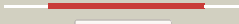



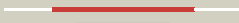
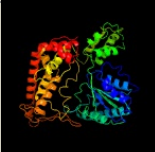



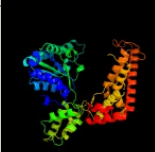





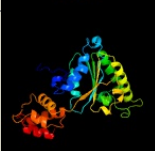



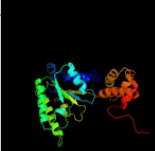


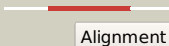
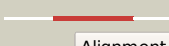


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3610c_(ftsH)_4050780_4053062
Date	Fri Aug 9 18:20:29 BST 2019
Unique Job ID	ec9e037e6e72ac69

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6nyyC_	 Alignment		100.0	46	PDB header: translocase Chain: C: PDB Molecule: afg3-like protein 2; PDBTitle: human m-aaa protease afg3l2, substrate-bound
2	c6nyyA_	 Alignment		100.0	47	PDB header: translocase Chain: A: PDB Molecule: afg3-like protein 2; PDBTitle: human m-aaa protease afg3l2, substrate-bound
3	c2dhrC_	 Alignment		100.0	56	PDB header: hydrolase Chain: C: PDB Molecule: ftsh; PDBTitle: whole cytosolic region of atp-dependent metalloprotease2 ftsh (g399l)
4	c6az0A_	 Alignment		100.0	46	PDB header: hydrolase Chain: A: PDB Molecule: mitochondrial inner membrane i-aaa protease supercomplex PDBTitle: mitochondrial atpase protease yme1
5	c2ce7B_	 Alignment		100.0	58	PDB header: cell division protein Chain: B: PDB Molecule: cell division protein ftsh; PDBTitle: edta treated
6	c4z8xC_	 Alignment		100.0	53	PDB header: hydrolase Chain: C: PDB Molecule: atp-dependent zinc metalloprotease ftsh; PDBTitle: truncated ftsh from a. aeolicus
7	c5g4gF_	 Alignment		100.0	41	PDB header: hydrolase Chain: F: PDB Molecule: vcvp-like atpase; PDBTitle: structure of the atpgs-bound vat complex
8	c5e7pA_	 Alignment		100.0	36	PDB header: hydrolase Chain: A: PDB Molecule: cell division control protein cdc48; PDBTitle: crystal structure of msmeg_0858 (uniprot a0qqs4), a aaa atpase.
9	c3cf1C_	 Alignment		100.0	39	PDB header: transport protein Chain: C: PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: structure of p97/vcp in complex with adp/adp.alfx
10	c6epdM_	 Alignment		100.0	38	PDB header: hydrolase Chain: M: PDB Molecule: 26s proteasome regulatory subunit 6a; PDBTitle: substrate processing state 26s proteasome (sps1)
11	c3cf2B_	 Alignment		100.0	36	PDB header: transport protein Chain: B: PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: structure of p97/vcp in complex with adp/amp-pnp

12	c3hu2C_	 Alignment		100.0	39	PDB header: transport protein Chain: C: PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: structure of p97 n-d1 r86a mutant in complex with atpgs
13	c6epcJ_	 Alignment		100.0	39	PDB header: hydrolase Chain: J: PDB Molecule: 26s proteasome regulatory subunit 8; PDBTitle: ground state 26s proteasome (gs2)
14	c4b4tK_	 Alignment		100.0	42	PDB header: hydrolase Chain: K: PDB Molecule: 26s protease regulatory subunit 6b homolog; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
15	c4b4tH_	 Alignment		100.0	44	PDB header: hydrolase Chain: H: PDB Molecule: 26s protease regulatory subunit 7 homolog; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
16	c5ifwB_	 Alignment		100.0	38	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
17	c4b4tI_	 Alignment		100.0	38	PDB header: hydrolase Chain: I: PDB Molecule: 26s protease regulatory subunit 4 homolog; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
18	c6hecH_	 Alignment		100.0	43	PDB header: hydrolase Chain: H: PDB Molecule: proteasome-activating nucleotidase; PDBTitle: pan-proteasome in state 4
19	c4b4tJ_	 Alignment		100.0	42	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	c5mpaL_	 Alignment		100.0	40	PDB header: hydrolase Chain: L: PDB Molecule: 26s protease subunit rpt4; PDBTitle: 26s proteasome in presence of atp (s2)
21	c5t0gA_	 Alignment	not modelled	100.0	40	PDB header: hydrolase Chain: A: PDB Molecule: 26s protease regulatory subunit 7; PDBTitle: structural basis for dynamic regulation of the human 26s proteasome
22	c4b4tL_	 Alignment	not modelled	100.0	41	PDB header: hydrolase Chain: L: PDB Molecule: 26s protease subunit rpt4; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
23	c1s3sA_	 Alignment	not modelled	100.0	44	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
24	c5gjql_	 Alignment	not modelled	100.0	38	PDB header: hydrolase Chain: L: PDB Molecule: 26s protease regulatory subunit 10b; PDBTitle: structure of the human 26s proteasome bound to usp14-ubal
25	c6matE_	 Alignment	not modelled	100.0	40	PDB header: ribosomal protein Chain: E: PDB Molecule: rix7 mutant; PDBTitle: cryo-em structure of the essential ribosome assembly aaa-atpase rix7
26	c3j96F_	 Alignment	not modelled	100.0	26	PDB header: hydrolase Chain: F: PDB Molecule: vesicle-fusing atpase; PDBTitle: structure of 20s supercomplex determined by single particle2 cryoelectron microscopy (state i)
27	c6opcF_	 Alignment	not modelled	100.0	39	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)
28	c4b4tM_	 Alignment	not modelled	100.0	38	PDB header: hydrolase Chain: M: PDB Molecule: 26s protease regulatory subunit 6a; PDBTitle: near-atomic resolution structural model of the yeast 26s

						proteasome
29	c5kzfl_	Alignment	not modelled	100.0	29	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
30	c1iy2A_	Alignment	not modelled	100.0	68	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent metalloprotease ftsh; PDBTitle: crystal structure of the ftsh atpase domain from thermus2 thermophilus
31	c1xwiA_	Alignment	not modelled	100.0	34	PDB header: protein transport Chain: A: PDB Molecule: skd1 protein; PDBTitle: crystal structure of vps4b
32	d2ce7a2	Alignment	not modelled	100.0	66	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
33	c2r65A_	Alignment	not modelled	100.0	60	PDB header: hydrolase Chain: A: PDB Molecule: cell division protease ftsh homolog; PDBTitle: crystal structure of helicobacter pylori atp dependent protease, ftsh2 adp complex
34	d1ixza_	Alignment	not modelled	100.0	70	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
35	c2zamA_	Alignment	not modelled	100.0	34	PDB header: protein transport Chain: A: PDB Molecule: vacuolar protein sorting-associated protein 4b; PDBTitle: crystal structure of mouse skd1/vps4b apo-form
36	c3h4mC_	Alignment	not modelled	100.0	45	PDB header: hydrolase Chain: C: PDB Molecule: proteasome-activating nucleotidase; PDBTitle: aaa atpase domain of the proteasome- activating nucleotidase
37	c3eihB_	Alignment	not modelled	100.0	39	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
38	c5ubvB_	Alignment	not modelled	100.0	55	PDB header: hydrolase Chain: B: PDB Molecule: atpase domain of i-aaa protease; PDBTitle: atpase domain of i-aaa protease from myceliophthora thermophila
39	c6b5cA_	Alignment	not modelled	100.0	33	PDB header: cell cycle Chain: A: PDB Molecule: katanin p60 atpase-containing subunit a-like 1; PDBTitle: structural basis for katanin self-assembly
40	c3zw6B_	Alignment	not modelled	100.0	19	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.
41	c5w0tA_	Alignment	not modelled	100.0	34	PDB header: hydrolase Chain: A: PDB Molecule: protein msp1; PDBTitle: crystal structure of monomeric msp1 from s. cerevisiae
42	c3b9pA_	Alignment	not modelled	100.0	38	PDB header: hydrolase Chain: A: PDB Molecule: cg5977-pa, isoform a; PDBTitle: spastin
43	c4l16A_	Alignment	not modelled	100.0	32	PDB header: hydrolase Chain: A: PDB Molecule: fidgetin-like protein 1; PDBTitle: crystal structure of figl-1 aaa domain in complex with adp
44	c3d8bB_	Alignment	not modelled	100.0	32	PDB header: hydrolase Chain: B: PDB Molecule: fidgetin-like protein 1; PDBTitle: crystal structure of human fidgetin-like protein 1 in complex with adp
45	c5wc0D_	Alignment	not modelled	100.0	37	PDB header: motor protein Chain: D: PDB Molecule: meiotic spindle formation protein mei-1; PDBTitle: katanin hexamer in spiral conformation
46	d1e32a2	Alignment	not modelled	100.0	43	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
47	c3vfdA_	Alignment	not modelled	100.0	36	PDB header: hydrolase Chain: A: PDB Molecule: spastin; PDBTitle: human spastin aaa domain
48	d1r7ra3	Alignment	not modelled	100.0	41	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
49	c2x8aA_	Alignment	not modelled	100.0	44	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
50	d1lv7a_	Alignment	not modelled	100.0	68	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
51	c2qz4A_	Alignment	not modelled	100.0	53	PDB header: hydrolase Chain: A: PDB Molecule: paraplegin; PDBTitle: human paraplegin, aaa domain in complex with adp
52	c5vq9D_	Alignment	not modelled	100.0	17	PDB header: protein binding Chain: D: PDB Molecule: pachytene checkpoint protein 2 homolog; PDBTitle: structure of human trip13, apo form
53	c4lcbA_	Alignment	not modelled	100.0	36	PDB header: protein transport Chain: A: PDB Molecule: cell division protein cdvc, vps4; PDBTitle: structure of vps4 homolog from acidianus hospitalis
54	d1oz4a3	Alignment	not modelled	100.0	41	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain

55	c4xguB_	Alignment	not modelled	100.0	19	PDB header: atp-binding protein Chain: B: PDB Molecule: putative pachytene checkpoint protein 2; PDBTitle: structure of c. elegans pch-2
56	d2ce7a1	Alignment	not modelled	100.0	46	Fold: FtsH protease domain-like Superfamily: FtsH protease domain-like Family: FtsH protease domain-like
57	c6mdnF_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: F: PDB Molecule: vesicle-fusing atpase; PDBTitle: the 20s supercomplex engaging the snap-25 n-terminus (class 2)
58	d2di4a1	Alignment	not modelled	100.0	35	Fold: FtsH protease domain-like Superfamily: FtsH protease domain-like Family: FtsH protease domain-like
59	c2di4B_	Alignment	not modelled	100.0	36	PDB header: hydrolase Chain: B: PDB Molecule: cell division protein ftsH homolog; PDBTitle: crystal structure of the ftsH protease domain
60	c4ww4B_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: B: PDB Molecule: ruvb-like 2; PDBTitle: double-heterohexameric rings of full-length rvb1(adp)/rvb2(adp)
61	c3sylB_	Alignment	not modelled	100.0	20	PDB header: chaperone Chain: B: PDB Molecule: protein cbbx; PDBTitle: crystal structure of the aaa+ protein cbbx, native structure
62	c1nsfA_	Alignment	not modelled	100.0	22	PDB header: protein transport Chain: A: PDB Molecule: n-ethylmaleimide sensitive factor; PDBTitle: d2 hexamerization domain of n-ethylmaleimide sensitive factor (nsf)
63	d1d2na_	Alignment	not modelled	100.0	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
64	c4ypnA_	Alignment	not modelled	100.0	27	PDB header: hydrolase Chain: A: PDB Molecule: lon protease; PDBTitle: crystal structure of a lona fragment containing the 3-helix bundle and2 the aaa-alpha/beta domain
65	c3pfiB_	Alignment	not modelled	100.0	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
66	c4ypIE_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: E: PDB Molecule: lon protease; PDBTitle: crystal structure of a hexameric lona protease bound to three adps
67	d1gvnb_	Alignment	not modelled	100.0	12	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Plasmid maintenance system epsilon/zeta, toxin zeta subunit
68	c1in8A_	Alignment	not modelled	99.9	19	PDB header: dna binding protein Chain: A: PDB Molecule: holliday junction dna helicase ruvb; PDBTitle: thermotoga maritima ruvb t158v
69	d1in4a2	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
70	d1ofha_	Alignment	not modelled	99.9	23	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
71	c5oafB_	Alignment	not modelled	99.9	22	PDB header: gene regulation Chain: B: PDB Molecule: ruvb-like 2; PDBTitle: human rvb1/rvb2 heterohexamer in ino80 complex
72	c4ciuA_	Alignment	not modelled	99.9	20	PDB header: chaperone Chain: A: PDB Molecule: chaperone protein clpb; PDBTitle: crystal structure of e. coli clpb
73	c3pxiB_	Alignment	not modelled	99.9	24	PDB header: protein binding Chain: B: PDB Molecule: negative regulator of genetic competence clpc/mecb; PDBTitle: structure of meca108:clpc
74	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
75	d1g41a_	Alignment	not modelled	99.9	25	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
76	d1e94e_	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
77	c1qvrB_	Alignment	not modelled	99.9	25	PDB header: chaperone Chain: B: PDB Molecule: clpb protein; PDBTitle: crystal structure analysis of clpb
78	c1r6bX_	Alignment	not modelled	99.9	24	PDB header: hydrolase Chain: X: PDB Molecule: clpa protein; PDBTitle: high resolution crystal structure of clpa
79	c5kneA_	Alignment	not modelled	99.9	20	PDB header: chaperone Chain: A: PDB Molecule: heat shock protein 104; PDBTitle: cryoem reconstruction of hsp104 hexamer
80	c2c9oC_	Alignment	not modelled	99.9	22	PDB header: hydrolase Chain: C: PDB Molecule: ruvb-like 1; PDBTitle: 3d structure of the human ruvb-like helicase ruvb1l
						PDB header: hydrolase Chain: A: PDB Molecule: holliday junction atp-dependent dna

81	c6blbA_	Alignment	not modelled	99.9	23	helicase ruvb; PDBTitle: 1.88 angstrom resolution crystal structure holliday junction atp-2 dependent dna helicase (ruvb) from pseudomonas aeruginosa in complex3 with adp
82	c5kneF_	Alignment	not modelled	99.9	24	PDB header: chaperone Chain: F: PDB Molecule: heat shock protein 104; PDBTitle: cryoem reconstruction of hsp104 hexamer
83	d1ixsb2	Alignment	not modelled	99.9	23	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
84	c6e111_	Alignment	not modelled	99.9	20	PDB header: protein transport Chain: 1: PDB Molecule: heat shock protein 101; PDBTitle: ptex core complex in the resetting (compact) state
85	c6genX_	Alignment	not modelled	99.9	29	PDB header: nuclear protein Chain: X: PDB Molecule: ruvb-like protein 1; PDBTitle: chromatin remodeller-nucleosome complex at 4.5 a resolution.
86	c2c9oA_	Alignment	not modelled	99.9	24	PDB header: hydrolase Chain: A: PDB Molecule: ruvb-like 1; PDBTitle: 3d structure of the human ruvb-like helicase ruvb1
87	c6em8F_	Alignment	not modelled	99.9	25	PDB header: chaperone Chain: F: PDB Molecule: atp-dependent clp protease atp-binding subunit clpC; PDBTitle: s.aureus clpC resting state, c2 symmetrised
88	d1l8qa2	Alignment	not modelled	99.9	23	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
89	c2hcbC_	Alignment	not modelled	99.9	25	PDB header: replication Chain: C: PDB Molecule: chromosomal replication initiator protein dnaa; PDBTitle: structure of amppcp-bound dnaa from aquifex aeolicus
90	c5d4wB_	Alignment	not modelled	99.9	22	PDB header: chaperone Chain: B: PDB Molecule: putative heat shock protein; PDBTitle: crystal structure of hsp104
91	c6em8E_	Alignment	not modelled	99.9	18	PDB header: chaperone Chain: E: PDB Molecule: atp-dependent clp protease atp-binding subunit clpC; PDBTitle: s.aureus clpC resting state, c2 symmetrised
92	c6qj8E_	Alignment	not modelled	99.9	19	PDB header: chaperone Chain: E: PDB Molecule: ruvb-like 2; PDBTitle: truncated human r2tp complex, structure 3 (adp-filled)
93	c2z4rB_	Alignment	not modelled	99.9	15	PDB header: dna binding protein Chain: B: PDB Molecule: chromosomal replication initiator protein dnaa; PDBTitle: crystal structure of domain iii from the thermotoga2 maritima replication initiation protein dnaa
94	c6azyA_	Alignment	not modelled	99.9	22	PDB header: chaperone Chain: A: PDB Molecule: heat shock protein hsp104; PDBTitle: crystal structure of hsp104 r328m/r757m mutant from calcarisporiella2 thermophila
95	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
96	d1r6bx3	Alignment	not modelled	99.9	24	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
97	c6djuA_	Alignment	not modelled	99.9	18	PDB header: chaperone Chain: A: PDB Molecule: chaperone protein clpB; PDBTitle: mtb clpB in complex with atpgamma and casein, conformer 1
98	c3pvsA_	Alignment	not modelled	99.9	23	PDB header: recombination Chain: A: PDB Molecule: replication-associated recombination protein a; PDBTitle: structure and biochemical activities of escherichia coli mgsa
99	d1qvra3	Alignment	not modelled	99.9	23	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
100	c4d2qC_	Alignment	not modelled	99.9	24	PDB header: chaperone Chain: C: PDB Molecule: clpB; PDBTitle: negative-stain electron microscopy of e. coli clpB mutant e432a (bap2 form bound to clpp)
101	d1r6bx2	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
102	d1um8a_	Alignment	not modelled	99.9	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
103	c3hteC_	Alignment	not modelled	99.9	24	PDB header: motor protein Chain: C: PDB Molecule: atp-dependent clp protease atp-binding subunit clpX; PDBTitle: crystal structure of nucleotide-free hexameric clpX
104	c5kneD_	Alignment	not modelled	99.9	23	PDB header: chaperone Chain: D: PDB Molecule: heat shock protein 104; PDBTitle: cryoem reconstruction of hsp104 hexamer
105	c3u5zM_	Alignment	not modelled	99.9	22	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
106	d1sxja2	Alignment	not modelled	99.9	25	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
						Fold: P-loop containing nucleoside triphosphate hydrolases

107	d1w5sa2	Alignment	not modelled	99.9	12	Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
108	c6djvE_	Alignment	not modelled	99.9	21	PDB header: chaperone Chain: E; PDB Molecule: chaperone protein clpb; PDBTitle: mtb clpb in complex with atpgammas and casein, conformer 2
109	c4ww4A_	Alignment	not modelled	99.9	28	PDB header: hydrolase Chain: A; PDB Molecule: ruvb-like 1; PDBTitle: double-heterohexameric rings of full-length rvb1(adp)/rvb2(adp)
110	c3bosA_	Alignment	not modelled	99.9	18	PDB header: hydrolase regulator,dna binding protein Chain: A; PDB Molecule: putative dna replication factor; PDBTitle: crystal structure of a putative dna replication regulator hda2 (sama_1916) from shewanella amazonensis sb2b at 1.75 a resolution
111	d1g8pa_	Alignment	not modelled	99.9	28	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
112	d1iqpa2	Alignment	not modelled	99.9	23	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
113	d1njfa_	Alignment	not modelled	99.9	25	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
114	d1jbka_	Alignment	not modelled	99.9	25	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
115	c6on2A_	Alignment	not modelled	99.8	19	PDB header: hydrolase Chain: A; PDB Molecule: atp-dependent protease la; PDBTitle: lon protease from yersinia pestis with y2853 substrate
116	d1fnna2	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
117	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
118	c1hqcb_	Alignment	not modelled	99.8	24	PDB header: hydrolase Chain: B; PDB Molecule: ruvb; PDBTitle: structure of ruvb from thermus thermophilus hb8
119	c3pxgA_	Alignment	not modelled	99.8	23	PDB header: protein binding Chain: A; PDB Molecule: negative regulator of genetic competence clpc/mecb; PDBTitle: structure of meca121 and clpc1-485 complex
120	d1sxic2	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