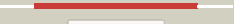



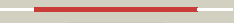










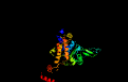



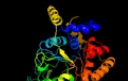


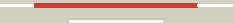

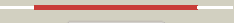















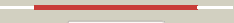

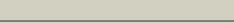
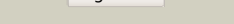
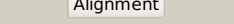
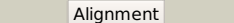




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1479_(moxR1)_1669289_1670422
Date	Fri Aug 2 13:30:06 BST 2019
Unique Job ID	94b194069857c2a2

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2r44A_	 Alignment		100.0	44	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
2	c3nbxX_	 Alignment		100.0	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
3	c4r7zB_	 Alignment		100.0	18	PDB header: hydrolase Chain: B; PDB Molecule: cell division control protein 21; PDBTitle: pfmcm-aaa double-octamer
4	c5udb7_	 Alignment		100.0	23	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	c3ja87_	 Alignment		100.0	23	PDB header: hydrolase Chain: 7; PDB Molecule: minichromosome maintenance 7; PDBTitle: cryo-em structure of the mcm2-7 double hexamer
6	c5h7i7_	 Alignment		100.0	23	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	c3f8tA_	 Alignment		100.0	20	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
8	c3jc76_	 Alignment		100.0	16	PDB header: hydrolase Chain: 6; PDB Molecule: dna replication licensing factor mcm6; PDBTitle: structure of the eukaryotic replicative cmg helicase and pumpjack2 motion
9	c3ja82_	 Alignment		100.0	20	PDB header: hydrolase Chain: 2; PDB Molecule: minichromosome maintenance 2; PDBTitle: cryo-em structure of the mcm2-7 double hexamer
10	c5udb3_	 Alignment		100.0	17	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
11	d1g8pa_	 Alignment		100.0	23	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain

12	c3jc57_	 Alignment		100.0	23	PDB header: hydrolase Chain: 7; PDB Molecule: dna replication licensing factor mcm7; PDBTitle: structure of the eukaryotic replicative cmg helicase and pumpjack2 motion
13	c6hv92_	 Alignment		100.0	18	PDB header: dna binding protein Chain: 2; PDB Molecule: dna replication licensing factor mcm2; PDBTitle: s. cerevisiae cmg-pol epsilon-dna
14	c3ja84_	 Alignment		100.0	20	PDB header: hydrolase Chain: 4; PDB Molecule: minichromosome maintenance 4; PDBTitle: cryo-em structure of the mcm2-7 double hexamer
15	c3ja83_	 Alignment		100.0	18	PDB header: hydrolase Chain: 3; PDB Molecule: minichromosome maintenance 3; PDBTitle: cryo-em structure of the mcm2-7 double hexamer
16	c3ja86_	 Alignment		100.0	14	PDB header: hydrolase Chain: 6; PDB Molecule: minichromosome maintenance 6; PDBTitle: cryo-em structure of the mcm2-7 double hexamer
17	c5v8f3_	 Alignment		100.0	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
18	c3ja85_	 Alignment		100.0	19	PDB header: hydrolase Chain: 5; PDB Molecule: minichromosome maintenance 5; PDBTitle: cryo-em structure of the mcm2-7 double hexamer
19	c5u8s4_	 Alignment		100.0	19	PDB header: replication Chain: 4; PDB Molecule: dna replication licensing factor mcm4; PDBTitle: structure of eukaryotic cmg helicase at a replication fork
20	c6hv96_	 Alignment		100.0	16	PDB header: dna binding protein Chain: 6; PDB Molecule: dna replication licensing factor mcm6; PDBTitle: s. cerevisiae cmg-pol epsilon-dna
21	c3jc72_	 Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: 2; PDB Molecule: dna replication licensing factor mcm2; PDBTitle: structure of the eukaryotic replicative cmg helicase and pumpjack2 motion
22	c5udb5_	 Alignment	not modelled	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
23	c6hv93_	 Alignment	not modelled	100.0	19	PDB header: dna binding protein Chain: 3; PDB Molecule: dna replication licensing factor mcm3; PDBTitle: s. cerevisiae cmg-pol epsilon-dna
24	c3jc55_	 Alignment	not modelled	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
25	c6hv97_	 Alignment	not modelled	100.0	24	PDB header: dna binding protein Chain: 7; PDB Molecule: dna replication licensing factor mcm7; PDBTitle: s. cerevisiae cmg-pol epsilon-dna
26	c3f9vA_	 Alignment	not modelled	100.0	20	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	c3jc73_	 Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: 3; PDB Molecule: dna replication licensing factor mcm3; PDBTitle: structure of the eukaryotic replicative cmg helicase and pumpjack2 motion
28	c3jc54_	 Alignment	not modelled	99.9	20	PDB header: hydrolase Chain: 4; PDB Molecule: dna replication licensing factor mcm4; PDBTitle: structure of the eukaryotic replicative cmg helicase and pumpjack2 motion

29	c3k1jA_	Alignment	not modelled	99.9	26	PDB header: hydrolase Chain: A; PDB Molecule: atp-dependent protease lon; PDBTitle: crystal structure of lon protease from thermococcus onnurineus na1
30	c6nyyC_	Alignment	not modelled	99.9	20	PDB header: translocase Chain: C; PDB Molecule: afg3-like protein 2; PDBTitle: human m-aaa protease afg3l2, substrate-bound
31	c5g4gF_	Alignment	not modelled	99.9	21	PDB header: hydrolase Chain: F; PDB Molecule: vcp-like atpase; PDBTitle: structure of the atpgs-bound vat complex
32	c2c9oA_	Alignment	not modelled	99.9	25	PDB header: hydrolase Chain: A; PDB Molecule: ruvb-like 1; PDBTitle: 3d structure of the human ruvb-like helicase ruvb1l
33	c1qvrB_	Alignment	not modelled	99.9	19	PDB header: chaperone Chain: B; PDB Molecule: clpb protein; PDBTitle: crystal structure analysis of clpb
34	d1um8a_	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
35	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
36	c6azyA_	Alignment	not modelled	99.9	17	PDB header: chaperone Chain: A; PDB Molecule: heat shock protein hsp104; PDBTitle: crystal structure of hsp104 r328m/r757m mutant from calcarisporiella2 thermophila
37	c4ww4A_	Alignment	not modelled	99.9	26	PDB header: hydrolase Chain: A; PDB Molecule: ruvb-like 1; PDBTitle: double-heterohexameric rings of full-length rvb1(adp)/rvb2(adp)
38	c6em8F_	Alignment	not modelled	99.9	20	PDB header: chaperone Chain: F; PDB Molecule: atp-dependent clp protease atp-binding subunit clpc; PDBTitle: s.aureus clpc resting state, c2 symmetrised
39	c1r6bX_	Alignment	not modelled	99.9	20	PDB header: hydrolase Chain: X; PDB Molecule: clpa protein; PDBTitle: high resolution crystal structure of clpa
40	c5e7pA_	Alignment	not modelled	99.9	21	PDB header: hydrolase Chain: A; PDB Molecule: cell division control protein cdc48; PDBTitle: crystal structure of msmeq_0858 (uniprot a0qqs4), a aaa atpase.
41	d1g41a_	Alignment	not modelled	99.9	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
42	c5kneD_	Alignment	not modelled	99.9	15	PDB header: chaperone Chain: D; PDB Molecule: heat shock protein 104; PDBTitle: cryoem reconstruction of hsp104 hexamer
43	c5kneF_	Alignment	not modelled	99.9	15	PDB header: chaperone Chain: F; PDB Molecule: heat shock protein 104; PDBTitle: cryoem reconstruction of hsp104 hexamer
44	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
45	c6nyyA_	Alignment	not modelled	99.9	17	PDB header: translocase Chain: A; PDB Molecule: afg3-like protein 2; PDBTitle: human m-aaa protease afg3l2, substrate-bound
46	c3pfiB_	Alignment	not modelled	99.9	20	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
47	c4ciuA_	Alignment	not modelled	99.9	18	PDB header: chaperone Chain: A; PDB Molecule: chaperone protein clpb; PDBTitle: crystal structure of e. coli clpb
48	d1qvra3	Alignment	not modelled	99.9	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
49	c6epcJ_	Alignment	not modelled	99.9	27	PDB header: hydrolase Chain: J; PDB Molecule: 26s proteasome regulatory subunit 8; PDBTitle: ground state 26s proteasome (gs2)
50	c6blbA_	Alignment	not modelled	99.9	22	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
51	c4b4tH_	Alignment	not modelled	99.9	23	PDB header: hydrolase Chain: H; PDB Molecule: 26s protease regulatory subunit 7 homolog; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
52	c3cf1C_	Alignment	not modelled	99.9	15	PDB header: transport protein Chain: C; PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: structure of p97/vcp in complex with adp/adp.afx
53	c2dhrC_	Alignment	not modelled	99.9	22	PDB header: hydrolase Chain: C; PDB Molecule: ftsh; PDBTitle: whole cytosolic region of atp-dependent metalloprotease2 ftsh (g399l)
54	c6epdM_	Alignment	not modelled	99.9	22	PDB header: hydrolase Chain: M; PDB Molecule: 26s proteasome regulatory subunit 6a; PDBTitle: substrate processing state 26s proteasome (sps1)

55	d1ofha_	Alignment	not modelled	99.9	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
56	c4b4tl_	Alignment	not modelled	99.9	23	PDB header: hydrolase Chain: I: PDB Molecule: 26s protease regulatory subunit 4 homolog; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
57	c4b4tj_	Alignment	not modelled	99.9	21	PDB header: hydrolase Chain: J: PDB Molecule: 26s protease regulatory subunit 8 homolog; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
58	c4d2qC_	Alignment	not modelled	99.9	17	PDB header: chaperone Chain: C: PDB Molecule: clpb; PDBTitle: negative-stain electron microscopy of e. coli clpb mutant e432a (bap2 form bound to clpp)
59	c3hteC_	Alignment	not modelled	99.9	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
60	c4b4tL_	Alignment	not modelled	99.9	21	PDB header: hydrolase Chain: L: PDB Molecule: 26s protease subunit rpt4; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
61	c6i26A_	Alignment	not modelled	99.9	22	PDB header: motor protein Chain: A: PDB Molecule: midasin,midasin,midasin,midasin; PDBTitle: rea1 wild type amppnp state
62	c5kzfl_	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: J: PDB Molecule: proteasome-associated atpase; PDBTitle: crystal structure of near full-length hexameric mycobacterium2 tuberculosis proteasomal atpase mpa in apo form
63	c6e111_	Alignment	not modelled	99.9	16	PDB header: protein transport Chain: 1: PDB Molecule: heat shock protein 101; PDBTitle: ptex core complex in the resetting (compact) state
64	c5vy9C_	Alignment	not modelled	99.9	17	PDB header: chaperone Chain: C: PDB Molecule: heat shock protein 104; PDBTitle: s. cerevisiae hsp104:casein complex, middle domain conformation
65	c5ifwB_	Alignment	not modelled	99.9	15	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
66	c5t0gA_	Alignment	not modelled	99.9	23	PDB header: hydrolase Chain: A: PDB Molecule: 26s protease regulatory subunit 7; PDBTitle: structural basis for dynamic regulation of the human 26s proteasome
67	c5oafB_	Alignment	not modelled	99.9	21	PDB header: gene regulation Chain: B: PDB Molecule: ruvb-like 2; PDBTitle: human rvb1/rvb2 heterohexameric in ino80 complex
68	c2c9oC_	Alignment	not modelled	99.9	20	PDB header: hydrolase Chain: C: PDB Molecule: ruvb-like 1; PDBTitle: 3d structure of the human ruvb-like helicase ruvb1
69	c3uk6H_	Alignment	not modelled	99.9	19	PDB header: hydrolase Chain: H: PDB Molecule: ruvb-like 2; PDBTitle: crystal structure of the tip48 (tip49b) hexamer
70	c6matE_	Alignment	not modelled	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
71	c5d4wB_	Alignment	not modelled	99.9	19	PDB header: chaperone Chain: B: PDB Molecule: putative heat shock protein; PDBTitle: crystal structure of hsp104
72	c4b4tK_	Alignment	not modelled	99.9	24	PDB header: hydrolase Chain: K: PDB Molecule: 26s protease regulatory subunit 6b homolog; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
73	c4ypnA_	Alignment	not modelled	99.9	26	PDB header: hydrolase Chain: A: PDB Molecule: lon protease; PDBTitle: crystal structure of a lon fragment containing the 3-helix bundle and2 the aaa-alpha/beta domain
74	c6hecH_	Alignment	not modelled	99.9	27	PDB header: hydrolase Chain: H: PDB Molecule: proteasome-activating nucleotidase; PDBTitle: pan-proteasome in state 4
75	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)
76	c6em8E_	Alignment	not modelled	99.9	19	PDB header: chaperone Chain: E: PDB Molecule: atp-dependent clp protease atp-binding subunit clpc; PDBTitle: s.aureus clpc resting state, c2 symmetrised
77	c5c3cB_	Alignment	not modelled	99.9	19	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
78	c5gjql_	Alignment	not modelled	99.9	20	PDB header: hydrolase Chain: L: PDB Molecule: 26s protease regulatory subunit 10b; PDBTitle: structure of the human 26s proteasome bound to usp14-ubal
79	c3b9pA_	Alignment	not modelled	99.9	23	PDB header: hydrolase Chain: A: PDB Molecule: cg5977-pa, isoform a; PDBTitle: spastin
80	c6em8H_	Alignment	not modelled	99.9	18	PDB header: chaperone Chain: H: PDB Molecule: atp-dependent clp protease atp-binding subunit clpc; PDBTitle: s.aureus clpc resting state, c2 symmetrised PDB header: chaperone

81	c6djuA	Alignment	not modelled	99.9	17	Chain: A; PDB Molecule: chaperone protein clpb; PDBTitle: mtb clpb in complex with atpgammas and casein, conformer 1
82	c3pxiB	Alignment	not modelled	99.8	18	PDB header: protein binding Chain: B; PDB Molecule: negative regulator of genetic competence clpc/mecb; PDBTitle: structure of meca108:clpc
83	c4b4tM	Alignment	not modelled	99.8	22	PDB header: hydrolase Chain: M; PDB Molecule: 26s protease regulatory subunit 6a; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
84	c1ojjD	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
85	c4xguB	Alignment	not modelled	99.8	17	PDB header: atp-binding protein Chain: B; PDB Molecule: putative pachytene checkpoint protein 2; PDBTitle: structure of c. elegans pch-2
86	c3hu2C	Alignment	not modelled	99.8	24	PDB header: transport protein Chain: C; PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: structure of p97 n-d1 r86a mutant in complex with atpgs
87	c4lcbA	Alignment	not modelled	99.8	22	PDB header: protein transport Chain: A; PDB Molecule: cell division protein cdvc, vps4; PDBTitle: structure of vps4 homolog from acidianus hospitalis
88	c1in8A	Alignment	not modelled	99.8	21	PDB header: dna binding protein Chain: A; PDB Molecule: holliday junction dna helicase ruvb; PDBTitle: thermotoga maritima ruvb t158v
89	c3cf2B	Alignment	not modelled	99.8	19	PDB header: transport protein Chain: B; PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: structure of p97/vcp in complex with adp/amp-pnp
90	c3vfdA	Alignment	not modelled	99.8	20	PDB header: hydrolase Chain: A; PDB Molecule: spastin; PDBTitle: human spastin aaa domain
91	c3d8bB	Alignment	not modelled	99.8	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
92	c6genX	Alignment	not modelled	99.8	29	PDB header: nuclear protein Chain: X; PDB Molecule: ruvb-like protein 1; PDBTitle: chromatin remodeller-nucleosome complex at 4.5 a resolution.
93	c1xwIA	Alignment	not modelled	99.8	17	PDB header: protein transport Chain: A; PDB Molecule: skd1 protein; PDBTitle: crystal structure of vps4b
94	c3eihB	Alignment	not modelled	99.8	14	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
95	c3h4mC	Alignment	not modelled	99.8	23	PDB header: hydrolase Chain: C; PDB Molecule: proteasome-activating nucleotidase; PDBTitle: aaa atpase domain of the proteasome- activating nucleotidase
96	c5ep4A	Alignment	not modelled	99.8	17	PDB header: transcription Chain: A; PDB Molecule: putative repressor protein luxo; PDBTitle: structure, regulation, and inhibition of the quorum-sensing signal2 integrator luxo
97	c4z8xC	Alignment	not modelled	99.8	20	PDB header: hydrolase Chain: C; PDB Molecule: atp-dependent zinc metalloprotease ftsh; PDBTitle: truncated ftsh from a. aeolicus
98	c6qi8E	Alignment	not modelled	99.8	17	PDB header: chaperone Chain: E; PDB Molecule: ruvb-like 2; PDBTitle: truncated human r2tp complex, structure 3 (adp-filled)
99	d1ixsb2	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
100	c2ce7B	Alignment	not modelled	99.8	21	PDB header: cell division protein Chain: B; PDB Molecule: cell division protein ftsh; PDBTitle: edta treated
101	d1in4a2	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	c6az0A	Alignment	not modelled	99.8	22	PDB header: hydrolase Chain: A; PDB Molecule: mitochondrial inner membrane i-aaa protease supercomplex PDBTitle: mitochondrial atpase protease yme1
103	d2ce7a2	Alignment	not modelled	99.8	23	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
104	c4l16A	Alignment	not modelled	99.8	15	PDB header: hydrolase Chain: A; PDB Molecule: fidgetin-like protein 1; PDBTitle: crystal structure of figl-1 aaa domain in complex with adp
105	d1ny5a2	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
106	c5kneA	Alignment	not modelled	99.8	19	PDB header: chaperone Chain: A; PDB Molecule: heat shock protein 104; PDBTitle: cryoem reconstruction of hsp104 hexamer
107	d1r6bx2	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	c4ww4B_	Alignment	not modelled	99.8	20	PDB header: hydrolase Chain: B; PDB Molecule: ruvb-like 2; PDBTitle: double-heterohexameric rings of full-length rvb1(adp)/rvb2(adp)
109	c6hz4B_	Alignment	not modelled	99.8	20	PDB header: dna binding protein Chain: B; PDB Molecule: 5-methylcytosine-specific restriction enzyme b; PDBTitle: structure of mcrbc without dna binding domains (one half of the full2 complex)
110	c4yp1E_	Alignment	not modelled	99.8	20	PDB header: hydrolase Chain: E; PDB Molecule: lon protease; PDBTitle: crystal structure of a hexameric lona protease bound to three adps
111	c2zamA_	Alignment	not modelled	99.8	18	PDB header: protein transport Chain: A; PDB Molecule: vacuolar protein sorting-associating protein 4b; PDBTitle: crystal structure of mouse skd1/vps4b apo-form
112	c6b5cA_	Alignment	not modelled	99.8	16	PDB header: cell cycle Chain: A; PDB Molecule: katanin p60 atpase-containing subunit a-like 1; PDBTitle: structural basis for katanin self-assembly
113	c5ubvB_	Alignment	not modelled	99.8	19	PDB header: hydrolase Chain: B; PDB Molecule: atpase domain of i-aaa protease; PDBTitle: atpase domain of i-aaa protease from myceliophthora thermophila
114	c6djvE_	Alignment	not modelled	99.8	19	PDB header: chaperone Chain: E; PDB Molecule: chaperone protein clpb; PDBTitle: mtb clpb in complex with atpgammas and casein, conformer 2
115	c5w0tA_	Alignment	not modelled	99.8	15	PDB header: hydrolase Chain: A; PDB Molecule: protein msp1; PDBTitle: crystal structure of monomeric msp1 from s. cerevisiae
116	c5exsA_	Alignment	not modelled	99.8	17	PDB header: transcription Chain: A; PDB Molecule: transcriptional regulator fleq; PDBTitle: aaa+ atpase fleq from pseudomonas aeruginosa bound to atp-gamma-s
117	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
118	c6i27A_	Alignment	not modelled	99.8	26	PDB header: motor protein Chain: A; PDB Molecule: midasin,midasin,midasin,midasin,midasin,midasin; PDBTitle: rea1 aaa2l-h2alpha deletion mutant in amppnp state
119	c6edoA_	Alignment	not modelled	99.8	24	PDB header: motor protein Chain: A; PDB Molecule: midasin; PDBTitle: full-length s. pombe mdn1 in the presence of amppnp (ring region)
120	c1o1f_	Alignment	not modelled	99.8	15	PDB header: response regulator Chain: F; PDB Molecule: transcriptional regulatory protein zrar; PDBTitle: crystal structure of a sigma54-activator suggests the mechanism for2 the conformational switch necessary for sigma54 binding