























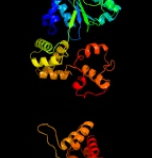

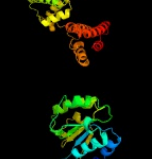

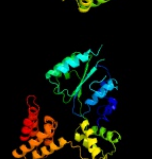
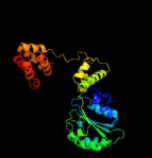
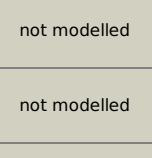


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2559c_(-)_2878581_2879939
Date	Wed Aug 7 12:50:19 BST 2019
Unique Job ID	6126dcfde5338714

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3pvsA_</a>	 Alignment		100.0	42	<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
2	<a href="#">d2r9ga1</a>	 Alignment		100.0	48	<b>Fold:</b> post-AAA+ oligomerization domain-like <b>Superfamily:</b> post-AAA+ oligomerization domain-like <b>Family:</b> MgsA/YrvN C-terminal domain-like
3	<a href="#">d3bgea1</a>	 Alignment		100.0	51	<b>Fold:</b> post-AAA+ oligomerization domain-like <b>Superfamily:</b> post-AAA+ oligomerization domain-like <b>Family:</b> MgsA/YrvN C-terminal domain-like
4	<a href="#">c3ctdB_</a>	 Alignment		100.0	44	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> putative atpase, aaa family; <b>PDBTitle:</b> crystal structure of a putative aaa family atpase from prochlorococcus2 marinus subsp. pastoris
5	<a href="#">d3ctda1</a>	 Alignment		100.0	44	<b>Fold:</b> post-AAA+ oligomerization domain-like <b>Superfamily:</b> post-AAA+ oligomerization domain-like <b>Family:</b> MgsA/YrvN C-terminal domain-like
6	<a href="#">c1xxhB_</a>	 Alignment		100.0	23	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> dna polymerase iii subunit gamma; <b>PDBTitle:</b> atpgs bound e. coli clamp loader complex
7	<a href="#">c5oafB_</a>	 Alignment		100.0	26	<b>PDB header:</b> gene regulation <b>Chain:</b> B: <b>PDB Molecule:</b> ruvb-like 2; <b>PDBTitle:</b> human rvb1/rvb2 heterohexamers in ino80 complex
8	<a href="#">c2c9oA_</a>	 Alignment		100.0	27	<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 ruvb1
9	<a href="#">c6genX_</a>	 Alignment		100.0	25	<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.
10	<a href="#">c1sxiC_</a>	 Alignment		100.0	20	<b>PDB header:</b> replication <b>Chain:</b> C: <b>PDB Molecule:</b> activator 1 40 kda subunit; <b>PDBTitle:</b> crystal structure of the eukaryotic clamp loader (replication factor2 c, rfc) bound to the dna sliding clamp (proliferating cell nuclear3 antigen, pcna)
11	<a href="#">d2qw6a1</a>	 Alignment		100.0	53	<b>Fold:</b> post-AAA+ oligomerization domain-like <b>Superfamily:</b> post-AAA+ oligomerization domain-like <b>Family:</b> MgsA/YrvN C-terminal domain-like

12	<a href="#">c2qw6A_</a>	Alignment		100.0	53	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> aaa atpase, central region; <b>PDBTitle:</b> crystal structure of the c-terminal domain of an aaa atpase from2 enterococcus faecium do
13	<a href="#">c1iqpF_</a>	Alignment		100.0	22	<b>PDB header:</b> replication <b>Chain:</b> F: <b>PDB Molecule:</b> rffc; <b>PDBTitle:</b> crystal structure of the clamp loader small subunit from2 pyrococcus furiosus
14	<a href="#">c6blbA_</a>	Alignment		100.0	23	<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
15	<a href="#">c1sxD_</a>	Alignment		100.0	20	<b>PDB header:</b> replication <b>Chain:</b> D: <b>PDB Molecule:</b> activator 1 41 kda subunit; <b>PDBTitle:</b> crystal structure of the eukaryotic clamp loader (replication factor2 c, rfc) bound to the dna sliding clamp (proliferating cell nuclear3 antigen, pcna)
16	<a href="#">c1sxB_</a>	Alignment		100.0	22	<b>PDB header:</b> replication <b>Chain:</b> B: <b>PDB Molecule:</b> activator 1 37 kda subunit; <b>PDBTitle:</b> crystal structure of the eukaryotic clamp loader (replication factor2 c, rfc) bound to the dna sliding clamp (proliferating cell nuclear3 antigen, pcna)
17	<a href="#">d1sxB2</a>	Alignment		100.0	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
18	<a href="#">c2chgB_</a>	Alignment		100.0	25	<b>PDB header:</b> dna-binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> replication factor c small subunit; <b>PDBTitle:</b> replication factor c domains 1 and 2
19	<a href="#">c1sxE_</a>	Alignment		100.0	15	<b>PDB header:</b> replication <b>Chain:</b> E: <b>PDB Molecule:</b> activator 1 40 kda subunit; <b>PDBTitle:</b> crystal structure of the eukaryotic clamp loader (replication factor2 c, rfc) bound to the dna sliding clamp (proliferating cell nuclear3 antigen, pcna)
20	<a href="#">c3u5zM_</a>	Alignment		100.0	20	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> M: <b>PDB Molecule:</b> dna polymerase accessory protein 44; <b>PDBTitle:</b> structure of t4 bacteriophage clamp loader bound to the t4 clamp,2 primer-template dna, and atp analog
21	<a href="#">d1iqa2</a>	Alignment	not modelled	100.0	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
22	<a href="#">d1njfa_</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
23	<a href="#">d1sxc2</a>	Alignment	not modelled	100.0	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
24	<a href="#">c1sxA_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> replication <b>Chain:</b> A: <b>PDB Molecule:</b> activator 1 95 kda subunit; <b>PDBTitle:</b> crystal structure of the eukaryotic clamp loader (replication factor2 c, rfc) bound to the dna sliding clamp (proliferating cell nuclear3 antigen, pcna)
25	<a href="#">c2chvE_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> dna-binding protein <b>Chain:</b> E: <b>PDB Molecule:</b> replication factor c small subunit; <b>PDBTitle:</b> replication factor c adnpn complex
26	<a href="#">d1sxd2</a>	Alignment	not modelled	100.0	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
27	<a href="#">c1in8A_</a>	Alignment	not modelled	100.0	23	<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
28	<a href="#">c1hqCB_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> ruvb; <b>PDBTitle:</b> structure of ruvb from thermus thermophilus hb8
						<b>PDB header:</b> hydrolase

29	<a href="#">c3pfiB_</a>	Alignment	not modelled	100.0	19	<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
30	<a href="#">d1sxja2</a>	Alignment	not modelled	100.0	22	<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
31	<a href="#">d1in4a2</a>	Alignment	not modelled	100.0	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
32	<a href="#">d1sxje2</a>	Alignment	not modelled	100.0	18	<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
33	<a href="#">c4ww4A_</a>	Alignment	not modelled	100.0	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 rvb1(adp)/rvb2(adp)
34	<a href="#">d1ixsb2</a>	Alignment	not modelled	100.0	31	<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
35	<a href="#">c4ww4B_</a>	Alignment	not modelled	100.0	29	<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)
36	<a href="#">c3bosA_</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> hydrolase regulator,dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative dna replication factor; <b>PDBTitle:</b> crystal structure of a putative dna replication regulator hda2 (sama_1916) from shewanella amazonensis sb2b at 1.75 a resolution
37	<a href="#">c2c9oC_</a>	Alignment	not modelled	99.9	22	<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 ruvb1l
38	<a href="#">c5kzfl_</a>	Alignment	not modelled	99.9	18	<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
39	<a href="#">c1jr3E_</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> transferase <b>Chain:</b> E: <b>PDB Molecule:</b> dna polymerase iii, delta' subunit; <b>PDBTitle:</b> crystal structure of the processivity clamp loader gamma complex of e.2 coli dna polymerase iii
40	<a href="#">c3b9pA_</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cg5977-pa, isoform a; <b>PDBTitle:</b> spastin
41	<a href="#">c3d8bB_</a>	Alignment	not modelled	99.9	17	<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
42	<a href="#">d1r6bx2</a>	Alignment	not modelled	99.9	18	<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
43	<a href="#">c2z4rB_</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> chromosomal replication initiator protein dnaa; <b>PDBTitle:</b> crystal structure of domain iii from the thermotoga2 maritima replication initiation protein dnaa
44	<a href="#">c6qi8E_</a>	Alignment	not modelled	99.9	26	<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)
45	<a href="#">c3vfdA_</a>	Alignment	not modelled	99.9	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> spastin; <b>PDBTitle:</b> human spastin aaa domain
46	<a href="#">c5kneA_</a>	Alignment	not modelled	99.9	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
47	<a href="#">c6nyyC_</a>	Alignment	not modelled	99.9	19	<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
48	<a href="#">c2ce7B_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> cell division protein <b>Chain:</b> B: <b>PDB Molecule:</b> cell division protein ftsh; <b>PDBTitle:</b> edta treated
49	<a href="#">c4l16A_</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
50	<a href="#">c2dhrC_</a>	Alignment	not modelled	99.9	20	<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)
51	<a href="#">d1a5ta2</a>	Alignment	not modelled	99.9	22	<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
52	<a href="#">c4lcbA_</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> cell division protein cdvc, vps4; <b>PDBTitle:</b> structure of vps4 homolog from acidianus hospitalis
53	<a href="#">d2gnoa2</a>	Alignment	not modelled	99.9	13	<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
54	<a href="#">c5g4gF_</a>	Alignment	not modelled	99.9	19	<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
						<b>PDB header:</b> hydrolase

55	<a href="#">c3h4mC_</a>	Alignment	not modelled	99.9	18	<b>Chain:</b> C: <b>PDB Molecule:</b> proteasome-activating nucleotidase; <b>PDBTitle:</b> aaa atpase domain of the proteasome- activating nucleotidase
56	<a href="#">c4z8xC_</a>	Alignment	not modelled	99.9	18	<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
57	<a href="#">c5wc0D_</a>	Alignment	not modelled	99.9	20	<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
58	<a href="#">d2ce7a2</a>	Alignment	not modelled	99.9	18	<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
59	<a href="#">c3uk6H_</a>	Alignment	not modelled	99.9	26	<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
60	<a href="#">c1xwiA_</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> skd1 protein; <b>PDBTitle:</b> crystal structure of vps4b
61	<a href="#">c3eihB_</a>	Alignment	not modelled	99.9	18	<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="#">d1um8a_</a>	Alignment	not modelled	99.9	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
63	<a href="#">c2zamA_</a>	Alignment	not modelled	99.9	18	<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
64	<a href="#">c4b4tL_</a>	Alignment	not modelled	99.9	25	<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
65	<a href="#">c5e7pA_</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cell division control protein cdc48; <b>PDBTitle:</b> crystal structure of msmeq_0858 (uniprot a0qqs4), a aaa atpase.
66	<a href="#">d1l8qa2</a>	Alignment	not modelled	99.9	18	<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
67	<a href="#">c4b4tH_</a>	Alignment	not modelled	99.9	19	<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
68	<a href="#">c4b4tJ_</a>	Alignment	not modelled	99.9	21	<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
69	<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 (sps1)
70	<a href="#">c3cf1C_</a>	Alignment	not modelled	99.9	20	<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
71	<a href="#">d1qvra2</a>	Alignment	not modelled	99.9	20	<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
72	<a href="#">c4b4tI_</a>	Alignment	not modelled	99.9	17	<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
73	<a href="#">c6az0A_</a>	Alignment	not modelled	99.9	18	<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
74	<a href="#">c6epcJ_</a>	Alignment	not modelled	99.9	23	<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)
75	<a href="#">c4xguB_</a>	Alignment	not modelled	99.9	19	<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
76	<a href="#">c4b4tM_</a>	Alignment	not modelled	99.9	18	<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
77	<a href="#">c6b5cA_</a>	Alignment	not modelled	99.9	22	<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
78	<a href="#">c5ubvB_</a>	Alignment	not modelled	99.9	19	<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
79	<a href="#">d1g41a_</a>	Alignment	not modelled	99.9	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
80	<a href="#">c5w0tA_</a>	Alignment	not modelled	99.9	21	<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

81	<a href="#">dlixza_</a>	Alignment	not modelled	99.9	20	<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
82	<a href="#">c6azyA_</a>	Alignment	not modelled	99.9	19	<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
83	<a href="#">d1fnna2</a>	Alignment	not modelled	99.9	17	<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
84	<a href="#">d1g8pa_</a>	Alignment	not modelled	99.9	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
85	<a href="#">c4b4tK_</a>	Alignment	not modelled	99.9	22	<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
86	<a href="#">d1w5sa2</a>	Alignment	not modelled	99.9	17	<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
87	<a href="#">c6hecH_</a>	Alignment	not modelled	99.9	23	<b>PDB header:</b> hydrolase <b>Chain:</b> H: <b>PDB Molecule:</b> proteasome-activating nucleotidase; <b>PDBTitle:</b> pan-proteasome in state 4
88	<a href="#">c5gjqL_</a>	Alignment	not modelled	99.9	21	<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
89	<a href="#">c6nyyA_</a>	Alignment	not modelled	99.9	17	<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
90	<a href="#">c5vq9D_</a>	Alignment	not modelled	99.9	16	<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
91	<a href="#">c3hu2C_</a>	Alignment	not modelled	99.9	22	<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
92	<a href="#">c5t0gA_</a>	Alignment	not modelled	99.8	21	<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
93	<a href="#">d1jbka_</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
94	<a href="#">c5zr1A_</a>	Alignment	not modelled	99.8	19	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> origin recognition complex subunit 1; <b>PDBTitle:</b> saccharomyces cerevisiae origin recognition complex bound to a 72-bp2 origin dna containing acs and b1 element
95	<a href="#">c2qz4A_</a>	Alignment	not modelled	99.8	18	<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
96	<a href="#">d1ofha_</a>	Alignment	not modelled	99.8	22	<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
97	<a href="#">c5ifwB_</a>	Alignment	not modelled	99.8	20	<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
98	<a href="#">c6djuA_</a>	Alignment	not modelled	99.8	22	<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
99	<a href="#">c3te6A_</a>	Alignment	not modelled	99.8	13	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> regulatory protein sir3; <b>PDBTitle:</b> crystal structure of the s. cerevisiae sir3 aaa+ domain
100	<a href="#">d1r6bx3</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
101	<a href="#">c6matE_</a>	Alignment	not modelled	99.8	15	<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
102	<a href="#">c5mpaL_</a>	Alignment	not modelled	99.8	21	<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)
103	<a href="#">c3sylB_</a>	Alignment	not modelled	99.8	20	<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
104	<a href="#">c2r65A_</a>	Alignment	not modelled	99.8	16	<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
105	<a href="#">c1qvrB_</a>	Alignment	not modelled	99.8	20	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> clpb protein; <b>PDBTitle:</b> crystal structure analysis of clpb
106	<a href="#">c6em8H_</a>	Alignment	not modelled	99.8	24	<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
						<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> transitional endoplasmic reticulum atpase

107	<a href="#">c1s3sA_</a>	Alignment	not modelled	99.8	21	(ter <b>PDBTitle:</b> crystal structure of aaa atpase p97/vcp nd1 in complex with2 p47 c
108	<a href="#">d1ny5a2</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
109	<a href="#">c6djvE_</a>	Alignment	not modelled	99.8	22	<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
110	<a href="#">c1iy2A_</a>	Alignment	not modelled	99.8	18	<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
111	<a href="#">c4ciuA_</a>	Alignment	not modelled	99.8	20	<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
112	<a href="#">d1lv7a_</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
113	<a href="#">c5uj7C_</a>	Alignment	not modelled	99.8	16	<b>PDB header:</b> dna binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> origin recognition complex subunit 4; <b>PDBTitle:</b> structure of the active form of human origin recognition complex2 atpase motor module, complex subunits 1, 4, 5
114	<a href="#">c3zh9B_</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> delta; <b>PDBTitle:</b> bacillus subtilis dna clamp loader delta protein (yqen)
115	<a href="#">c2hcbC_</a>	Alignment	not modelled	99.8	20	<b>PDB header:</b> replication <b>Chain:</b> C: <b>PDB Molecule:</b> chromosomal replication initiator protein dnaa; <b>PDBTitle:</b> structure of amppcp-bound dnaa from aquifex aeolicus
116	<a href="#">c1r6bX_</a>	Alignment	not modelled	99.8	24	<b>PDB header:</b> hydrolase <b>Chain:</b> X: <b>PDB Molecule:</b> clpa protein; <b>PDBTitle:</b> high resolution crystal structure of clpa
117	<a href="#">c5kneF_</a>	Alignment	not modelled	99.8	22	<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
118	<a href="#">c2p65A_</a>	Alignment	not modelled	99.8	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein pf08_0063; <b>PDBTitle:</b> crystal structure of the first nucleotide binding domain of2 chaperone clpb1, putative, (pv089580) from plasmodium vivax
119	<a href="#">d1qvra3</a>	Alignment	not modelled	99.8	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="#">c5ep4A_</a>	Alignment	not modelled	99.8	19	<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