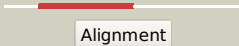







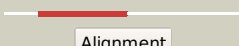



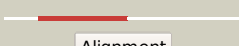









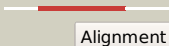
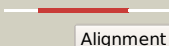





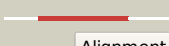






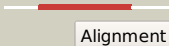
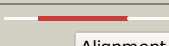
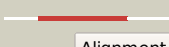

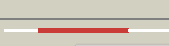


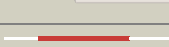


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2850c_(-)_3158175_3160064
Date	Wed Aug 7 12:50:51 BST 2019
Unique Job ID	Oea1a13e2403f024

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1g8pa_	 Alignment		100.0	53	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
2	c4r7zB_	 Alignment		100.0	23	PDB header: hydrolase Chain: B: PDB Molecule: cell division control protein 21; PDBTitle: pfmcm-aaa double-octamer
3	c3ja87_	 Alignment		100.0	21	PDB header: hydrolase Chain: 7: PDB Molecule: minichromosome maintenance 7; PDBTitle: cryo-em structure of the mcm2-7 double hexamer
4	c5udb7_	 Alignment		100.0	21	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
5	c3ja84_	 Alignment		100.0	21	PDB header: hydrolase Chain: 4: PDB Molecule: minichromosome maintenance 4; PDBTitle: cryo-em structure of the mcm2-7 double hexamer
6	c5h7i7_	 Alignment		100.0	21	PDB header: hydrolase Chain: 7: PDB Molecule: dna replication licensing factor mcm7; PDBTitle: cryo-em structure of the cdt1-mcm2-7 complex in amppnp state
7	c3ja85_	 Alignment		100.0	18	PDB header: hydrolase Chain: 5: PDB Molecule: minichromosome maintenance 5; PDBTitle: cryo-em structure of the mcm2-7 double hexamer
8	c3ja82_	 Alignment		100.0	22	PDB header: hydrolase Chain: 2: PDB Molecule: minichromosome maintenance 2; PDBTitle: cryo-em structure of the mcm2-7 double hexamer
9	c3ja83_	 Alignment		100.0	26	PDB header: hydrolase Chain: 3: PDB Molecule: minichromosome maintenance 3; PDBTitle: cryo-em structure of the mcm2-7 double hexamer
10	c5u8s4_	 Alignment		100.0	20	PDB header: replication Chain: 4: PDB Molecule: dna replication licensing factor mcm4; PDBTitle: structure of eukaryotic cmg helicase at a replication fork
11	c5udb3_	 Alignment		100.0	26	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

12	c3nbxX_	 Alignment		100.0	18	PDB header: hydrolase Chain: X; PDB Molecule: atpase rava; PDBTitle: crystal structure of e. coli rava (regulatory atpase variant a) in2 complex with adp
13	c6hv93_	 Alignment		100.0	27	PDB header: dna binding protein Chain: 3; PDB Molecule: dna replication licensing factor mcm3; PDBTitle: s. cerevisiae cmg-pol epsilon-dna
14	c3jc72_	 Alignment		100.0	22	PDB header: hydrolase Chain: 2; PDB Molecule: dna replication licensing factor mcm2; PDBTitle: structure of the eukaryotic replicative cmg helicase and pumpjack2 motion
15	c3ja86_	 Alignment		100.0	19	PDB header: hydrolase Chain: 6; PDB Molecule: minichromosome maintenance 6; PDBTitle: cryo-em structure of the mcm2-7 double hexamer
16	c5v8f3_	 Alignment		100.0	27	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
17	c3jc57_	 Alignment		100.0	22	PDB header: hydrolase Chain: 7; PDB Molecule: dna replication licensing factor mcm7; PDBTitle: structure of the eukaryotic replicative cmg helicase and pumpjack2 motion
18	c3jc76_	 Alignment		100.0	18	PDB header: hydrolase Chain: 6; PDB Molecule: dna replication licensing factor mcm6; PDBTitle: structure of the eukaryotic replicative cmg helicase and pumpjack2 motion
19	c3jc55_	 Alignment		100.0	18	PDB header: hydrolase Chain: 5; PDB Molecule: minichromosome maintenance protein 5; PDBTitle: structure of the eukaryotic replicative cmg helicase and pumpjack2 motion
20	c5udb5_	 Alignment		100.0	19	PDB header: replication Chain: 5; PDB Molecule: minichromosome maintenance protein 5; PDBTitle: structural basis of mcm2-7 replicative helicase loading by orc-cdc62 and cdt1
21	c6hv92_	 Alignment	not modelled	100.0	22	PDB header: dna binding protein Chain: 2; PDB Molecule: dna replication licensing factor mcm2; PDBTitle: s. cerevisiae cmg-pol epsilon-dna
22	c3jc73_	 Alignment	not modelled	100.0	28	PDB header: hydrolase Chain: 3; PDB Molecule: dna replication licensing factor mcm3; PDBTitle: structure of the eukaryotic replicative cmg helicase and pumpjack2 motion
23	c3f8tA_	 Alignment	not modelled	100.0	24	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
24	c2r44A_	 Alignment	not modelled	100.0	22	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
25	c6hv96_	 Alignment	not modelled	99.9	19	PDB header: dna binding protein Chain: 6; PDB Molecule: dna replication licensing factor mcm6; PDBTitle: s. cerevisiae cmg-pol epsilon-dna
26	c3f9vA_	 Alignment	not modelled	99.9	24	PDB header: hydrolase Chain: A; PDB Molecule: minichromosome maintenance protein mcm; PDBTitle: crystal structure of a near full-length archaeal mcm: functional2 insights for an aaa+ hexameric helicase
27	c6hv97_	 Alignment	not modelled	99.9	21	PDB header: dna binding protein Chain: 7; PDB Molecule: dna replication licensing factor mcm7; PDBTitle: s. cerevisiae cmg-pol epsilon-dna
28	c3k1jA_	 Alignment	not modelled	99.9	21	PDB header: hydrolase Chain: A; PDB Molecule: atp-dependent protease lon; PDBTitle: crystal structure of lon protease from thermococcus

						onnurineus na1
29	c4fx5A_	Alignment	not modelled	99.9	16	PDB header: blood clotting Chain: A; PDB Molecule: von willebrand factor type a; PDBTitle: von willebrand factor type a from catenulispora acidiphila
30	c4ww4A_	Alignment	not modelled	99.9	23	PDB header: hydrolase Chain: A; PDB Molecule: ruvb-like 1; PDBTitle: double-heterohexameric rings of full-length ruv1(adp)/ruv2(adp)
31	c5oafB_	Alignment	not modelled	99.9	26	PDB header: gene regulation Chain: B; PDB Molecule: ruvb-like 2; PDBTitle: human ruv1/ruv2 heterohexamer in ino80 complex
32	c2c9oA_	Alignment	not modelled	99.9	19	PDB header: hydrolase Chain: A; PDB Molecule: ruvb-like 1; PDBTitle: 3d structure of the human ruvb-like helicase ruvb1
33	c6genX_	Alignment	not modelled	99.9	24	PDB header: nuclear protein Chain: X; PDB Molecule: ruvb-like protein 1; PDBTitle: chromatin remodeller-nucleosome complex at 4.5 a resolution.
34	c6blbA_	Alignment	not modelled	99.9	24	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
35	c3jc54_	Alignment	not modelled	99.9	23	PDB header: hydrolase Chain: 4; PDB Molecule: dna replication licensing factor mcm4; PDBTitle: structure of the eukaryotic replicative cmg helicase and pumpjack2 motion
36	c5a8jA_	Alignment	not modelled	99.9	14	PDB header: transcription Chain: A; PDB Molecule: vwa2; PDBTitle: crystal structure of the arnb paralog vwa2 from2 sulfobolus acidocaldarius
37	c6fpzA_	Alignment	not modelled	99.9	19	PDB header: structural protein Chain: A; PDB Molecule: inter-alpha-trypsin inhibitor heavy chain h1; PDBTitle: inter-alpha-inhibitor heavy chain 1, d298a
38	c6nyyC_	Alignment	not modelled	99.9	17	PDB header: translocase Chain: C; PDB Molecule: afg3-like protein 2; PDBTitle: human m-aaa protease afg3l2, substrate-bound
39	c3pvsA_	Alignment	not modelled	99.8	21	PDB header: recombination Chain: A; PDB Molecule: replication-associated recombination protein a; PDBTitle: structure and biochemical activities of escherichia coli mgsa
40	c5g4gF_	Alignment	not modelled	99.8	19	PDB header: hydrolase Chain: F; PDB Molecule: vcp-like atpase; PDBTitle: structure of the atpgs-bound vat complex
41	c6nmiE_	Alignment	not modelled	99.8	16	PDB header: transcription Chain: E; PDB Molecule: general transcription factor iih subunit 2, p44; PDBTitle: cryo-em structure of the human tfiih core complex
42	c3uk6H_	Alignment	not modelled	99.8	21	PDB header: hydrolase Chain: H; PDB Molecule: ruvb-like 2; PDBTitle: crystal structure of the tip48 (tip49b) hexamer
43	c6o9l6_	Alignment	not modelled	99.8	16	PDB header: transcription/dna Chain: 6; PDB Molecule: general transcription factor iih subunit 2; PDBTitle: human holo-pic in the closed state
44	c2x31F_	Alignment	not modelled	99.8	34	PDB header: ligase Chain: F; PDB Molecule: magnesium-chelatase 60 kda subunit; PDBTitle: modelling of the complex between subunits bchi and bchd of magnesium2 chelatase based on single-particle cryo-em reconstruction at 7.5 ang
45	c3pfiB_	Alignment	not modelled	99.8	19	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
46	c1in8A_	Alignment	not modelled	99.8	18	PDB header: dna binding protein Chain: A; PDB Molecule: holliday junction dna helicase ruvb; PDBTitle: thermotoga maritima ruvb t158v
47	c4rckB_	Alignment	not modelled	99.8	25	PDB header: membrane protein Chain: B; PDB Molecule: hypothetical membrane spanning protein; PDBTitle: crystal structure of uncharacterized membrane spanning protein from2 vibrio fischeri
48	d1ixsb2	Alignment	not modelled	99.8	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
49	c2dhrC_	Alignment	not modelled	99.8	21	PDB header: hydrolase Chain: C; PDB Molecule: ftsh; PDBTitle: whole cytosolic region of atp-dependent metalloprotease2 ftsh (g399l)
50	c2c9oC_	Alignment	not modelled	99.8	17	PDB header: hydrolase Chain: C; PDB Molecule: ruvb-like 1; PDBTitle: 3d structure of the human ruvb-like helicase ruvb1
51	c1rs0A_	Alignment	not modelled	99.8	15	PDB header: hydrolase Chain: A; PDB Molecule: complement factor b; PDBTitle: crystal structure analysis of the bb segment of factor b2 complexed with di-isopropyl-phosphate (dip)
52	d1in4a2	Alignment	not modelled	99.8	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
53	c5e7pA_	Alignment	not modelled	99.8	26	PDB header: hydrolase Chain: A; PDB Molecule: cell division control protein cdc48; PDBTitle: crystal structure of msmeg_0858 (uniprot a0qqs4), a aaa

						atpase.
54	c2i6sA_	Alignment	not modelled	99.8	16	PDB header: hydrolase Chain: A: PDB Molecule: complement c2a fragment; PDBTitle: complement component c2a
55	c1xxhB_	Alignment	not modelled	99.8	21	PDB header: transferase Chain: B: PDB Molecule: dna polymerase iii subunit gamma; PDBTitle: atpgs bound e. coli clamp loader complex
56	c3ibsA_	Alignment	not modelled	99.8	25	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved hypothetical protein batb; PDBTitle: crystal structure of conserved hypothetical protein batb from 2 bacteroides thetaiotaomicron
57	c5iy70_	Alignment	not modelled	99.8	15	PDB header: transcription, transferase/dna Chain: 0: PDB Molecule: general transcription factor iih subunit 2; PDBTitle: human holo-pic in the open state
58	c4b4tW_	Alignment	not modelled	99.8	14	PDB header: hydrolase Chain: W: PDB Molecule: 26s proteasome regulatory subunit rpn10; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
59	c2ok5A_	Alignment	not modelled	99.8	16	PDB header: hydrolase Chain: A: PDB Molecule: complement factor b; PDBTitle: human complement factor b
60	d1um8a_	Alignment	not modelled	99.8	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
61	c6epdM_	Alignment	not modelled	99.8	20	PDB header: hydrolase Chain: M: PDB Molecule: 26s proteasome regulatory subunit 6a; PDBTitle: substrate processing state 26s proteasome (sps1)
62	c3cf1C_	Alignment	not modelled	99.8	17	PDB header: transport protein Chain: C: PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: structure of p97/vcp in complex with adp/adp.alfx
63	c6qi8E_	Alignment	not modelled	99.8	23	PDB header: chaperone Chain: E: PDB Molecule: ruvb-like 2; PDBTitle: truncated human r2tp complex, structure 3 (adp-filled)
64	c1hqcb_	Alignment	not modelled	99.8	21	PDB header: hydrolase Chain: B: PDB Molecule: ruvb; PDBTitle: structure of ruvb from thermus thermophilus hb8
65	c6epcJ_	Alignment	not modelled	99.8	16	PDB header: hydrolase Chain: J: PDB Molecule: 26s proteasome regulatory subunit 8; PDBTitle: ground state 26s proteasome (gs2)
66	c4b4tK_	Alignment	not modelled	99.8	20	PDB header: hydrolase Chain: K: PDB Molecule: 26s protease regulatory subunit 6b homolog; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
67	d1g41a_	Alignment	not modelled	99.8	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
68	d2ok5a1	Alignment	not modelled	99.8	15	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
69	c4b4tH_	Alignment	not modelled	99.8	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
70	d1r6bx3	Alignment	not modelled	99.8	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
71	c3b9pA_	Alignment	not modelled	99.8	24	PDB header: hydrolase Chain: A: PDB Molecule: cg5977-pa, isoform a; PDBTitle: spastin
72	c5vq9D_	Alignment	not modelled	99.8	18	PDB header: protein binding Chain: D: PDB Molecule: pacchytene checkpoint protein 2 homolog; PDBTitle: structure of human trip13, apo form
73	c1qvrB_	Alignment	not modelled	99.8	23	PDB header: chaperone Chain: B: PDB Molecule: clpb protein; PDBTitle: crystal structure analysis of clpb
74	c4b4tI_	Alignment	not modelled	99.8	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
75	c3jbrF_	Alignment	not modelled	99.8	13	PDB header: membrane protein Chain: F: PDB Molecule: voltage-dependent calcium channel subunit alpha-2/delta-1; PDBTitle: cryo-em structure of the rabbit voltage-gated calcium channel cav1.12 complex at 4.2 angstrom
76	c4fw9A_	Alignment	not modelled	99.8	23	PDB header: hydrolase Chain: A: PDB Molecule: ttc1975 peptidase; PDBTitle: crystal structure of the lon-like protease mtalonc
77	c1r6bX_	Alignment	not modelled	99.8	19	PDB header: hydrolase Chain: X: PDB Molecule: clpa protein; PDBTitle: high resolution crystal structure of clpa
78	c4ww4B_	Alignment	not modelled	99.8	24	PDB header: hydrolase Chain: B: PDB Molecule: ruvb-like 2; PDBTitle: double-heterohexameric rings of full-length rvb1(adp)/rvb2(adp)
79	c2chgB_	Alignment	not modelled	99.7	17	PDB header: dna-binding protein Chain: B: PDB Molecule: replication factor c small subunit; PDBTitle: replication factor c domains 1 and 2

80	c6matE	Alignment	not modelled	99.7	19	PDB header: ribosomal protein Chain: E: PDB Molecule: rix7 mutant; PDBTitle: cryo-em structure of the essential ribosome assembly aaa-atpase rix7
81	d1sxic2	Alignment	not modelled	99.7	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
82	c4b4tL	Alignment	not modelled	99.7	22	PDB header: hydrolase Chain: L: PDB Molecule: 26s protease subunit rpt4; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
83	c6hecH	Alignment	not modelled	99.7	21	PDB header: hydrolase Chain: H: PDB Molecule: proteasome-activating nucleotidase; PDBTitle: pan-proteasome in state 4
84	c4b4tJ	Alignment	not modelled	99.7	16	PDB header: hydrolase Chain: J: PDB Molecule: 26s protease regulatory subunit 8 homolog; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
85	c1sxC	Alignment	not modelled	99.7	15	PDB header: replication Chain: C: PDB Molecule: activator 1 40 kda subunit; PDBTitle: crystal structure of the eukaryotic clamp loader (replication factor 2 c, rfc) bound to the dna sliding clamp (proliferating cell nuclear 3 antigen, pcna)
86	c5kzfl	Alignment	not modelled	99.7	17	PDB header: hydrolase Chain: J: PDB Molecule: proteasome-associated atpase; PDBTitle: crystal structure of near full-length hexameric mycobacterium 2 tuberculosis proteasomal atpase mpa in apo form
87	c3pxiB	Alignment	not modelled	99.7	20	PDB header: protein binding Chain: B: PDB Molecule: negative regulator of genetic competence clpc/mecb; PDBTitle: structure of meca108:clpc
88	c2x5nA	Alignment	not modelled	99.7	11	PDB header: nuclear protein Chain: A: PDB Molecule: 26s proteasome regulatory subunit rpn10; PDBTitle: crystal structure of the sprpn10 vwa domain
89	d1ofha	Alignment	not modelled	99.7	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
90	c1xwiA	Alignment	not modelled	99.7	17	PDB header: protein transport Chain: A: PDB Molecule: skd1 protein; PDBTitle: crystal structure of vps4b
91	c5gjfV	Alignment	not modelled	99.7	14	PDB header: membrane protein Chain: F: PDB Molecule: voltage-dependent calcium channel subunit alpha-2/delta-1; PDBTitle: structure of the mammalian voltage-gated calcium channel cav1.12 complex at near atomic resolution
92	c6nyyA	Alignment	not modelled	99.7	16	PDB header: translocase Chain: A: PDB Molecule: afg3-like protein 2; PDBTitle: human m-aaa protease afg3l2, substrate-bound
93	c2chvE	Alignment	not modelled	99.7	17	PDB header: dna-binding protein Chain: E: PDB Molecule: replication factor c small subunit; PDBTitle: replication factor c adpnp complex
94	c6az0A	Alignment	not modelled	99.7	19	PDB header: hydrolase Chain: A: PDB Molecule: mitochondrial inner membrane i-aaa protease supercomplex PDBTitle: mitochondrial atpase protease yme1
95	c4lcbA	Alignment	not modelled	99.7	17	PDB header: protein transport Chain: A: PDB Molecule: cell division protein cdvc, vps4; PDBTitle: structure of vps4 homolog from acidianus hospitalis
96	c4ciuA	Alignment	not modelled	99.7	18	PDB header: chaperone Chain: A: PDB Molecule: chaperone protein clpb; PDBTitle: crystal structure of e. coli clpb
97	c4wfqA	Alignment	not modelled	99.7	18	PDB header: transcription Chain: A: PDB Molecule: suppressor of stem-loop protein 1; PDBTitle: crystal structure of tfiih subunit
98	d1sxb2	Alignment	not modelled	99.7	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
99	c3d8bB	Alignment	not modelled	99.7	19	PDB header: hydrolase Chain: B: PDB Molecule: fidgetin-like protein 1; PDBTitle: crystal structure of human fidgetin-like protein 1 in complex with adp
100	c3cf2B	Alignment	not modelled	99.7	24	PDB header: transport protein Chain: B: PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: structure of p97/vcp in complex with adp/amp-pnp
101	c5oqj6	Alignment	not modelled	99.7	20	PDB header: transcription Chain: 6: PDB Molecule: suppressor of stem-loop protein 1; PDBTitle: structure of yeast transcription pre-initiation complex with tfiih
102	c5mpaL	Alignment	not modelled	99.7	22	PDB header: hydrolase Chain: L: PDB Molecule: 26s protease subunit rpt4; PDBTitle: 26s proteasome in presence of atp (s2)
103	c6azyA	Alignment	not modelled	99.7	18	PDB header: chaperone Chain: A: PDB Molecule: heat shock protein hsp104; PDBTitle: crystal structure of hsp104 r328m/r757m mutant from calcarisporiella2 thermophila
104	c1ojlD	Alignment	not modelled	99.7	23	PDB header: response regulator Chain: D: PDB Molecule: transcriptional regulatory protein zrar; PDBTitle: crystal structure of a sigma54-activator suggests the mechanism for2 the conformational switch necessary for sigma54 binding
105	d1sxd2	Alignment	not modelled	99.7	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain

106	c3hu2C_	Alignment	not modelled	99.7	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
107	c5ifwB_	Alignment	not modelled	99.7	19	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
108	c5qjL_	Alignment	not modelled	99.7	21	PDB header: hydrolase Chain: L; PDB Molecule: 26s protease regulatory subunit 10b; PDBTitle: structure of the human 26s proteasome bound to usp14-ubal
109	c3vfdA_	Alignment	not modelled	99.7	21	PDB header: hydrolase Chain: A; PDB Molecule: spastin; PDBTitle: human spastin aaa domain
110	d1njfa_	Alignment	not modelled	99.7	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
111	d1ny5a2	Alignment	not modelled	99.7	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
112	c3hteC_	Alignment	not modelled	99.7	19	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	c5exsA_	Alignment	not modelled	99.7	17	PDB header: transcription Chain: A; PDB Molecule: transcriptional regulator fleq; PDBTitle: aaa+ atpase fleq from pseudomonas aeruginosa bound to atp-gamma-s
114	c4l16A_	Alignment	not modelled	99.7	22	PDB header: hydrolase Chain: A; PDB Molecule: figetin-like protein 1; PDBTitle: crystal structure of figl-1 aaa domain in complex with adp
115	d1iqpa2	Alignment	not modelled	99.7	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
116	d1r6bx2	Alignment	not modelled	99.7	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
117	c2ce7B_	Alignment	not modelled	99.7	18	PDB header: cell division protein Chain: B; PDB Molecule: cell division protein ftsh; PDBTitle: edta treated
118	c5d4wB_	Alignment	not modelled	99.7	16	PDB header: chaperone Chain: B; PDB Molecule: putative heat shock protein; PDBTitle: crystal structure of hsp104
119	c5kneD_	Alignment	not modelled	99.7	19	PDB header: chaperone Chain: D; PDB Molecule: heat shock protein 104; PDBTitle: cryoem reconstruction of hsp104 hexamer
120	c4d2qC_	Alignment	not modelled	99.7	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)