for katanin self-assembly
39	d1e32a2	Alignment	not modelled	99.9	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
40	d2ce7a2	Alignment	not modelled	99.9	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
41	d1g41a	Alignment	not modelled	99.9	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
42	c1iy2A	Alignment	not modelled	99.9	24	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent metalloprotease ftsh; PDBTitle: crystal structure of the ftsh atpase domain from thermus2 thermophilus
43	c5wc0D	Alignment	not modelled	99.9	22	PDB header: motor protein Chain: D: PDB Molecule: meiotic spindle formation protein mei-1; PDBTitle: katanin hexamer in spiral conformation
44	c2c9oA	Alignment	not modelled	99.9	24	PDB header: hydrolase Chain: A: PDB Molecule: ruvb-like 1; PDBTitle: 3d structure of the human ruvb-like helicase ruvb1
45	c3vfdA	Alignment	not modelled	99.9	19	PDB header: hydrolase Chain: A: PDB Molecule: spastin; PDBTitle: human spastin aaa domain
46	d1ixza	Alignment	not modelled	99.9	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
47	c3pxiB	Alignment	not modelled	99.9	23	PDB header: protein binding Chain: B: PDB Molecule: negative regulator of genetic competence clpc/mechb; PDBTitle: structure of meca108:clpc
48	c5oafB	Alignment	not modelled	99.9	28	PDB header: gene regulation Chain: B: PDB Molecule: ruvb-like 2; PDBTitle: human rvb1/rvb2 heterohexamer in ino80 complex
49	c4xguB	Alignment	not modelled	99.9	21	PDB header: atp-binding protein Chain: B: PDB Molecule: putative pachytene checkpoint protein 2; PDBTitle: structure of c. elegans pch-2
50	c2r65A	Alignment	not modelled	99.9	21	PDB header: hydrolase Chain: A: PDB Molecule: cell division protease ftsh homolog; PDBTitle: crystal structure of helicobacter pylori atp dependent protease, ftsh2 adp complex
51	c3pfiB	Alignment	not modelled	99.9	25	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
52	c3h4mC	Alignment	not modelled	99.9	23	PDB header: hydrolase Chain: C: PDB Molecule: proteasome-activating nucleotidase; PDBTitle: aaa atpase domain of the proteasome- activating nucleotidase
53	c3pvsA	Alignment	not modelled	99.9	23	PDB header: recombination Chain: A: PDB Molecule: replication-associated recombination protein a; PDBTitle: structure and biochemical activities of escherichia coli mgsa
54	c5ubvB	Alignment	not modelled	99.9	19	PDB header: hydrolase Chain: B: PDB Molecule: atpase domain of i-aaa protease; PDBTitle: atpase domain of i-aaa protease from myceliophthora

						thermophila
55	c6opcF_	Alignment	not modelled	99.9	22	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)
56	c5vq9D_	Alignment	not modelled	99.9	15	PDB header: protein binding Chain: D: PDB Molecule: pachytene checkpoint protein 2 homolog; PDBTitle: structure of human trip13, apo form
57	c4ww4B_	Alignment	not modelled	99.9	27	PDB header: hydrolase Chain: B: PDB Molecule: ruvb-like 2; PDBTitle: double-heterohexameric rings of full-length rvb1(adp)/rvb2(adp)
58	d1ofha_	Alignment	not modelled	99.9	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
59	c4ww4A_	Alignment	not modelled	99.9	25	PDB header: hydrolase Chain: A: PDB Molecule: ruvb-like 1; PDBTitle: double-heterohexameric rings of full-length rvb1(adp)/rvb2(adp)
60	c4lcbA_	Alignment	not modelled	99.9	21	PDB header: protein transport Chain: A: PDB Molecule: cell division protein cdvc, vps4; PDBTitle: structure of vps4 homolog from acidianus hospitalis
61	c3j96F_	Alignment	not modelled	99.9	21	PDB header: hydrolase Chain: F: PDB Molecule: vesicle-fusing atpase; PDBTitle: structure of 20s supercomplex determined by single particle2 cryoelectron microscopy (state i)
62	c4ciuA_	Alignment	not modelled	99.9	17	PDB header: chaperone Chain: A: PDB Molecule: chaperone protein clpb; PDBTitle: crystal structure of e. coli clpb
63	c6azyA_	Alignment	not modelled	99.9	15	PDB header: chaperone Chain: A: PDB Molecule: heat shock protein hsp104; PDBTitle: crystal structure of hsp104 r328m/r757m mutant from calcarisporiella2 thermophila
64	c5kneA_	Alignment	not modelled	99.9	24	PDB header: chaperone Chain: A: PDB Molecule: heat shock protein 104; PDBTitle: cryoem reconstruction of hsp104 hexamer
65	c5d4wB_	Alignment	not modelled	99.9	19	PDB header: chaperone Chain: B: PDB Molecule: putative heat shock protein; PDBTitle: crystal structure of hsp104
66	c5kneF_	Alignment	not modelled	99.9	18	PDB header: chaperone Chain: F: PDB Molecule: heat shock protein 104; PDBTitle: cryoem reconstruction of hsp104 hexamer
67	c1qvrB_	Alignment	not modelled	99.9	18	PDB header: chaperone Chain: B: PDB Molecule: clpb protein; PDBTitle: crystal structure analysis of clpb
68	c6blbA_	Alignment	not modelled	99.9	28	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
69	c2qz4A_	Alignment	not modelled	99.9	19	PDB header: hydrolase Chain: A: PDB Molecule: paraplegin; PDBTitle: human paraplegin, aaa domain in complex with adp
70	c6mdnF_	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: F: PDB Molecule: vesicle-fusing atpase; PDBTitle: the 20s supercomplex engaging the snap-25 n-terminus (class 2)
71	c5vy9C_	Alignment	not modelled	99.9	22	PDB header: chaperone Chain: C: PDB Molecule: heat shock protein 104; PDBTitle: s. cerevisiae hsp104:casein complex, middle domain conformation
72	d1lv7a_	Alignment	not modelled	99.9	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
73	c6em8F_	Alignment	not modelled	99.9	18	PDB header: chaperone Chain: F: PDB Molecule: atp-dependent clp protease atp-binding subunit clpc; PDBTitle: s.aureus clpc resting state, c2 symmetrised
74	d1in4a2	Alignment	not modelled	99.9	32	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
75	c1r6bX_	Alignment	not modelled	99.9	21	PDB header: hydrolase Chain: X: PDB Molecule: clpa protein; PDBTitle: high resolution crystal structure of clpa
76	c1in8A_	Alignment	not modelled	99.9	32	PDB header: dna binding protein Chain: A: PDB Molecule: holliday junction dna helicase ruvb; PDBTitle: thermotoga maritima ruvb t158v
77	c2x8aA_	Alignment	not modelled	99.9	19	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
78	d1r6bx2	Alignment	not modelled	99.9	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
79	d1qvra3	Alignment	not modelled	99.9	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
80	d1r7ra3	Alignment	not modelled	99.9	23	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
						PDB header: chaperone

81	c6djuA	Alignment	not modelled	99.9	21	Chain: A: PDB Molecule: chaperone protein clpb; PDBTitle: mtb clpb in complex with atpgammas and casein, conformer 1
82	d1r6bx3	Alignment	not modelled	99.9	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
83	c3pxgA	Alignment	not modelled	99.9	21	PDB header: protein binding Chain: A: PDB Molecule: negative regulator of genetic competence clpc/meccb; PDBTitle: structure of meca121 and clpc1-485 complex
84	c6e111	Alignment	not modelled	99.9	18	PDB header: protein transport Chain: 1: PDB Molecule: heat shock protein 101; PDBTitle: ptx core complex in the resetting (compact) state
85	c2c9oC	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: C: PDB Molecule: ruvb-like 1; PDBTitle: 3d structure of the human ruvb-like helicase ruvb1l
86	c3zw6B	Alignment	not modelled	99.9	15	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.
87	c5kneD	Alignment	not modelled	99.9	16	PDB header: chaperone Chain: D: PDB Molecule: heat shock protein 104; PDBTitle: cryoem reconstruction of hsp104 hexamer
88	c3f8tA	Alignment	not modelled	99.9	17	PDB header: hydrolase Chain: A: PDB Molecule: predicted atpase involved in replication control, cdc46/mcm PDBTitle: crystal structure analysis of a full-length mcm homolog from2 methanopyrus kandleri
89	d1um8a	Alignment	not modelled	99.9	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
90	c4r7zB	Alignment	not modelled	99.9	21	PDB header: hydrolase Chain: B: PDB Molecule: cell division control protein 21; PDBTitle: pfmcm-aaa double-octamer
91	c6qj8E	Alignment	not modelled	99.9	19	PDB header: chaperone Chain: E: PDB Molecule: ruvb-like 2; PDBTitle: truncated human r2tp complex, structure 3 (adp-filled)
92	c6djevE	Alignment	not modelled	99.9	21	PDB header: chaperone Chain: E: PDB Molecule: chaperone protein clpb; PDBTitle: mtb clpb in complex with atpgammas and casein, conformer 2
93	d1g8pa	Alignment	not modelled	99.9	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
94	c6em8H	Alignment	not modelled	99.9	19	PDB header: chaperone Chain: H: PDB Molecule: atp-dependent clp protease atp-binding subunit clpc; PDBTitle: s.aureus clpc resting state, c2 symmetrised
95	c1xxhB	Alignment	not modelled	99.9	20	PDB header: transferase Chain: B: PDB Molecule: dna polymerase iii subunit gamma; PDBTitle: atpgs bound e. coli clamp loader complex
96	c4d2qC	Alignment	not modelled	99.9	20	PDB header: chaperone Chain: C: PDB Molecule: clpb; PDBTitle: negative-stain electron microscopy of e. coli clpb mutant e432a (bap2 form bound to clpp)
97	d1ixsb2	Alignment	not modelled	99.9	29	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
98	d1iqpa2	Alignment	not modelled	99.9	27	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
99	c5u8s4	Alignment	not modelled	99.8	18	PDB header: replication Chain: 4: PDB Molecule: dna replication licensing factor mcm4; PDBTitle: structure of eukaryotic cmg helicase at a replication fork
100	c5nnrD	Alignment	not modelled	99.8	15	PDB header: transferase Chain: D: PDB Molecule: n-terminal acetyltransferase-like protein; PDBTitle: structure of naa15/naa10 bound to hypk-thb
101	d1w5sa2	Alignment	not modelled	99.8	12	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
102	d1jbka	Alignment	not modelled	99.8	24	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
103	c5udb3	Alignment	not modelled	99.8	18	PDB header: replication Chain: 3: PDB Molecule: dna replication licensing factor mcm3; PDBTitle: structural basis of mcm2-7 replicative helicase loading by orc-cdc62 and cdt1
104	d1sxb2	Alignment	not modelled	99.8	27	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
105	c3hteC	Alignment	not modelled	99.8	23	PDB header: motor protein Chain: C: PDB Molecule: atp-dependent clp protease atp-binding subunit clpx; PDBTitle: crystal structure of nucleotide-free hexameric clpx
106	c2chgB	Alignment	not modelled	99.8	24	PDB header: dna-binding protein Chain: B: PDB Molecule: replication factor c small subunit; PDBTitle: replication factor c domains 1 and 2
107	d1qvra2	Alignment	not modelled	99.8	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain

108	c2r44A_	Alignment	not modelled	99.8	13	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
109	c3jc55_	Alignment	not modelled	99.8	17	PDB header: hydrolase Chain: 5; PDB Molecule: minichromosome maintenance protein 5; PDBTitle: structure of the eukaryotic replicative cmg helicase and pumpjack2 motion
110	c6em8E_	Alignment	not modelled	99.8	22	PDB header: chaperone Chain: E; PDB Molecule: atp-dependent clp protease atp-binding subunit clpc; PDBTitle: s.aureus clpc resting state, c2 symmetrised
111	c4ypnA_	Alignment	not modelled	99.8	27	PDB header: hydrolase Chain: A; PDB Molecule: lon protease; PDBTitle: crystal structure of a lona fragment containing the 3-helix bundle and2 the aaa-alpha/beta domain
112	c5ep4A_	Alignment	not modelled	99.8	16	PDB header: transcription Chain: A; PDB Molecule: putative repressor protein luxo; PDBTitle: structure, regulation, and inhibition of the quorum-sensing signal2 integrator luxo
113	c6c95A_	Alignment	not modelled	99.8	11	PDB header: transferase Chain: A; PDB Molecule: n-alpha-acetyltransferase 15, nata auxiliary subunit; PDBTitle: the human nata (naa10/naa15) amino-terminal acetyltransferase complex2 bound to hypk
114	d1njfa_	Alignment	not modelled	99.8	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
115	c1nsfA_	Alignment	not modelled	99.8	18	PDB header: protein transport Chain: A; PDB Molecule: n-ethylmaleimide sensitive factor; PDBTitle: d2 hexamerization domain of n-ethylmaleimide sensitive factor (nsf)
116	c4yplE_	Alignment	not modelled	99.8	22	PDB header: hydrolase Chain: E; PDB Molecule: lon protease; PDBTitle: crystal structure of a hexameric lona protease bound to three adps
117	c5udb7_	Alignment	not modelled	99.8	17	PDB header: replication Chain: 7; PDB Molecule: dna replication licensing factor mcm7; PDBTitle: structural basis of mcm2-7 replicative helicase loading by orc-cdc62 and cdt1
118	c4buJF_	Alignment	not modelled	99.8	8	PDB header: hydrolase Chain: F; PDB Molecule: superkiller protein 3; PDBTitle: crystal structure of the s. cerevisiae ski2-3-8 complex
119	d1sxd2	Alignment	not modelled	99.8	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
120	c3ja82_	Alignment	not modelled	99.8	16	PDB header: hydrolase Chain: 2; PDB Molecule: minichromosome maintenance 2; PDBTitle: cryo-em structure of the mcm2-7 double hexamer