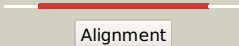



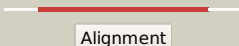

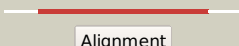

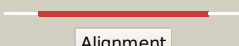

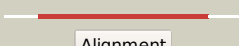

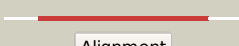








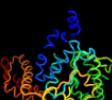


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2457c_clpX_2758218_2759498
Date	Wed Aug 7 12:50:08 BST 2019
Unique Job ID	70c49d68a3101bde

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1um8a_</a>	 Alignment		100.0	53	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
2	<a href="#">d1e94e_</a>	 Alignment		100.0	28	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
3	<a href="#">c1qvrB_</a>	 Alignment		100.0	27	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> clpb protein; <b>PDBTitle:</b> crystal structure analysis of clpb
4	<a href="#">d1g41a_</a>	 Alignment		100.0	40	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
5	<a href="#">c5kneD_</a>	 Alignment		100.0	20	<b>PDB header:</b> chaperone <b>Chain:</b> D: <b>PDB Molecule:</b> heat shock protein 104; <b>PDBTitle:</b> cryoem reconstruction of hsp104 hexamer
6	<a href="#">c6e111_</a>	 Alignment		100.0	20	<b>PDB header:</b> protein transport <b>Chain:</b> 1: <b>PDB Molecule:</b> heat shock protein 101; <b>PDBTitle:</b> ptex core complex in the resetting (compact) state
7	<a href="#">c6em8F_</a>	 Alignment		100.0	25	<b>PDB header:</b> chaperone <b>Chain:</b> F: <b>PDB Molecule:</b> atp-dependent clp protease atp-binding subunit clpc; <b>PDBTitle:</b> s.aureus clpc resting state, c2 symmetrised
8	<a href="#">c1r6bX_</a>	 Alignment		100.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> X: <b>PDB Molecule:</b> clpa protein; <b>PDBTitle:</b> high resolution crystal structure of clpa
9	<a href="#">c6azyA_</a>	 Alignment		100.0	22	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> heat shock protein hsp104; <b>PDBTitle:</b> crystal structure of hsp104 r328m/r757m mutant from calcarisporiella2 thermophila
10	<a href="#">c5vy9C_</a>	 Alignment		100.0	21	<b>PDB header:</b> chaperone <b>Chain:</b> C: <b>PDB Molecule:</b> heat shock protein 104; <b>PDBTitle:</b> s. cerevisiae hsp104:casein complex, middle domain conformation
11	<a href="#">c4d2qC_</a>	 Alignment		100.0	23	<b>PDB header:</b> chaperone <b>Chain:</b> C: <b>PDB Molecule:</b> clpb; <b>PDBTitle:</b> negative-stain electron microscopy of e. coli clpb mutant e432a (bap2 form bound to clpb)

12	<a href="#">d1ofha_</a>	Alignment		100.0	40	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
13	<a href="#">c3pxiB_</a>	Alignment		100.0	25	<b>PDB header:</b> protein binding <b>Chain:</b> B; <b>PDB Molecule:</b> negative regulator of genetic competence clpc/mecb; <b>PDBTitle:</b> structure of meca108:clpc
14	<a href="#">c3hteC_</a>	Alignment		100.0	62	<b>PDB header:</b> motor protein <b>Chain:</b> C; <b>PDB Molecule:</b> atp-dependent clp protease atp-binding subunit clpx; <b>PDBTitle:</b> crystal structure of nucleotide-free hexameric clpx
15	<a href="#">c4ciuA_</a>	Alignment		100.0	24	<b>PDB header:</b> chaperone <b>Chain:</b> A; <b>PDB Molecule:</b> chaperone protein clpb; <b>PDBTitle:</b> crystal structure of e. coli clpb
16	<a href="#">c5d4wB_</a>	Alignment		100.0	23	<b>PDB header:</b> chaperone <b>Chain:</b> B; <b>PDB Molecule:</b> putative heat shock protein; <b>PDBTitle:</b> crystal structure of hsp104
17	<a href="#">c5kneF_</a>	Alignment		100.0	19	<b>PDB header:</b> chaperone <b>Chain:</b> F; <b>PDB Molecule:</b> heat shock protein 104; <b>PDBTitle:</b> cryoem reconstruction of hsp104 hexamer
18	<a href="#">c6djuA_</a>	Alignment		100.0	26	<b>PDB header:</b> chaperone <b>Chain:</b> A; <b>PDB Molecule:</b> chaperone protein clpb; <b>PDBTitle:</b> mtb clpb in complex with atpgammas and casein, conformer 1
19	<a href="#">d1r6bx3</a>	Alignment		100.0	21	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
20	<a href="#">c6em8H_</a>	Alignment		100.0	25	<b>PDB header:</b> chaperone <b>Chain:</b> H; <b>PDB Molecule:</b> atp-dependent clp protease atp-binding subunit clpc; <b>PDBTitle:</b> s.aureus clpc resting state, c2 symmetrised
21	<a href="#">d1qvra3</a>	Alignment	not modelled	100.0	27	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
22	<a href="#">c5kneA_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> chaperone <b>Chain:</b> A; <b>PDB Molecule:</b> heat shock protein 104; <b>PDBTitle:</b> cryoem reconstruction of hsp104 hexamer
23	<a href="#">c6djvE_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> chaperone <b>Chain:</b> E; <b>PDB Molecule:</b> chaperone protein clpb; <b>PDBTitle:</b> mtb clpb in complex with atpgammas and casein, conformer 2
24	<a href="#">c6em8E_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> chaperone <b>Chain:</b> E; <b>PDB Molecule:</b> atp-dependent clp protease atp-binding subunit clpc; <b>PDBTitle:</b> s.aureus clpc resting state, c2 symmetrised
25	<a href="#">c6on2A_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> atp-dependent protease la; <b>PDBTitle:</b> lon protease from yersinia pestis with y2853 substrate
26	<a href="#">c5g4gF_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> hydrolase <b>Chain:</b> F; <b>PDB Molecule:</b> vcp-like atpase; <b>PDBTitle:</b> structure of the atpgs-bound vat complex
27	<a href="#">c3cf1C_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> transport protein <b>Chain:</b> C; <b>PDB Molecule:</b> transitional endoplasmic reticulum atpase; <b>PDBTitle:</b> structure of p97/vcp in complex with adp/adp.alfx
28	<a href="#">c5e7pA_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> cell division control protein cdc48; <b>PDBTitle:</b> crystal structure of msmeg_0858 (uniprot a0qqs4), a aaa atpase.
29	<a href="#">c4vplE_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> E; <b>PDB Molecule:</b> lon protease;

29	<a href="#">c4ypE_</a>	Alignment	not modelled	100.0	19	<b>PDBTitle:</b> crystal structure of a hexameric Iona protease bound to three adps
30	<a href="#">c3cf2B_</a>	Alignment	not modelled	99.9	25	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> transitional endoplasmic reticulum atpase; <b>PDBTitle:</b> structure of p97/vcp in complex with adp/amp-pnp
31	<a href="#">c6matE_</a>	Alignment	not modelled	99.9	24	<b>PDB header:</b> ribosomal protein <b>Chain:</b> E: <b>PDB Molecule:</b> rix7 mutant; <b>PDBTitle:</b> cryo-em structure of the essential ribosome assembly aaa-atpase rix7
32	<a href="#">c1ny5A_</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator (ntrc family); <b>PDBTitle:</b> crystal structure of sigm54 activator (aaa+ atpase) in the inactive2 state
33	<a href="#">c5m7nA_</a>	Alignment	not modelled	99.9	23	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> nitrogen assimilation regulatory protein; <b>PDBTitle:</b> crystal structure of ntrx from brucella abortus in complex with atp2 processed with the crystaldirect automated mounting and cryo-cooling3 technology
34	<a href="#">c6nyyC_</a>	Alignment	not modelled	99.9	22	<b>PDB header:</b> translocase <b>Chain:</b> C: <b>PDB Molecule:</b> afg3-like protein 2; <b>PDBTitle:</b> human m-aaa protease afg3l2, substrate-bound
35	<a href="#">c3dzdA_</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator (ntrc family); <b>PDBTitle:</b> crystal structure of sigma54 activator ntrc4 in the inactive2 state
36	<a href="#">c6epdM_</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> hydrolase <b>Chain:</b> M: <b>PDB Molecule:</b> 26s proteasome regulatory subunit 6a; <b>PDBTitle:</b> substrate processing state 26s proteasome (sp51)
37	<a href="#">c2c9oA_</a>	Alignment	not modelled	99.9	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ruvb-like 1; <b>PDBTitle:</b> 3d structure of the human ruvb-like helicase ruvb1l
38	<a href="#">c5oafB_</a>	Alignment	not modelled	99.9	25	<b>PDB header:</b> gene regulation <b>Chain:</b> B: <b>PDB Molecule:</b> ruvb-like 2; <b>PDBTitle:</b> human rvb1/rvb2 heterohexameric in ino80 complex
39	<a href="#">c5ep0A_</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative repressor protein luxo; <b>PDBTitle:</b> quorum-sensing signal integrator luxo - receiver+catalytic domains
40	<a href="#">c5ifwB_</a>	Alignment	not modelled	99.9	28	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> transitional endoplasmic reticulum atpase; <b>PDBTitle:</b> quantitative interaction mapping reveals an extended ubiquitin2 regulatory domain in aspl that disrupts functional p97 hexamers and3 induces cell death
41	<a href="#">c5j1sA_</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> torsin-1a; <b>PDBTitle:</b> torsina-lull1 complex, h. sapiens, bound to vhh-bs2
42	<a href="#">c4ww4B_</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> ruvb-like 2; <b>PDBTitle:</b> double-heterohexameric rings of full-length rvb1(adp)/rvb2(adp)
43	<a href="#">c3sylB_</a>	Alignment	not modelled	99.9	23	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> protein cbbx; <b>PDBTitle:</b> crystal structure of the aaa+ protein cbbx, native structure
44	<a href="#">c6epcJ_</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> hydrolase <b>Chain:</b> J: <b>PDB Molecule:</b> 26s proteasome regulatory subunit 8; <b>PDBTitle:</b> ground state 26s proteasome (gs2)
45	<a href="#">c5kzfJ_</a>	Alignment	not modelled	99.9	27	<b>PDB header:</b> hydrolase <b>Chain:</b> J: <b>PDB Molecule:</b> proteasome-associated atpase; <b>PDBTitle:</b> crystal structure of near full-length hexameric mycobacterium2 tuberculosis proteasomal atpase mpa in apo form
46	<a href="#">c4b4tH_</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> hydrolase <b>Chain:</b> H: <b>PDB Molecule:</b> 26s protease regulatory subunit 7 homolog; <b>PDBTitle:</b> near-atomic resolution structural model of the yeast 26s proteasome
47	<a href="#">c4b4tJ_</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> hydrolase <b>Chain:</b> J: <b>PDB Molecule:</b> 26s protease regulatory subunit 8 homolog; <b>PDBTitle:</b> near-atomic resolution structural model of the yeast 26s proteasome
48	<a href="#">c5ep4A_</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative repressor protein luxo; <b>PDBTitle:</b> structure, regulation, and inhibition of the quorum-sensing signal2 integrator luxo
49	<a href="#">c3hu2C_</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> transitional endoplasmic reticulum atpase; <b>PDBTitle:</b> structure of p97 n-d1 r86a mutant in complex with atpgs
50	<a href="#">c4b4tK_</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> hydrolase <b>Chain:</b> K: <b>PDB Molecule:</b> 26s protease regulatory subunit 6b homolog; <b>PDBTitle:</b> near-atomic resolution structural model of the yeast 26s proteasome
51	<a href="#">c3b9pA_</a>	Alignment	not modelled	99.9	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cg5977-pa, isoform a; <b>PDBTitle:</b> spastin
52	<a href="#">c2dhrC_</a>	Alignment	not modelled	99.9	27	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> ftsh; <b>PDBTitle:</b> whole cytosolic region of atp-dependent metalloprotease2 ftsh (g399l)
53	<a href="#">c5gjql_</a>	Alignment	not modelled	99.9	23	<b>PDB header:</b> hydrolase <b>Chain:</b> L: <b>PDB Molecule:</b> 26s protease regulatory subunit 10b; <b>PDBTitle:</b> structure of the human 26s proteasome bound to usp14-ubal
54	<a href="#">c2c99A_</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> transcription regulation <b>Chain:</b> A: <b>PDB Molecule:</b> psp operon transcriptional activator; <b>PDBTitle:</b> structural basis of the nucleotide driven conformational2

						changes in the aaa domain of transcription activator pspf <b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> holliday junction atp-dependent dna helicase ruvb; <b>PDBTitle:</b> 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
55	<a href="#">c3pfiB_</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> fidgetin-like protein 1; <b>PDBTitle:</b> crystal structure of figl-1 aaa domain in complex with adp
56	<a href="#">c4i16A_</a>	Alignment	not modelled	99.9	26	<b>PDB header:</b> response regulator <b>Chain:</b> D: <b>PDB Molecule:</b> transcriptional regulatory protein zrar; <b>PDBTitle:</b> crystal structure of a sigma54-activator suggests the mechanism for2 the conformational switch necessary for sigma54 binding
57	<a href="#">c1ojlD_</a>	Alignment	not modelled	99.9	22	<b>PDB header:</b> hydrolase <b>Chain:</b> H: <b>PDB Molecule:</b> proteasome-activating nucleotidase; <b>PDBTitle:</b> pan-proteasome in state 4
58	<a href="#">c6hecH_</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> vesicle-fusing atpase; <b>PDBTitle:</b> structure of 20s supercomplex determined by single particle2 cryoelectron microscopy (state i)
59	<a href="#">c3j96F_</a>	Alignment	not modelled	99.9	22	<b>PDB header:</b> hydrolase <b>Chain:</b> I: <b>PDB Molecule:</b> 26s protease regulatory subunit 4 homolog; <b>PDBTitle:</b> near-atomic resolution structural model of the yeast 26s proteasome
60	<a href="#">c4b4tI_</a>	Alignment	not modelled	99.9	15	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
61	<a href="#">d1ny5a2</a>	Alignment	not modelled	99.9	22	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> vacuolar protein sorting-associated protein 4; <b>PDBTitle:</b> crystal structure of s.cerevisiae vps4 in the presence of atpgammas
62	<a href="#">c3eihB_</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator fleq; <b>PDBTitle:</b> aaa+ atpase fleq from pseudomonas aeruginosa bound to atp-gamma-s
63	<a href="#">c5exsA_</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 26s protease regulatory subunit 7; <b>PDBTitle:</b> structural basis for dynamic regulation of the human 26s proteasome
64	<a href="#">c5t0gA_</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lon protease; <b>PDBTitle:</b> crystal structure of a lona fragment containing the 3-helix bundle and2 the aaa-alpha/beta domain
65	<a href="#">c4ypnA_</a>	Alignment	not modelled	99.9	22	<b>PDB header:</b> hydrolase <b>Chain:</b> L: <b>PDB Molecule:</b> 26s protease subunit rpt4; <b>PDBTitle:</b> near-atomic resolution structural model of the yeast 26s proteasome
66	<a href="#">c4b4tL_</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> hydrolase <b>Chain:</b> L: <b>PDB Molecule:</b> 26s protease subunit rpt4; <b>PDBTitle:</b> 26s proteasome in presence of atp (s2)
67	<a href="#">c5mpaL_</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> holliday junction atp-dependent dna helicase ruvb; <b>PDBTitle:</b> 1.88 angstrom resolution crystal structure holliday junction atp-2 dependent dna helicase (ruvb) from pseudomonas aeruginosa in complex3 with adp
68	<a href="#">c6blbA_</a>	Alignment	not modelled	99.9	23	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> skd1 protein; <b>PDBTitle:</b> crystal structure of vps4b
69	<a href="#">c1xwiA_</a>	Alignment	not modelled	99.9	22	<b>PDB header:</b> response regulator <b>Chain:</b> F: <b>PDB Molecule:</b> transcriptional regulatory protein zrar; <b>PDBTitle:</b> crystal structure of a sigma54-activator suggests the mechanism for2 the conformational switch necessary for sigma54 binding
70	<a href="#">c1ojlF_</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> transitional endoplasmic reticulum atpase (ter) <b>PDBTitle:</b> crystal structure of aaa atpase p97/vcp nd1 in complex with2 p47 c
71	<a href="#">c1s3sA_</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> vesicle-fusing atpase; <b>PDBTitle:</b> the 20s supercomplex engaging the snap-25 n-terminus (class 2)
72	<a href="#">c6mdnF_</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> atp-dependent protease la 1; <b>PDBTitle:</b> crystal structure of bacillus subtilis lon c-terminal domain
73	<a href="#">c3m6aC_</a>	Alignment	not modelled	99.9	23	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> fidgetin-like protein 1; <b>PDBTitle:</b> crystal structure of human fidgetin-like protein 1 in complex with adp
74	<a href="#">c3d8bB_</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a putative atpase (chu_0153) from cytophaga2 hutchinsonii atcc 33406 at 2.00 a resolution
75	<a href="#">c2r44A_</a>	Alignment	not modelled	99.9	24	<b>PDB header:</b> hydrolase <b>Chain:</b> M: <b>PDB Molecule:</b> 26s protease regulatory subunit 6a; <b>PDBTitle:</b> near-atomic resolution structural model of the yeast 26s proteasome
76	<a href="#">c4b4tM_</a>	Alignment	not modelled	99.9	22	<b>PDB header:</b> nuclear protein <b>Chain:</b> X: <b>PDB Molecule:</b> ruvb-like protein 1; <b>PDBTitle:</b> chromatin remodeller-nucleosome complex at 4.5 a resolution.
77	<a href="#">c6genX_</a>	Alignment	not modelled	99.9	30	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> cell division protein cdvc, vps4;
78	<a href="#">c4lcbA_</a>	Alignment	not modelled	99.9	25	

					<b>PDBTitle:</b> structure of vps4 homolog from acidianus hospitalis
79	<a href="#">c3vfdA_</a>	Alignment	not modelled	99.9	25 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> spastin; <b>PDBTitle:</b> human spastin aaa domain
80	<a href="#">c6nyyA_</a>	Alignment	not modelled	99.9	16 <b>PDB header:</b> translocase <b>Chain:</b> A: <b>PDB Molecule:</b> afg3-like protein 2; <b>PDBTitle:</b> human m-aaa protease afg3l2, substrate-bound
81	<a href="#">c2zamA_</a>	Alignment	not modelled	99.8	23 <b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> vacuolar protein sorting-associating protein 4b; <b>PDBTitle:</b> crystal structure of mouse skd1/vps4b apo-form
82	<a href="#">c5w0tA_</a>	Alignment	not modelled	99.8	24 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protein msp1; <b>PDBTitle:</b> crystal structure of monomeric msp1 from s. cerevisiae
83	<a href="#">c5wc0D_</a>	Alignment	not modelled	99.8	18 <b>PDB header:</b> motor protein <b>Chain:</b> D: <b>PDB Molecule:</b> meiotic spindle formation protein mei-1; <b>PDBTitle:</b> katanin hexamer in spiral conformation
84	<a href="#">c3pvsA_</a>	Alignment	not modelled	99.8	30 <b>PDB header:</b> recombination <b>Chain:</b> A: <b>PDB Molecule:</b> replication-associated recombination protein a; <b>PDBTitle:</b> structure and biochemical activities of escherichia coli mgsa
85	<a href="#">c3h4mC_</a>	Alignment	not modelled	99.8	26 <b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> proteasome-activating nucleotidase; <b>PDBTitle:</b> aaa atpase domain of the proteasome- activating nucleotidase
86	<a href="#">c6az0A_</a>	Alignment	not modelled	99.8	22 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> mitochondrial inner membrane i-aaa protease supercomplex <b>PDBTitle:</b> mitochondrial atpase protease yme1
87	<a href="#">c6b5cA_</a>	Alignment	not modelled	99.8	21 <b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> katanin p60 atpase-containing subunit a-like 1; <b>PDBTitle:</b> structural basis for katanin self-assembly
88	<a href="#">d1g8pa_</a>	Alignment	not modelled	99.8	24 <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
89	<a href="#">c5vq9D_</a>	Alignment	not modelled	99.8	18 <b>PDB header:</b> protein binding <b>Chain:</b> D: <b>PDB Molecule:</b> pachytene checkpoint protein 2 homolog; <b>PDBTitle:</b> structure of human trip13, apo form
90	<a href="#">c3zw6B_</a>	Alignment	not modelled	99.8	12 <b>PDB header:</b> photosynthesis <b>Chain:</b> B: <b>PDB Molecule:</b> ribulose biphosphate carboxylase/oxygenase activase 1, <b>PDBTitle:</b> model of hexameric aaa domain arrangement of green-type rubisco2 activase from tobacco.
91	<a href="#">c1in8A_</a>	Alignment	not modelled	99.8	22 <b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> holliday junction dna helicase ruvb; <b>PDBTitle:</b> thermotoga maritima ruvb t158v
92	<a href="#">c4z8xC_</a>	Alignment	not modelled	99.8	25 <b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> atp-dependent zinc metalloprotease ftsh; <b>PDBTitle:</b> truncated ftsh from a. aeolicus
93	<a href="#">c4xquB_</a>	Alignment	not modelled	99.8	20 <b>PDB header:</b> atp-binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> putative pachytene checkpoint protein 2; <b>PDBTitle:</b> structure of c. elegans pch-2
94	<a href="#">c4ww4A_</a>	Alignment	not modelled	99.8	28 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ruvb-like 1; <b>PDBTitle:</b> double-heterohexameric rings of full-length ruvb1(adp)/ruvb2(adp)
95	<a href="#">c2ce7B_</a>	Alignment	not modelled	99.8	27 <b>PDB header:</b> cell division protein <b>Chain:</b> B: <b>PDB Molecule:</b> cell division protein ftsh; <b>PDBTitle:</b> edta treated
96	<a href="#">c6opcF_</a>	Alignment	not modelled	99.8	21 <b>PDB header:</b> motor protein <b>Chain:</b> F: <b>PDB Molecule:</b> cell division control protein 48; <b>PDBTitle:</b> cdc48 hexamer in a complex with substrate and shp1(ubx domain)
97	<a href="#">c1nsfA_</a>	Alignment	not modelled	99.8	22 <b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> n-ethylmaleimide sensitive factor; <b>PDBTitle:</b> d2 hexamerization domain of n-ethylmaleimide sensitive factor (nsf)
98	<a href="#">d1d2na_</a>	Alignment	not modelled	99.8	23 <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
99	<a href="#">d1ixza_</a>	Alignment	not modelled	99.8	28 <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
100	<a href="#">c4r7zB_</a>	Alignment	not modelled	99.8	18 <b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> cell division control protein 21; <b>PDBTitle:</b> pfmcm-aaa double-octamer
101	<a href="#">c2x8aA_</a>	Alignment	not modelled	99.8	27 <b>PDB header:</b> nuclear protein <b>Chain:</b> A: <b>PDB Molecule:</b> nuclear valosin-containing protein-like; <b>PDBTitle:</b> human nuclear valosin containing protein like (nv), c-2 terminal aaa-atpase domain
102	<a href="#">c5ubvB_</a>	Alignment	not modelled	99.8	23 <b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> atpase domain of i-aaa protease; <b>PDBTitle:</b> atpase domain of i-aaa protease from myceliophthora thermophila
103	<a href="#">c3nbxX_</a>	Alignment	not modelled	99.8	17 <b>PDB header:</b> hydrolase <b>Chain:</b> X: <b>PDB Molecule:</b> atpase rava; <b>PDBTitle:</b> crystal structure of e. coli rava (regulatory atpase variant a) in2 complex with adp
104	<a href="#">c2c9oC_</a>	Alignment	not modelled	99.8	18 <b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> ruvb-like 1; <b>PDBTitle:</b> 3d structure of the human ruvb-like helicase ruvb1

105	<a href="#">c6qi8E_</a>	Alignment	not modelled	99.8	16	<b>PDB header:</b> chaperone <b>Chain:</b> E; <b>PDB Molecule:</b> ruvb-like 2; <b>PDBTitle:</b> truncated human r2tp complex, structure 3 (adp-filled)
106	<a href="#">c2r65A_</a>	Alignment	not modelled	99.8	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> cell division protease ftsh homolog; <b>PDBTitle:</b> crystal structure of helicobacter pylori atp dependent protease, ftsh2 adp complex
107	<a href="#">c3k1jA_</a>	Alignment	not modelled	99.8	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> atp-dependent protease lon; <b>PDBTitle:</b> crystal structure of lon protease from thermococcus onnurineus na1
108	<a href="#">d1r7ra3</a>	Alignment	not modelled	99.8	26	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
109	<a href="#">d2ce7a2</a>	Alignment	not modelled	99.8	19	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
110	<a href="#">d1e32a2</a>	Alignment	not modelled	99.8	16	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
111	<a href="#">d1in4a2</a>	Alignment	not modelled	99.7	23	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
112	<a href="#">c5u8s4_</a>	Alignment	not modelled	99.7	16	<b>PDB header:</b> replication <b>Chain:</b> 4; <b>PDB Molecule:</b> dna replication licensing factor mcm4; <b>PDBTitle:</b> structure of eukaryotic cmg helicase at a replication fork
113	<a href="#">d1ixsb2</a>	Alignment	not modelled	99.7	25	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
114	<a href="#">c2qz4A_</a>	Alignment	not modelled	99.7	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> paraplegin; <b>PDBTitle:</b> human paraplegin, aaa domain in complex with adp
115	<a href="#">c1iy2A_</a>	Alignment	not modelled	99.7	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> atp-dependent metalloprotease ftsh; <b>PDBTitle:</b> crystal structure of the ftsh atpase domain from thermus2 thermophilus
116	<a href="#">c5udb3_</a>	Alignment	not modelled	99.7	18	<b>PDB header:</b> replication <b>Chain:</b> 3; <b>PDB Molecule:</b> dna replication licensing factor mcm3; <b>PDBTitle:</b> structural basis of mcm2-7 replicative helicase loading by orc-cdc62 and cdt1
117	<a href="#">c1hqcb_</a>	Alignment	not modelled	99.7	25	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> ruvb; <b>PDBTitle:</b> structure of ruvb from thermus thermophilus hb8
118	<a href="#">c3uk6H_</a>	Alignment	not modelled	99.7	22	<b>PDB header:</b> hydrolase <b>Chain:</b> H; <b>PDB Molecule:</b> ruvb-like 2; <b>PDBTitle:</b> crystal structure of the tip48 (tip49b) hexamer
119	<a href="#">d1lv7a_</a>	Alignment	not modelled	99.7	21	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
120	<a href="#">d1l8qa2</a>	Alignment	not modelled	99.7	21	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain