










Phyre2

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 Description RVBD3692_(moxR2)_4133694_4134770
 Date Fri Aug 9 18:20:38 BST 2019
 Unique Job ID ec6053c295b73f15

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2r44A_	Alignment		100.0	40	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	22	PDB header: hydrolase Chain: B; PDB Molecule: cell division control protein 21; PDBTitle: pfmcm-aaa double-octamer
4	d1g8pa_	Alignment		100.0	27	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
5	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
6	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
7	c5h7i7_	Alignment		100.0	22	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
8	c5udb3_	Alignment		100.0	21	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
9	c3f8tA_	Alignment		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
10	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
11	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

12	c3ja82_	Alignment		100.0	19	PDB header: hydrolase Chain: 2; PDB Molecule: minichromosome maintenance 2; PDBTitle: cryo-em structure of the mcm2-7 double hexamer
13	c3ja83_	Alignment		100.0	21	PDB header: hydrolase Chain: 3; PDB Molecule: minichromosome maintenance 3; PDBTitle: cryo-em structure of the mcm2-7 double hexamer
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	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
16	c5v8f3_	Alignment		100.0	21	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	c5u8s4_	Alignment		100.0	21	PDB header: replication Chain: 4; PDB Molecule: dna replication licensing factor mcm4; PDBTitle: structure of eukaryotic cmg helicase at a replication fork
18	c6hv92_	Alignment		100.0	19	PDB header: dna binding protein Chain: 2; PDB Molecule: dna replication licensing factor mcm2; PDBTitle: s. cerevisiae cmg-pol epsilon-dna
19	c6hv96_	Alignment		100.0	19	PDB header: dna binding protein Chain: 6; PDB Molecule: dna replication licensing factor mcm6; PDBTitle: s. cerevisiae cmg-pol epsilon-dna
20	c3f9vA_	Alignment		100.0	22	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
21	c3jc57_	Alignment	not modelled	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
22	c3jc72_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: 2; PDB Molecule: dna replication licensing factor mcm2; PDBTitle: structure of the eukaryotic replicative cmg helicase and pumpjack2 motion
23	c6hv93_	Alignment	not modelled	100.0	20	PDB header: dna binding protein Chain: 3; PDB Molecule: dna replication licensing factor mcm3; PDBTitle: s. cerevisiae cmg-pol epsilon-dna
24	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
25	c3jc55_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: 5; PDB Molecule: minichromosome maintenance protein 5; PDBTitle: structure of the eukaryotic replicative cmg helicase and pumpjack2 motion
26	c3jc73_	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: 3; PDB Molecule: dna replication licensing factor mcm3; PDBTitle: structure of the eukaryotic replicative cmg helicase and pumpjack2 motion
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	23	PDB header: hydrolase Chain: A; PDB Molecule: atp-dependent protease lon; PDBTitle: crystal structure of lon protease from thermococcus onnurineus na1
						PDB header: translocase

29	c6nyyC_	Alignment	not modelled	99.9	18	Chain: C: PDB Molecule: afg3-like protein 2; PDBTitle: human m-aaa protease afg3l2, substrate-bound
30	c5g4gF_	Alignment	not modelled	99.9	21	PDB header: hydrolase Chain: F: PDB Molecule: vcvp-like atpase; PDBTitle: structure of the atpgs-bound vat complex
31	c3jc54_	Alignment	not modelled	99.9	21	PDB header: hydrolase Chain: 4: PDB Molecule: dna replication licensing factor mcm4; PDBTitle: structure of the eukaryotic replicative cmg helicase and pumpjack2 motion
32	c6i26A_	Alignment	not modelled	99.9	23	PDB header: motor protein Chain: A: PDB Molecule: midasin,midasin,midasin,midasin; PDBTitle: rea1 wild type amppnp state
33	c5e7pA_	Alignment	not modelled	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.
34	c3cf1C_	Alignment	not modelled	99.9	19	PDB header: transport protein Chain: C: PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: structure of p97/vcp in complex with adp/adp.alfx
35	c1r6bX_	Alignment	not modelled	99.9	20	PDB header: hydrolase Chain: X: PDB Molecule: clpa protein; PDBTitle: high resolution crystal structure of clpa
36	d1r6bx3	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
37	d1g41a_	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
38	c5kneD_	Alignment	not modelled	99.9	18	PDB header: chaperone Chain: D: PDB Molecule: heat shock protein 104; PDBTitle: cryoem reconstruction of hsp104 hexamer
39	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 ruvb1l
40	c1qvrB_	Alignment	not modelled	99.9	19	PDB header: chaperone Chain: B: PDB Molecule: clpb protein; PDBTitle: crystal structure analysis of clpb
41	c6azyA_	Alignment	not modelled	99.9	18	PDB header: chaperone Chain: A: PDB Molecule: heat shock protein hsp104; PDBTitle: crystal structure of hsp104 r328m/r757m mutant from calcarisporiella2 thermophila
42	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
43	c6blbA_	Alignment	not modelled	99.9	23	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
44	c3pfiB_	Alignment	not modelled	99.9	22	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
45	c6epcJ_	Alignment	not modelled	99.9	25	PDB header: hydrolase Chain: J: PDB Molecule: 26s proteasome regulatory subunit 8; PDBTitle: ground state 26s proteasome (gs2)
46	c2dhrC_	Alignment	not modelled	99.9	23	PDB header: hydrolase Chain: C: PDB Molecule: ftsh; PDBTitle: whole cytosolic region of atp-dependent metalloprotease2 ftsh (g399l)
47	c6nyyA_	Alignment	not modelled	99.9	16	PDB header: translocase Chain: A: PDB Molecule: afg3-like protein 2; PDBTitle: human m-aaa protease afg3l2, substrate-bound
48	c5kneF_	Alignment	not modelled	99.9	20	PDB header: chaperone Chain: F: PDB Molecule: heat shock protein 104; PDBTitle: cryoem reconstruction of hsp104 hexamer
49	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
50	c4b4tH_	Alignment	not modelled	99.9	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
51	c4b4tI_	Alignment	not modelled	99.9	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
52	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
53	c6epdM_	Alignment	not modelled	99.9	21	PDB header: hydrolase Chain: M: PDB Molecule: 26s proteasome regulatory subunit 6a; PDBTitle: substrate processing state 26s proteasome (sps1)
54	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
55	c4ww4A_	Alignment	not modelled	99.9	23	PDB header: hydrolase Chain: A: PDB Molecule: ruvb-like 1; PDBTitle: double-heterohexameric rings of full-length rvb1(adp)/rvb2(adp)
56	c4b4tL_	Alignment	not modelled	99.9	20	PDB header: hydrolase Chain: L: PDB Molecule: 26s protease subunit rpt4; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
57	c5vq9D_	Alignment	not modelled	99.9	18	PDB header: protein binding Chain: D: PDB Molecule: pachytene checkpoint protein 2 homolog; PDBTitle: structure of human trip13, apo form
58	c3cf2B_	Alignment	not modelled	99.9	21	PDB header: transport protein Chain: B: PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: structure of p97/vcp in complex with adp/amp-pnp
59	d1qvra3	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
60	c6hecH_	Alignment	not modelled	99.9	26	PDB header: hydrolase Chain: H: PDB Molecule: proteasome-activating nucleotidase; PDBTitle: pan-proteasome in state 4
61	c3hteC_	Alignment	not modelled	99.9	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
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	c5ifwB_	Alignment	not modelled	99.9	20	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
64	c5kzfl_	Alignment	not modelled	99.8	20	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
65	c4b4tK_	Alignment	not modelled	99.8	19	PDB header: hydrolase Chain: K: PDB Molecule: 26s protease regulatory subunit 6b homolog; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
66	c4b4tM_	Alignment	not modelled	99.8	21	PDB header: hydrolase Chain: M: PDB Molecule: 26s protease regulatory subunit 6a; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
67	c3hu2C_	Alignment	not modelled	99.8	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
68	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
69	c4d2qC_	Alignment	not modelled	99.8	18	PDB header: chaperone Chain: C: PDB Molecule: clpb; PDBTitle: negative-stain electron microscopy of e. coli clpb mutant e432a (bap2 form bound to clpp)
70	c6edoA_	Alignment	not modelled	99.8	19	PDB header: motor protein Chain: A: PDB Molecule: midasin; PDBTitle: full-length s. pombe mdn1 in the presence of amppnp (ring region)
71	c5mpaL_	Alignment	not modelled	99.8	21	PDB header: hydrolase Chain: L: PDB Molecule: 26s protease subunit rpt4; PDBTitle: 26s proteasome in presence of atp (s2)
72	c6matE_	Alignment	not modelled	99.8	18	PDB header: ribosomal protein Chain: E: PDB Molecule: rix7 mutant; PDBTitle: cryo-em structure of the essential ribosome assembly aaa-atpase rix7
73	c5c3cB_	Alignment	not modelled	99.8	20	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
74	c5t0gA_	Alignment	not modelled	99.8	21	PDB header: hydrolase Chain: A: PDB Molecule: 26s protease regulatory subunit 7; PDBTitle: structural basis for dynamic regulation of the human 26s proteasome
75	c5vy9C_	Alignment	not modelled	99.8	18	PDB header: chaperone Chain: C: PDB Molecule: heat shock protein 104; PDBTitle: s. cerevisiae hsp104:casein complex, middle domain conformation
76	c5gjqL_	Alignment	not modelled	99.8	23	PDB header: hydrolase Chain: L: PDB Molecule: 26s protease regulatory subunit 10b; PDBTitle: structure of the human 26s proteasome bound to usp14-ubal
77	c6az0A_	Alignment	not modelled	99.8	21	PDB header: hydrolase Chain: A: PDB Molecule: mitochondrial inner membrane i-aaa protease supercomplex PDBTitle: mitochondrial atpase protease yme1
78	c6e11L_	Alignment	not modelled	99.8	17	PDB header: protein transport Chain: 1: PDB Molecule: heat shock protein 101; PDBTitle: ptex core complex in the resetting (compact) state
79	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
						PDB header: dna binding protein

80	c1in8A_	Alignment	not modelled	99.8	25	Chain: A: PDB Molecule: holliday junction dna helicase ruvb; PDBTitle: thermotoga maritima ruvb t158v
81	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
82	c5d4wB_	Alignment	not modelled	99.8	18	PDB header: chaperone Chain: B: PDB Molecule: putative heat shock protein; PDBTitle: crystal structure of hsp104
83	c4ypnA_	Alignment	not modelled	99.8	20	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
84	c2ce7B_	Alignment	not modelled	99.8	22	PDB header: cell division protein Chain: B: PDB Molecule: cell division protein ftsh; PDBTitle: edta treated
85	c3b9pA_	Alignment	not modelled	99.8	25	PDB header: hydrolase Chain: A: PDB Molecule: cg5977-pa, isoform a; PDBTitle: spastin
86	c4i16A_	Alignment	not modelled	99.8	22	PDB header: hydrolase Chain: A: PDB Molecule: fidgetin-like protein 1; PDBTitle: crystal structure of figl-1 aaa domain in complex with adp
87	c5oafB_	Alignment	not modelled	99.8	23	PDB header: gene regulation Chain: B: PDB Molecule: ruvb-like 2; PDBTitle: human rvb1/rvb2 heterohexamers in ino80 complex
88	c4lcbA_	Alignment	not modelled	99.8	23	PDB header: protein transport Chain: A: PDB Molecule: cell division protein cdvc, vps4; PDBTitle: structure of vps4 homolog from acidianus hospitalis
89	c6em8H_	Alignment	not modelled	99.8	19	PDB header: chaperone Chain: H: PDB Molecule: atp-dependent clp protease atp-binding subunit clpc; PDBTitle: s.aureus clpc resting state, c2 symmetrised
90	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
91	d1in4a2	Alignment	not modelled	99.8	26	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
92	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
93	c3pxiB_	Alignment	not modelled	99.8	19	PDB header: protein binding Chain: B: PDB Molecule: negative regulator of genetic competence clpc/mecb; PDBTitle: structure of meca108:clpc
94	c6em8E_	Alignment	not modelled	99.8	20	PDB header: chaperone Chain: E: PDB Molecule: atp-dependent clp protease atp-binding subunit clpc; PDBTitle: s.aureus clpc resting state, c2 symmetrised
95	c6djuA_	Alignment	not modelled	99.8	17	PDB header: chaperone Chain: A: PDB Molecule: chaperone protein clpb; PDBTitle: mtb clpb in complex with atpgammas and casein, conformer 1
96	c6orbA_	Alignment	not modelled	99.8	18	PDB header: motor protein Chain: A: PDB Molecule: midasin; PDBTitle: full-length s. pombe mdn1 in the presence of atp and rbin-1
97	c6qi8E_	Alignment	not modelled	99.8	21	PDB header: chaperone Chain: E: PDB Molecule: ruvb-like 2; PDBTitle: truncated human r2tp complex, structure 3 (adp-filled)
98	c5kneA_	Alignment	not modelled	99.8	18	PDB header: chaperone Chain: A: PDB Molecule: heat shock protein 104; PDBTitle: cryoem reconstruction of hsp104 hexamer
99	c3vfdA_	Alignment	not modelled	99.8	19	PDB header: hydrolase Chain: A: PDB Molecule: spastin; PDBTitle: human spastin aaa domain
100	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
101	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
102	c3h4mC_	Alignment	not modelled	99.8	21	PDB header: hydrolase Chain: C: PDB Molecule: proteasome-activating nucleotidase; PDBTitle: aaa atpase domain of the proteasome- activating nucleotidase
103	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
104	c3eihB_	Alignment	not modelled	99.8	18	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
105	c1xwiA_	Alignment	not modelled	99.8	18	PDB header: protein transport Chain: A: PDB Molecule: skd1 protein; PDBTitle: crystal structure of vps4b
106	c1s3sA_	Alignment	not modelled	99.8	23	PDB header: protein binding Chain: A: PDB Molecule: transitional endoplasmic reticulum atpase (ter

						PDBTitle: crystal structure of aaa atpase p97/vcp nd1 in complex with2 p47 c
107	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
108	d1ny5a2	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
109	c5ep4A_	Alignment	not modelled	99.8	15	PDB header: transcription Chain: A; PDB Molecule: putative repressor protein luxo; PDBTitle: structure, regulation, and inhibition of the quorum-sensing signal2 integrator luxo
110	c5exsA_	Alignment	not modelled	99.8	16	PDB header: transcription Chain: A; PDB Molecule: transcriptional regulator fleq; PDBTitle: aaa+ atpase fleq from pseudomonas aeruginosa bound to atp-gamma-s
111	d1ixza_	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
112	c1hqcB_	Alignment	not modelled	99.8	25	PDB header: hydrolase Chain: B; PDB Molecule: ruvb; PDBTitle: structure of ruvb from thermus thermophilus hb8
113	c1iy2A_	Alignment	not modelled	99.8	24	PDB header: hydrolase Chain: A; PDB Molecule: atp-dependent metalloprotease ftsh; PDBTitle: crystal structure of the ftsh atpase domain from thermus2 thermophilus
114	c5ubvB_	Alignment	not modelled	99.8	21	PDB header: hydrolase Chain: B; PDB Molecule: atpase domain of i-aaa protease; PDBTitle: atpase domain of i-aaa protease from myceliophthora thermophila
115	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 mcrcb without dna binding domains (one half of the full2 complex)
116	c2zamA_	Alignment	not modelled	99.8	17	PDB header: protein transport Chain: A; PDB Molecule: vacuolar protein sorting-associating protein 4b; PDBTitle: crystal structure of mouse skd1/vps4b apo-form
117	c5wc0D_	Alignment	not modelled	99.8	26	PDB header: motor protein Chain: D; PDB Molecule: meiotic spindle formation protein mei-1; PDBTitle: katanin hexamer in spiral conformation
118	d1fnna2	Alignment	not modelled	99.8	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
119	c2r65A_	Alignment	not modelled	99.8	22	PDB header: hydrolase Chain: A; PDB Molecule: cell division protease ftsh homolog; PDBTitle: crystal structure of helicobacter pylori atp dependent protease, ftsh2 adp complex
120	c6genX_	Alignment	not modelled	99.8	32	PDB header: nuclear protein Chain: X; PDB Molecule: ruvb-like protein 1; PDBTitle: chromatin remodeller-nucleosome complex at 4.5 a resolution.