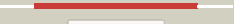





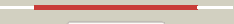












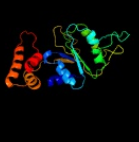




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2426c (-)_2723318_2724193
Date	Wed Aug 7 12:50:04 BST 2019
Unique Job ID	92521db99a1a44f4

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6i26A_	 Alignment		100.0	24	PDB header: motor protein Chain: A; PDB Molecule: midasin,midasin,midasin,midasin; PDBTitle: rea1 wild type amppnp state
2	c6orbA_	 Alignment		100.0	23	PDB header: motor protein Chain: A; PDB Molecule: midasin; PDBTitle: full-length s. pombe mdn1 in the presence of atp and rbin-1
3	c5g4gF_	 Alignment		99.9	24	PDB header: hydrolase Chain: F; PDB Molecule: vcp-like atpase; PDBTitle: structure of the atpgs-bound vat complex
4	c3nbxX_	 Alignment		99.9	20	PDB header: hydrolase Chain: X; PDB Molecule: atpase rava; PDBTitle: crystal structure of e. coli rava (regulatory atpase variant a) in2 complex with adp
5	c2r44A_	 Alignment		99.9	18	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
6	c5e7pA_	 Alignment		99.9	23	PDB header: hydrolase Chain: A; PDB Molecule: cell division control protein cdc48; PDBTitle: crystal structure of msmeq_0858 (uniprot a0qqs4), a aaa atpase.
7	c3cf1C_	 Alignment		99.9	22	PDB header: transport protein Chain: C; PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: structure of p97/vcp in complex with adp/adp.alfx
8	c6nyyC_	 Alignment		99.9	19	PDB header: translocase Chain: C; PDB Molecule: afg3-like protein 2; PDBTitle: human m-aaa protease afg3l2, substrate-bound
9	c6azyA_	 Alignment		99.9	25	PDB header: chaperone Chain: A; PDB Molecule: heat shock protein hsp104; PDBTitle: crystal structure of hsp104 r328m/r757m mutant from calcarisporiella2 thermophila
10	c6edoA_	 Alignment		99.9	20	PDB header: motor protein Chain: A; PDB Molecule: midasin; PDBTitle: full-length s. pombe mdn1 in the presence of amppnp (ring region)
11	c6epdM_	 Alignment		99.9	23	PDB header: hydrolase Chain: M; PDB Molecule: 26s proteasome regulatory subunit 6a; PDBTitle: substrate processing state 26s proteasome (sps1)

12	c6i27A_	Alignment		99.9	25	PDB header: motor protein Chain: A; PDB Molecule: midasin,midasin,midasin,midasin,midasin,midasin,midasin; PDBTitle: rea1 aaa2l-h2alpha deletion mutant in amppnp state
13	c4b4tH_	Alignment		99.9	24	PDB header: hydrolase Chain: H; PDB Molecule: 26s protease regulatory subunit 7 homolog; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
14	c6matE_	Alignment		99.9	20	PDB header: ribosomal protein Chain: E; PDB Molecule: rix7 mutant; PDBTitle: cryo-em structure of the essential ribosome assembly aaa-atpase rix7
15	c5c3cB_	Alignment		99.9	17	PDB header: protein binding Chain: B; PDB Molecule: cbbq/nirq/norq domain protein; PDBTitle: structural characterization of a newly identified component of alpha-2 carboxysomes: the aaa+ domain protein cso-cbbq
16	c1qvrB_	Alignment		99.9	29	PDB header: chaperone Chain: B; PDB Molecule: clpb protein; PDBTitle: crystal structure analysis of clpb
17	c3cf2B_	Alignment		99.9	23	PDB header: transport protein Chain: B; PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: structure of p97/vcp in complex with adp/amp-pnp
18	c6epcJ_	Alignment		99.9	26	PDB header: hydrolase Chain: J; PDB Molecule: 26s proteasome regulatory subunit 8; PDBTitle: ground state 26s proteasome (gs2)
19	c4b4tj_	Alignment		99.9	23	PDB header: hydrolase Chain: J; PDB Molecule: 26s protease regulatory subunit 8 homolog; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
20	c6hecH_	Alignment		99.9	23	PDB header: hydrolase Chain: H; PDB Molecule: proteasome-activating nucleotidase; PDBTitle: pan-proteasome in state 4
21	c4b4tl_	Alignment	not modelled	99.9	22	PDB header: hydrolase Chain: I; PDB Molecule: 26s protease regulatory subunit 4 homolog; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
22	c6nyyA_	Alignment	not modelled	99.9	18	PDB header: translocase Chain: A; PDB Molecule: afg3-like protein 2; PDBTitle: human m-aaa protease afg3l2, substrate-bound
23	c4ciuA_	Alignment	not modelled	99.9	25	PDB header: chaperone Chain: A; PDB Molecule: chaperone protein clpb; PDBTitle: crystal structure of e. coli clpb
24	c1r6bX_	Alignment	not modelled	99.9	21	PDB header: hydrolase Chain: X; PDB Molecule: clpa protein; PDBTitle: high resolution crystal structure of clpa
25	c4b4tL_	Alignment	not modelled	99.9	22	PDB header: hydrolase Chain: L; PDB Molecule: 26s protease subunit rpt4; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
26	c5t0gA_	Alignment	not modelled	99.9	21	PDB header: hydrolase Chain: A; PDB Molecule: 26s protease regulatory subunit 7; PDBTitle: structural basis for dynamic regulation of the human 26s proteasome
27	c5ifwB_	Alignment	not modelled	99.9	22	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
28	c4b4tM_	Alignment	not modelled	99.9	24	PDB header: hydrolase Chain: M; PDB Molecule: 26s protease regulatory subunit 6a; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome

29	c3hu2C_	Alignment	not modelled	99.9	22	PDB header: transport protein Chain: C; PDB Molecule: translational endoplasmic reticulum atpase; PDBTitle: structure of p97 n-d1 r86a mutant in complex with atpgs
30	c5kzfj_	Alignment	not modelled	99.9	24	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
31	c4ypnA_	Alignment	not modelled	99.9	26	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
32	c5mpaL_	Alignment	not modelled	99.9	21	PDB header: hydrolase Chain: L; PDB Molecule: 26s protease subunit rpt4; PDBTitle: 26s proteasome in presence of atp (s2)
33	c5gjqL_	Alignment	not modelled	99.9	25	PDB header: hydrolase Chain: L; PDB Molecule: 26s protease regulatory subunit 10b; PDBTitle: structure of the human 26s proteasome bound to usp14-ubal
34	c2dhrC_	Alignment	not modelled	99.9	26	PDB header: hydrolase Chain: C; PDB Molecule: ftsh; PDBTitle: whole cytosolic region of atp-dependent metalloprotease2 ftsh (g399l)
35	c4b4tK_	Alignment	not modelled	99.9	22	PDB header: hydrolase Chain: K; PDB Molecule: 26s protease regulatory subunit 6b homolog; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
36	c5kneD_	Alignment	not modelled	99.9	24	PDB header: chaperone Chain: D; PDB Molecule: heat shock protein 104; PDBTitle: cryoem reconstruction of hsp104 hexamer
37	d1r6bx3	Alignment	not modelled	99.9	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
38	c4d2qC_	Alignment	not modelled	99.9	25	PDB header: chaperone Chain: C; PDB Molecule: clpb; PDBTitle: negative-stain electron microscopy of e. coli clpb mutant e432a (bap2 form bound to clpp)
39	c5kneF_	Alignment	not modelled	99.9	28	PDB header: chaperone Chain: F; PDB Molecule: heat shock protein 104; PDBTitle: cryoem reconstruction of hsp104 hexamer
40	c6e111_	Alignment	not modelled	99.9	22	PDB header: protein transport Chain: 1; PDB Molecule: heat shock protein 101; PDBTitle: ptex core complex in the resetting (compact) state
41	d1g41a_	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
42	c6em8F_	Alignment	not modelled	99.9	30	PDB header: chaperone Chain: F; PDB Molecule: atp-dependent clp protease atp-binding subunit clpc; PDBTitle: s.aureus clpc resting state, c2 symmetrised
43	c6genX_	Alignment	not modelled	99.9	24	PDB header: nuclear protein Chain: X; PDB Molecule: ruvb-like protein 1; PDBTitle: chromatin remodeler-nucleosome complex at 4.5 a resolution.
44	c2zamA_	Alignment	not modelled	99.9	26	PDB header: protein transport Chain: A; PDB Molecule: vacuolar protein sorting-associating protein 4b; PDBTitle: crystal structure of mouse skd1/vps4b apo-form
45	c3pfiB_	Alignment	not modelled	99.9	18	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	c3b9pA_	Alignment	not modelled	99.9	22	PDB header: hydrolase Chain: A; PDB Molecule: cg5977-pa, isoform a; PDBTitle: spastin
47	c6blbA_	Alignment	not modelled	99.9	18	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
48	c5d4wB_	Alignment	not modelled	99.9	23	PDB header: chaperone Chain: B; PDB Molecule: putative heat shock protein; PDBTitle: crystal structure of hsp104
49	c2c9oA_	Alignment	not modelled	99.9	23	PDB header: hydrolase Chain: A; PDB Molecule: ruvb-like 1; PDBTitle: 3d structure of the human ruvb-like helicase ruvb1
50	c3zw6B_	Alignment	not modelled	99.9	22	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.
51	c5vy9C_	Alignment	not modelled	99.9	21	PDB header: chaperone Chain: C; PDB Molecule: heat shock protein 104; PDBTitle: s. cerevisiae hsp104:casein complex, middle domain conformation
52	c4z8xC_	Alignment	not modelled	99.9	20	PDB header: hydrolase Chain: C; PDB Molecule: atp-dependent zinc metalloprotease ftsh; PDBTitle: truncated ftsh from a. aeolicus
53	c3vkhB_	Alignment	not modelled	99.9	16	PDB header: motor protein Chain: B; PDB Molecule: dynein heavy chain, cytoplasmic; PDBTitle: x-ray structure of a functional full-length dynein motor domain
						PDB header: chaperone

54	c6em8E_	Alignment	not modelled	99.9	27	Chain: E; PDB Molecule: atp-dependent clp protease atp-binding subunit clpc; PDBTitle: s.aureus clpc resting state, c2 symmetrised
55	c1xwiA_	Alignment	not modelled	99.9	28	PDB header: protein transport Chain: A; PDB Molecule: skd1 protein; PDBTitle: crystal structure of vps4b
56	d1g8pa_	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
57	c4r7zB_	Alignment	not modelled	99.9	19	PDB header: hydrolase Chain: B; PDB Molecule: cell division control protein 21; PDBTitle: pfmc-aaa double-octamer
58	c5vq9D_	Alignment	not modelled	99.9	21	PDB header: protein binding Chain: D; PDB Molecule: pachytene checkpoint protein 2 homolog; PDBTitle: structure of human trip13, apo form
59	c5oafB_	Alignment	not modelled	99.9	22	PDB header: gene regulation Chain: B; PDB Molecule: ruvb-like 2; PDBTitle: human rvb1/rvb2 heterohexameric in ino80 complex
60	c3d8bB_	Alignment	not modelled	99.9	24	PDB header: hydrolase Chain: B; PDB Molecule: fidgetin-like protein 1; PDBTitle: crystal structure of human fidgetin-like protein 1 in complex with adp
61	d1um8a_	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
62	c3pxiB_	Alignment	not modelled	99.8	26	PDB header: protein binding Chain: B; PDB Molecule: negative regulator of genetic competence clpc/mecb; PDBTitle: structure of meca108:clpc
63	c3h4mC_	Alignment	not modelled	99.8	22	PDB header: hydrolase Chain: C; PDB Molecule: proteasome-activating nucleotidase; PDBTitle: aaa atpase domain of the proteasome- activating nucleotidase
64	c3vfdA_	Alignment	not modelled	99.8	23	PDB header: hydrolase Chain: A; PDB Molecule: spastin; PDBTitle: human spastin aaa domain
65	c4xguB_	Alignment	not modelled	99.8	22	PDB header: atp-binding protein Chain: B; PDB Molecule: putative pachytene checkpoint protein 2; PDBTitle: structure of c. elegans pch-2
66	c3pvsA_	Alignment	not modelled	99.8	20	PDB header: recombination Chain: A; PDB Molecule: replication-associated recombination protein a; PDBTitle: structure and biochemical activities of escherichia coli mgsa
67	c6az0A_	Alignment	not modelled	99.8	21	PDB header: hydrolase Chain: A; PDB Molecule: mitochondrial inner membrane f-aaa protease supercomplex PDBTitle: mitochondrial atpase protease yme1
68	c1s3sA_	Alignment	not modelled	99.8	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
69	c4i16A_	Alignment	not modelled	99.8	23	PDB header: hydrolase Chain: A; PDB Molecule: fidgetin-like protein 1; PDBTitle: crystal structure of figl-1 aaa domain in complex with adp
70	c6opcF_	Alignment	not modelled	99.8	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)
71	d1qvra3	Alignment	not modelled	99.8	25	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
72	c3eihB_	Alignment	not modelled	99.8	24	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
73	c1iy2A_	Alignment	not modelled	99.8	23	PDB header: hydrolase Chain: A; PDB Molecule: atp-dependent metalloprotease ftsH; PDBTitle: crystal structure of the ftsH atpase domain from thermus2 thermophilus
74	d1ofha_	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
75	c4ww4A_	Alignment	not modelled	99.8	23	PDB header: hydrolase Chain: A; PDB Molecule: ruvb-like 1; PDBTitle: double-heterohexameric rings of full-length rvb1(adp)/rvb2(adp)
76	c2c9oC_	Alignment	not modelled	99.8	19	PDB header: hydrolase Chain: C; PDB Molecule: ruvb-like 1; PDBTitle: 3d structure of the human ruvb-like helicase ruvb1
77	c1in8A_	Alignment	not modelled	99.8	19	PDB header: dna binding protein Chain: A; PDB Molecule: holliday junction dna helicase ruvb; PDBTitle: thermotoga maritima ruvb t158v
78	c3hteC_	Alignment	not modelled	99.8	18	PDB header: motor protein Chain: C; PDB Molecule: atp-dependent clp protease atp-binding subunit clpx; PDBTitle: crystal structure of nucleotide-free hexameric clpx
79	c6b5cA_	Alignment	not modelled	99.8	29	PDB header: cell cycle Chain: A; PDB Molecule: katanin p60 atpase-containing subunit a-like 1; PDBTitle: structural basis for katanin self-assembly
80	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
81	c3vkhA	Alignment	not modelled	99.8	19	PDB header: motor protein Chain: A; PDB Molecule: dynein heavy chain, cytoplasmic; PDBTitle: x-ray structure of a functional full-length dynein motor domain
82	c1xxhB	Alignment	not modelled	99.8	23	PDB header: transferase Chain: B; PDB Molecule: dna polymerase iii subunit gamma; PDBTitle: atpgs bound e. coli clamp loader complex
83	c1nsfA	Alignment	not modelled	99.8	16	PDB header: protein transport Chain: A; PDB Molecule: n-ethylmaleimide sensitive factor; PDBTitle: d2 hexamerization domain of n-ethylmaleimide sensitive factor (nsf)
84	c3uk6H	Alignment	not modelled	99.8	17	PDB header: hydrolase Chain: H; PDB Molecule: ruvb-like 2; PDBTitle: crystal structure of the tip48 (tip49b) hexamer
85	c5wc0D	Alignment	not modelled	99.8	24	PDB header: motor protein Chain: D; PDB Molecule: meiotic spindle formation protein mei-1; PDBTitle: katanin hexamer in spiral conformation
86	c5w0tA	Alignment	not modelled	99.8	20	PDB header: hydrolase Chain: A; PDB Molecule: protein msp1; PDBTitle: crystal structure of monomeric msp1 from s. cerevisiae
87	c4ww4B	Alignment	not modelled	99.8	19	PDB header: hydrolase Chain: B; PDB Molecule: ruvb-like 2; PDBTitle: double-heterohexameric rings of full-length rvb1(adp)/rvb2(adp)
88	d2ce7a2	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
89	d1ny5a2	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
90	c2ce7B	Alignment	not modelled	99.8	22	PDB header: cell division protein Chain: B; PDB Molecule: cell division protein ftsh; PDBTitle: edta treated
91	d1njfa	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
92	c6em8H	Alignment	not modelled	99.8	24	PDB header: chaperone Chain: H; PDB Molecule: atp-dependent clp protease atp-binding subunit clpc; PDBTitle: s.aureus clpc resting state, c2 symmetrised
93	c4lcbA	Alignment	not modelled	99.8	18	PDB header: protein transport Chain: A; PDB Molecule: cell division protein cdvc, vps4; PDBTitle: structure of vps4 homolog from acidianus hospitalis
94	c3j96F	Alignment	not modelled	99.8	23	PDB header: hydrolase Chain: F; PDB Molecule: vesicle-fusing atpase; PDBTitle: structure of 20s supercomplex determined by single particle2 cryoelectron microscopy (state i)
95	c6djuA	Alignment	not modelled	99.8	24	PDB header: chaperone Chain: A; PDB Molecule: chaperone protein clpb; PDBTitle: mtb clpb in complex with atpgammas and casein, conformer 1
96	c6hypA	Alignment	not modelled	99.8	20	PDB header: motor protein Chain: A; PDB Molecule: midasin,midasin; PDBTitle: rea1 wild type adp state (aaa+ ring part)
97	c2x8aA	Alignment	not modelled	99.8	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
98	c6or5A	Alignment	not modelled	99.8	17	PDB header: motor protein Chain: A; PDB Molecule: midasin; PDBTitle: full-length s. pombe mdn1 in the presence of amppnp (ring region)
99	c6mdnF	Alignment	not modelled	99.8	15	PDB header: hydrolase Chain: F; PDB Molecule: vesicle-fusing atpase; PDBTitle: the 20s supercomplex engaging the snap-25 n-terminus (class 2)
100	c2qz4A	Alignment	not modelled	99.8	23	PDB header: hydrolase Chain: A; PDB Molecule: paraplegin; PDBTitle: human paraplegin, aaa domain in complex with adp
101	d1ixsb2	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
102	c5nugB	Alignment	not modelled	99.8	20	PDB header: motor protein Chain: B; PDB Molecule: cytoplasmic dynein 1 heavy chain 1; PDBTitle: motor domains from human cytoplasmic dynein-1 in the phi-particle2 conformation
103	c3k1jA	Alignment	not modelled	99.8	17	PDB header: hydrolase Chain: A; PDB Molecule: atp-dependent protease lon; PDBTitle: crystal structure of lon protease from thermococcus onnurineus na1
104	d1d2na	Alignment	not modelled	99.8	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
105	c2chgB	Alignment	not modelled	99.8	16	PDB header: dna-binding protein Chain: B; PDB Molecule: replication factor c small subunit; PDBTitle: replication factor c domains 1 and 2
106	c3vkgA	Alignment	not modelled	99.8	17	PDB header: motor protein Chain: A; PDB Molecule: dynein heavy chain, cytoplasmic; PDBTitle: x-ray structure of an mtbd truncation mutant of dynein motor domain
107	c5op4A	Alignment	not modelled	99.8	16	PDB header: transcription Chain: A; PDB Molecule: putative repressor protein luxo;

107	c3ep4A_	Alignment	not modelled	99.8	10	PDBTitle: structure, regulation, and inhibition of the quorum-sensing signal2 integrator luxo
108	d1iqpa2	Alignment	not modelled	99.8	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
109	c1sxjA_	Alignment	not modelled	99.8	15	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)
110	c5kneA_	Alignment	not modelled	99.8	20	PDB header: chaperone Chain: A; PDB Molecule: heat shock protein 104; PDBTitle: cryoem reconstruction of hsp104 hexamer
111	c4akgB_	Alignment	not modelled	99.8	17	PDB header: motor protein Chain: B; PDB Molecule: glutathione s-transferase class-mu 26 kda isozyme, dynein PDBTitle: dynein motor domain - atp complex
112	c5ubvB_	Alignment	not modelled	99.8	23	PDB header: hydrolase Chain: B; PDB Molecule: atpase domain of i-aaa protease; PDBTitle: atpase domain of i-aaa protease from myceliophthora thermophila
113	c5j1sA_	Alignment	not modelled	99.8	14	PDB header: hydrolase Chain: A; PDB Molecule: torsin-1a; PDBTitle: torsina-lul1 complex, h. sapiens, bound to vhh-bs2
114	c3u5zM_	Alignment	not modelled	99.8	19	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
115	c4yplE_	Alignment	not modelled	99.8	23	PDB header: hydrolase Chain: E; PDB Molecule: lon protease; PDBTitle: crystal structure of a hexameric lona protease bound to three adps
116	c1ojlD_	Alignment	not modelled	99.8	16	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
117	c2r65A_	Alignment	not modelled	99.8	20	PDB header: hydrolase Chain: A; PDB Molecule: cell division protease ftsh homolog; PDBTitle: crystal structure of helicobacter pylori atp dependent protease, ftsh2 adp complex
118	c4w8fA_	Alignment	not modelled	99.8	16	PDB header: motor protein Chain: A; PDB Molecule: dynein heavy chain lysozyme chimera; PDBTitle: crystal structure of the dynein motor domain in the amppnp-bound state
119	c3vkgB_	Alignment	not modelled	99.8	19	PDB header: motor protein Chain: B; PDB Molecule: dynein heavy chain, cytoplasmic; PDBTitle: x-ray structure of an mtbd truncation mutant of dynein motor domain
120	c6hz4B_	Alignment	not modelled	99.8	17	PDB header: dna binding protein Chain: B; PDB Molecule: 5-methylcytosine-specific restriction enzyme b; PDBTitle: structure of mcrcb without dna binding domains (one half of the full2 complex)