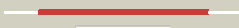











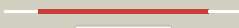

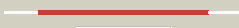










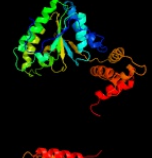

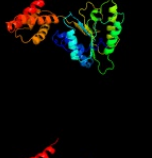

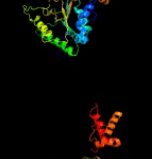
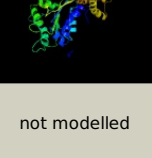


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2115c (-)_2374469_2376298
Date	Mon Aug 5 13:25:23 BST 2019
Unique Job ID	977831d47a29696b

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5kzfj_	 Alignment		100.0	100	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
2	c5g4gF_	 Alignment		100.0	30	PDB header: hydrolase Chain: F: PDB Molecule: vcp-like atpase; PDBTitle: structure of the atpgs-bound vat complex
3	c3cf1C_	 Alignment		100.0	30	PDB header: transport protein Chain: C: PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: structure of p97/vcp in complex with adp/adp.alfx
4	c5e7pA_	 Alignment		100.0	26	PDB header: hydrolase Chain: A: PDB Molecule: cell division control protein cdc48; PDBTitle: crystal structure of msmeg_0858 (uniprot a0qq54), a aaa atpase.
5	c3cf2B_	 Alignment		100.0	29	PDB header: transport protein Chain: B: PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: structure of p97/vcp in complex with adp/amp-pnp
6	c6matE_	 Alignment		100.0	26	PDB header: ribosomal protein Chain: E: PDB Molecule: rix7 mutant; PDBTitle: cryo-em structure of the essential ribosome assembly aaa-atpase rix7
7	c6opcF_	 Alignment		100.0	31	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)
8	c5ifwB_	 Alignment		100.0	30	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
9	c3hu2C_	 Alignment		100.0	37	PDB header: transport protein Chain: C: PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: structure of p97 n-d1 r86a mutant in complex with atpgs
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	c6nyyC_	 Alignment		100.0	29	PDB header: translocase Chain: C: PDB Molecule: afg3-like protein 2; PDBTitle: human m-aaa protease afg3l2, substrate-bound

12	c6epcJ_	Alignment		100.0	38	PDB header: hydrolase Chain: J: PDB Molecule: 26s proteasome regulatory subunit 8; PDBTitle: ground state 26s proteasome (gs2)
13	c1s3sA_	Alignment		100.0	37	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
14	c4b4tH_	Alignment		100.0	35	PDB header: hydrolase Chain: H: PDB Molecule: 26s protease regulatory subunit 7 homolog; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
15	c4b4tK_	Alignment		100.0	38	PDB header: hydrolase Chain: K: PDB Molecule: 26s protease regulatory subunit 6b homolog; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
16	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
17	c6hecH_	Alignment		100.0	43	PDB header: hydrolase Chain: H: PDB Molecule: proteasome-activating nucleotidase; PDBTitle: pan-proteasome in state 4
18	c4b4tJ_	Alignment		100.0	38	PDB header: hydrolase Chain: J: PDB Molecule: 26s protease regulatory subunit 8 homolog; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
19	c5mpaL_	Alignment		100.0	36	PDB header: hydrolase Chain: L: PDB Molecule: 26s protease subunit rpt4; PDBTitle: 26s proteasome in presence of atp (s2)
20	c3j96F_	Alignment		100.0	32	PDB header: hydrolase Chain: F: PDB Molecule: vesicle-fusing atpase; PDBTitle: structure of 20s supercomplex determined by single particle2 cryoelectron microscopy (state i)
21	c5t0gA_	Alignment	not modelled	100.0	36	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	35	PDB header: hydrolase Chain: L: PDB Molecule: 26s protease subunit rpt4; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
23	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
24	c6nyyA_	Alignment	not modelled	100.0	29	PDB header: translocase Chain: A: PDB Molecule: afg3-like protein 2; PDBTitle: human m-aaa protease afg3l2, substrate-bound
25	c4b4tM_	Alignment	not modelled	100.0	35	PDB header: hydrolase Chain: M: PDB Molecule: 26s protease regulatory subunit 6a; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
26	c2dhrC_	Alignment	not modelled	100.0	30	PDB header: hydrolase Chain: C: PDB Molecule: ftsh; PDBTitle: whole cytosolic region of atp-dependent metalloprotease2 ftsh (g399l)
27	c1xwiA_	Alignment	not modelled	100.0	32	PDB header: protein transport Chain: A: PDB Molecule: skd1 protein; PDBTitle: crystal structure of vps4b
28	c2zamA_	Alignment	not modelled	100.0	31	PDB header: protein transport Chain: A: PDB Molecule: vacuolar protein sorting-associated protein 4b; PDBTitle: crystal structure of mouse skd1/vps4b apo-form PDB header: hydrolase

29	c1iy2A_	Alignment	not modelled	100.0	34	Chain: A: PDB Molecule: atp-dependent metalloprotease ftsh; PDBTitle: crystal structure of the ftsh atpase domain from thermus2 thermophilus
30	c5w0tA_	Alignment	not modelled	100.0	28	PDB header: hydrolase Chain: A: PDB Molecule: protein msp1; PDBTitle: crystal structure of monomeric msp1 from s. cerevisiae
31	c3eihB_	Alignment	not modelled	100.0	33	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
32	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
33	c3b9pA_	Alignment	not modelled	100.0	31	PDB header: hydrolase Chain: A: PDB Molecule: cg5977-pa, isoform a; PDBTitle: spastin
34	d2ce7a2	Alignment	not modelled	100.0	35	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
35	d1ixza_	Alignment	not modelled	100.0	36	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
36	c3d8bB_	Alignment	not modelled	100.0	30	PDB header: hydrolase Chain: B: PDB Molecule: fidgetin-like protein 1; PDBTitle: crystal structure of human fidgetin-like protein 1 in complex with adp
37	c6az0A_	Alignment	not modelled	100.0	26	PDB header: hydrolase Chain: A: PDB Molecule: mitochondrial inner membrane i-aaa protease supercomplex PDBTitle: mitochondrial atpase protease yme1
38	c4i16A_	Alignment	not modelled	100.0	30	PDB header: hydrolase Chain: A: PDB Molecule: fidgetin-like protein 1; PDBTitle: crystal structure of figl-1 aaa domain in complex with adp
39	c3h4mC_	Alignment	not modelled	100.0	38	PDB header: hydrolase Chain: C: PDB Molecule: proteasome-activating nucleotidase; PDBTitle: aaa atpase domain of the proteasome- activating nucleotidase
40	c3zw6B_	Alignment	not modelled	100.0	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.
41	c4z8xC_	Alignment	not modelled	100.0	33	PDB header: hydrolase Chain: C: PDB Molecule: atp-dependent zinc metalloprotease ftsh; PDBTitle: truncated ftsh from a. aeolicus
42	c5vq9D_	Alignment	not modelled	100.0	23	PDB header: protein binding Chain: D: PDB Molecule: pachytene checkpoint protein 2 homolog; PDBTitle: structure of human trip13, apo form
43	c2r65A_	Alignment	not modelled	100.0	32	PDB header: hydrolase Chain: A: PDB Molecule: cell division protease ftsh homolog; PDBTitle: crystal structure of helicobacter pylori atp dependent protease, ftsh2 adp complex
44	d1e32a2	Alignment	not modelled	100.0	37	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
45	c2ce7B_	Alignment	not modelled	100.0	36	PDB header: cell division protein Chain: B: PDB Molecule: cell division protein ftsh; PDBTitle: edta treated
46	c3vfdA_	Alignment	not modelled	100.0	31	PDB header: hydrolase Chain: A: PDB Molecule: spastin; PDBTitle: human spastin aaa domain
47	d1r7ra3	Alignment	not modelled	100.0	42	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
48	c5wc0D_	Alignment	not modelled	100.0	28	PDB header: motor protein Chain: D: PDB Molecule: meiotic spindle formation protein mei-1; PDBTitle: katanin hexamer in spiral conformation
49	c5ubvB_	Alignment	not modelled	100.0	33	PDB header: hydrolase Chain: B: PDB Molecule: atpase domain of i-aaa protease; PDBTitle: atpase domain of i-aaa protease from myceliophthora thermophila
50	c2x8aA_	Alignment	not modelled	100.0	39	PDB header: nuclear protein Chain: A: PDB Molecule: nuclear valosin-containing protein-like; PDBTitle: human nuclear valosin containing protein like (nv1), c-2 terminal aaa-atpase domain
51	c4xquB_	Alignment	not modelled	100.0	22	PDB header: atp-binding protein Chain: B: PDB Molecule: putative pachytene checkpoint protein 2; PDBTitle: structure of c. elegans pch-2
52	c4lcbA_	Alignment	not modelled	100.0	31	PDB header: protein transport Chain: A: PDB Molecule: cell division protein cdvc, vps4; PDBTitle: structure of vps4 homolog from acidianus hospitalis
53	c2qz4A_	Alignment	not modelled	100.0	35	PDB header: hydrolase Chain: A: PDB Molecule: paraplegin; PDBTitle: human paraplegin, aaa domain in complex with adp
54	c6mdnF_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: F: PDB Molecule: vesicle-fusing atpase; PDBTitle: the 20s supercomplex engaging the snap-25 n-terminus (class 2)
55	d1oz4a3	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
56	d1lv7a_	Alignment	not modelled	100.0	33	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
57	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
58	c4ypnA_	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: A; PDB Molecule: lon protease; PDBTitle: crystal structure of a lon fragment containing the 3-helix bundle and 2 the aaa-alpha/beta domain
59	c1nsfA_	Alignment	not modelled	100.0	18	PDB header: protein transport Chain: A; PDB Molecule: n-ethylmaleimide sensitive factor; PDBTitle: d2 hexamerization domain of n-ethylmaleimide sensitive factor (nsf)
60	c4ww4B_	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: B; PDB Molecule: rvub-like 2; PDBTitle: double-heterohexameric rings of full-length rvb1(adp)/rvb2(adp)
61	c1qvrB_	Alignment	not modelled	100.0	18	PDB header: chaperone Chain: B; PDB Molecule: clpb protein; PDBTitle: crystal structure analysis of clpb
62	c3pxiB_	Alignment	not modelled	100.0	20	PDB header: protein binding Chain: B; PDB Molecule: negative regulator of genetic competence clpc/mecb; PDBTitle: structure of meca108:clpc
63	c4ciuA_	Alignment	not modelled	100.0	18	PDB header: chaperone Chain: A; PDB Molecule: chaperone protein clpb; PDBTitle: crystal structure of e. coli clpb
64	d1d2na_	Alignment	not modelled	100.0	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
65	c6em8F_	Alignment	not modelled	99.9	18	PDB header: chaperone Chain: F; PDB Molecule: atp-dependent clp protease atp-binding subunit clpc; PDBTitle: s.aureus clpc resting state, c2 symmetrised
66	d1gvnb_	Alignment	not modelled	99.9	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Plasmid maintenance system epsilon/zeta, toxin zeta subunit
67	d1ofha_	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
68	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
69	c4yplE_	Alignment	not modelled	99.9	20	PDB header: hydrolase Chain: E; PDB Molecule: lon protease; PDBTitle: crystal structure of a hexameric lon protease bound to three adps
70	c5kneF_	Alignment	not modelled	99.9	25	PDB header: chaperone Chain: F; PDB Molecule: heat shock protein 104; PDBTitle: cryoem reconstruction of hsp104 hexamer
71	c5kneA_	Alignment	not modelled	99.9	13	PDB header: chaperone Chain: A; PDB Molecule: heat shock protein 104; PDBTitle: cryoem reconstruction of hsp104 hexamer
72	c1r6bX_	Alignment	not modelled	99.9	19	PDB header: hydrolase Chain: X; PDB Molecule: clpa protein; PDBTitle: high resolution crystal structure of clpa
73	c6djuA_	Alignment	not modelled	99.9	14	PDB header: chaperone Chain: A; PDB Molecule: chaperone protein clpb; PDBTitle: mtb clpb in complex with atpgammas and casein, conformer 1
74	c6e111_	Alignment	not modelled	99.9	21	PDB header: protein transport Chain: 1; PDB Molecule: heat shock protein 101; PDBTitle: ptex core complex in the resetting (compact) state
75	c5d4wB_	Alignment	not modelled	99.9	23	PDB header: chaperone Chain: B; PDB Molecule: putative heat shock protein; PDBTitle: crystal structure of hsp104
76	c3pfiB_	Alignment	not modelled	99.9	17	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
77	c5oafB_	Alignment	not modelled	99.9	17	PDB header: gene regulation Chain: B; PDB Molecule: rvub-like 2; PDBTitle: human rvb1/rvb2 heterohexamer in ino80 complex
78	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
79	c5vy9C_	Alignment	not modelled	99.9	16	PDB header: chaperone Chain: C; PDB Molecule: heat shock protein 104; PDBTitle: s. cerevisiae hsp104:casein complex, middle domain conformation
80	c5kneD_	Alignment	not modelled	99.9	24	PDB header: chaperone Chain: D; PDB Molecule: heat shock protein 104; PDBTitle: cryoem reconstruction of hsp104 hexamer
81	c6on2A_	Alignment	not modelled	99.9	17	PDB header: hydrolase Chain: A; PDB Molecule: atp-dependent protease la; PDBTitle: lon protease from yersinia pestis with y2853 substrate

82	c6em8H_	Alignment	not modelled	99.9	21	PDB header: chaperone Chain: H: PDB Molecule: atp-dependent clp protease atp-binding subunit clpc; PDBTitle: s.aureus clpc resting state, c2 symmetrised
83	c6em8E_	Alignment	not modelled	99.9	17	PDB header: chaperone Chain: E: PDB Molecule: atp-dependent clp protease atp-binding subunit clpc; PDBTitle: s.aureus clpc resting state, c2 symmetrised
84	d1jbka_	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
85	c3pvsA_	Alignment	not modelled	99.9	20	PDB header: recombination Chain: A: PDB Molecule: replication-associated recombination protein a; PDBTitle: structure and biochemical activities of escherichia coli mgsa
86	d1in4a2	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
87	c6djvE_	Alignment	not modelled	99.9	18	PDB header: chaperone Chain: E: PDB Molecule: chaperone protein clpb; PDBTitle: mtb clpb in complex with atpgammas and casein, conformer 2
88	c3pxqA_	Alignment	not modelled	99.9	17	PDB header: protein binding Chain: A: PDB Molecule: negative regulator of genetic competence clpc/meccb; PDBTitle: structure of meca121 and clpc1-485 complex
89	d1l8qa2	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
90	d1r6bx2	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
91	c4d2qC_	Alignment	not modelled	99.9	19	PDB header: chaperone Chain: C: PDB Molecule: clpb; PDBTitle: negative-stain electron microscopy of e. coli clpb mutant e432a (bap2 form bound to clpp)
92	c6genX_	Alignment	not modelled	99.9	28	PDB header: nuclear protein Chain: X: PDB Molecule: ruvb-like protein 1; PDBTitle: chromatin remodeller-nucleosome complex at 4.5 a resolution.
93	clin8A_	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
94	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
95	c2p65A_	Alignment	not modelled	99.9	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein pf08_0063; PDBTitle: crystal structure of the first nucleotide binding domain of2 chaperone clpb1, putative, (pv089580) from plasmodium vivax
96	c2c9oC_	Alignment	not modelled	99.9	24	PDB header: hydrolase Chain: C: PDB Molecule: ruvb-like 1; PDBTitle: 3d structure of the human ruvb-like helicase ruvb1
97	c2hcbC_	Alignment	not modelled	99.9	15	PDB header: replication Chain: C: PDB Molecule: chromosomal replication initiator protein dnaa; PDBTitle: structure of amppcp-bound dnaa from aquifex aeolicus
98	d1qvra2	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
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	c3u5zM_	Alignment	not modelled	99.9	21	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
101	c2c9oA_	Alignment	not modelled	99.9	27	PDB header: hydrolase Chain: A: PDB Molecule: ruvb-like 1; PDBTitle: 3d structure of the human ruvb-like helicase ruvb1
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	c6blbA_	Alignment	not modelled	99.9	19	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
104	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
105	d1sxja2	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
106	c3hteC_	Alignment	not modelled	99.9	26	PDB header: motor protein Chain: C: PDB Molecule: atp-dependent clp protease atp-binding subunit clpc; PDBTitle: crystal structure of nucleotide-free hexameric clpx
107	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

108	c3m6aC_	Alignment	not modelled	99.8	19	PDB header: hydrolase Chain: C: PDB Molecule: atp-dependent protease la 1; PDBTitle: crystal structure of bacillus subtilis lon c-terminal domain
109	d1e94e_	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
110	c5j1sA_	Alignment	not modelled	99.8	15	PDB header: hydrolase Chain: A: PDB Molecule: torsin-1a; PDBTitle: torsina-lull1 complex, h. sapiens, bound to vhh-bs2
111	d1w5sa2	Alignment	not modelled	99.8	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
112	c6qi8E_	Alignment	not modelled	99.8	19	PDB header: chaperone Chain: E: PDB Molecule: rvvb-like 2; PDBTitle: truncated human r2tp complex, structure 3 (adp-filled)
113	c2p5tD_	Alignment	not modelled	99.8	12	PDB header: transcription regulator Chain: D: PDB Molecule: pez2; PDBTitle: molecular and structural characterization of the pez2 chromosomal2 toxin-antitoxin system of the human pathogen streptococcus pneumoniae
114	c2z4rB_	Alignment	not modelled	99.8	19	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
115	d1iqa2	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
116	d1njfa_	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
117	c1xxhB_	Alignment	not modelled	99.8	16	PDB header: transferase Chain: B: PDB Molecule: dna polymerase iii subunit gamma; PDBTitle: atpgs bound e. coli clamp loader complex
118	c2r44A_	Alignment	not modelled	99.8	16	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
119	c2chgB_	Alignment	not modelled	99.8	19	PDB header: dna-binding protein Chain: B: PDB Molecule: replication factor c small subunit; PDBTitle: replication factor c domains 1 and 2
120	c4ww4A_	Alignment	not modelled	99.8	30	PDB header: hydrolase Chain: A: PDB Molecule: rvvb-like 1; PDBTitle: double-heterohexameric rings of full-length rvb1(adp)/rvb2(adp)