







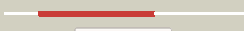




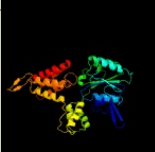









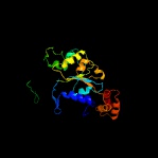
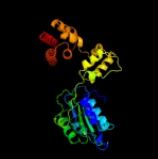








# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3644c (- )_4081695_4082900
Date	Fri Aug 9 18:20:33 BST 2019
Unique Job ID	236197b2b78a89c9

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<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
2	<a href="#">c1jr3E_</a>	 Alignment		100.0	31	<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
3	<a href="#">c3u5zM_</a>	 Alignment		100.0	13	<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
4	<a href="#">c2gnoA_</a>	 Alignment		100.0	17	<b>PDB header:</b> replication <b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase iii, gamma subunit-related protein; <b>PDBTitle:</b> crystal structure of a dna polymerase iii, gamma subunit-related2 protein (tm0771) from thermotoga maritima msb8 at 2.00 a resolution
5	<a href="#">c6genX_</a>	 Alignment		100.0	24	<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.
6	<a href="#">d2gnoa2</a>	 Alignment		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
7	<a href="#">c1sxiE_</a>	 Alignment		100.0	16	<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)
8	<a href="#">d1a5ta2</a>	 Alignment		100.0	36	<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
9	<a href="#">c1sxiC_</a>	 Alignment		100.0	18	<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)
10	<a href="#">c2chvE_</a>	 Alignment		100.0	21	<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 adpnp complex
11	<a href="#">c3pvsA_</a>	 Alignment		100.0	24	<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

12	<a href="#">c1iqpF_</a>	Alignment		100.0	21	<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
13	<a href="#">c5oafB_</a>	Alignment		100.0	20	<b>PDB header:</b> gene regulation <b>Chain:</b> B: <b>PDB Molecule:</b> ruvb-like 2; <b>PDBTitle:</b> human rvb1/rvb2 heterohexamer in ino80 complex
14	<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)
15	<a href="#">c1sxD_</a>	Alignment		100.0	17	<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="#">c2c9oA_</a>	Alignment		100.0	18	<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
17	<a href="#">d1njfa_</a>	Alignment		99.9	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
18	<a href="#">c4ww4A_</a>	Alignment		99.9	22	<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)/rvb2(adp)
19	<a href="#">c3zh9B_</a>	Alignment		99.9	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)
20	<a href="#">c5g4gF_</a>	Alignment		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
21	<a href="#">c2chgB_</a>	Alignment	not modelled	99.9	23	<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
22	<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
23	<a href="#">c3cf1C_</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/vcp in complex with adp/adp.alfx
24	<a href="#">c5e7pA_</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cell division control protein cdc48; <b>PDBTitle:</b> crystal structure of msme9_0858 (uniprot a0qqs4), a aaa atpase.
25	<a href="#">c3pfiB_</a>	Alignment	not modelled	99.9	19	<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
26	<a href="#">d1sxje2</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
27	<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-associated protein 4b; <b>PDBTitle:</b> crystal structure of mouse skd1/vps4b apo-form
28	<a href="#">d1sxb2</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

29	<a href="#">c1sxa</a>	Alignment	not modelled	99.9	20	<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)
30	<a href="#">d1sxc2</a>	Alignment	not modelled	99.9	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
31	<a href="#">c5kzfl</a>	Alignment	not modelled	99.9	15	<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
32	<a href="#">c4ww4B</a>	Alignment	not modelled	99.9	18	<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)
33	<a href="#">c1xwiA</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> skd1 protein; <b>PDBTitle:</b> crystal structure of vps4b
34	<a href="#">c2dhrC</a>	Alignment	not modelled	99.9	21	<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)
35	<a href="#">d1iqa2</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
36	<a href="#">c6epcj</a>	Alignment	not modelled	99.9	16	<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)
37	<a href="#">c3hu2C</a>	Alignment	not modelled	99.9	21	<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
38	<a href="#">c3d8bB</a>	Alignment	not modelled	99.9	19	<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
39	<a href="#">c6blbA</a>	Alignment	not modelled	99.9	20	<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
40	<a href="#">c6epdM</a>	Alignment	not modelled	99.9	19	<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)
41	<a href="#">c4i16A</a>	Alignment	not modelled	99.9	18	<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
42	<a href="#">d1in4a2</a>	Alignment	not modelled	99.9	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
43	<a href="#">c3vfdA</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> spastin; <b>PDBTitle:</b> human spastin aaa domain
44	<a href="#">c6matE</a>	Alignment	not modelled	99.9	17	<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
45	<a href="#">c4xguB</a>	Alignment	not modelled	99.9	21	<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
46	<a href="#">c3h4mC</a>	Alignment	not modelled	99.9	18	<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
47	<a href="#">d1sxa2</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
48	<a href="#">c6az0A</a>	Alignment	not modelled	99.9	19	<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
49	<a href="#">c3b9pA</a>	Alignment	not modelled	99.9	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cg5977-pa, isoform a; <b>PDBTitle:</b> spastin
50	<a href="#">c4lcbA</a>	Alignment	not modelled	99.9	14	<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
51	<a href="#">c3cf2B</a>	Alignment	not modelled	99.9	15	<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
52	<a href="#">c5vq9D</a>	Alignment	not modelled	99.9	23	<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
53	<a href="#">c1s3sA</a>	Alignment	not modelled	99.9	21	<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
54	<a href="#">c5w0tA</a>	Alignment	not modelled	99.9	15	<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

55	<a href="#">c4b4tH</a>	Alignment	not modelled	99.9	17	<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
56	<a href="#">c3eihB</a>	Alignment	not modelled	99.9	17	<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
57	<a href="#">c6b5cA</a>	Alignment	not modelled	99.9	17	<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
58	<a href="#">c5gjql</a>	Alignment	not modelled	99.9	17	<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
59	<a href="#">c5wc0D</a>	Alignment	not modelled	99.9	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
60	<a href="#">c6hecH</a>	Alignment	not modelled	99.8	18	<b>PDB header:</b> hydrolase <b>Chain:</b> H: <b>PDB Molecule:</b> proteasome-activating nucleotidase; <b>PDBTitle:</b> pan-proteasome in state 4
61	<a href="#">c5ifwB</a>	Alignment	not modelled	99.8	21	<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
62	<a href="#">c4b4tL</a>	Alignment	not modelled	99.8	17	<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
63	<a href="#">c4b4tI</a>	Alignment	not modelled	99.8	15	<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
64	<a href="#">c2c9oC</a>	Alignment	not modelled	99.8	14	<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
65	<a href="#">c1qvrB</a>	Alignment	not modelled	99.8	16	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> clpb protein; <b>PDBTitle:</b> crystal structure analysis of clpb
66	<a href="#">d1sxd2</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
67	<a href="#">c4b4tJ</a>	Alignment	not modelled	99.8	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
68	<a href="#">c6nyyA</a>	Alignment	not modelled	99.8	18	<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
69	<a href="#">c1xxiF</a>	Alignment	not modelled	99.8	11	<b>PDB header:</b> transferase <b>Chain:</b> F: <b>PDB Molecule:</b> dna polymerase iii, delta subunit; <b>PDBTitle:</b> adp bound e. coli clamp loader complex
70	<a href="#">c4b4tM</a>	Alignment	not modelled	99.8	21	<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
71	<a href="#">c2ce7B</a>	Alignment	not modelled	99.8	18	<b>PDB header:</b> cell division protein <b>Chain:</b> B: <b>PDB Molecule:</b> cell division protein ftsh; <b>PDBTitle:</b> edta treated
72	<a href="#">c1in8A</a>	Alignment	not modelled	99.8	21	<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
73	<a href="#">c4b4tK</a>	Alignment	not modelled	99.8	13	<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
74	<a href="#">d1ixsb2</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
75	<a href="#">c4z8xC</a>	Alignment	not modelled	99.8	19	<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
76	<a href="#">c5mpaL</a>	Alignment	not modelled	99.8	16	<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)
77	<a href="#">c5t0gA</a>	Alignment	not modelled	99.8	14	<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
78	<a href="#">d1e32a2</a>	Alignment	not modelled	99.8	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
79	<a href="#">c3sylB</a>	Alignment	not modelled	99.8	22	<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
						<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases

80	<a href="#">d2ce7a2</a>	Alignment	not modelled	99.8	20	<b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
81	<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
82	<a href="#">c2qz4A</a>	Alignment	not modelled	99.8	16	<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
83	<a href="#">c1iy2A</a>	Alignment	not modelled	99.8	21	<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
84	<a href="#">c5ubvB</a>	Alignment	not modelled	99.8	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
85	<a href="#">d1r6bx3</a>	Alignment	not modelled	99.8	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
86	<a href="#">c3pxiB</a>	Alignment	not modelled	99.8	16	<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
87	<a href="#">d1g41a</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
88	<a href="#">c5j1sA</a>	Alignment	not modelled	99.8	15	<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
89	<a href="#">d1lixza</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
90	<a href="#">d1um8a</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
91	<a href="#">c5d4wB</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> putative heat shock protein; <b>PDBTitle:</b> crystal structure of hsp104
92	<a href="#">d1r7ra3</a>	Alignment	not modelled	99.8	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
93	<a href="#">c4ciuA</a>	Alignment	not modelled	99.8	15	<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
94	<a href="#">c6azyA</a>	Alignment	not modelled	99.8	15	<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
95	<a href="#">c3j96F</a>	Alignment	not modelled	99.8	15	<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)
96	<a href="#">c2r65A</a>	Alignment	not modelled	99.8	18	<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
97	<a href="#">d1g8pa</a>	Alignment	not modelled	99.8	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
98	<a href="#">c6qi8E</a>	Alignment	not modelled	99.8	19	<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)
99	<a href="#">c6opcF</a>	Alignment	not modelled	99.8	17	<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)
100	<a href="#">c3zw6B</a>	Alignment	not modelled	99.8	10	<b>PDB header:</b> photosynthesis <b>Chain:</b> B: <b>PDB Molecule:</b> ribulose bisphosphate carboxylase/oxygenase activase 1, <b>PDBTitle:</b> model of hexameric aaa domain arrangement of green-type rubisco2 activase from tobacco.
101	<a href="#">c1r6bX</a>	Alignment	not modelled	99.8	20	<b>PDB header:</b> hydrolase <b>Chain:</b> X: <b>PDB Molecule:</b> clpa protein; <b>PDBTitle:</b> high resolution crystal structure of clpa
102	<a href="#">d1lv7a</a>	Alignment	not modelled	99.8	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
103	<a href="#">c4d2qC</a>	Alignment	not modelled	99.8	15	<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 clpp)
104	<a href="#">d1d2na</a>	Alignment	not modelled	99.8	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
105	<a href="#">c5kneD</a>	Alignment	not modelled	99.8	12	<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
106	<a href="#">c3hteC</a>	Alignment	not modelled	99.7	21	<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

107	<a href="#">d1qvra2</a>	Alignment	not modelled	99.7	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
108	<a href="#">c3uk6H</a>	Alignment	not modelled	99.7	16	<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
109	<a href="#">c1hqcB</a>	Alignment	not modelled	99.7	23	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> ruvb; <b>PDBTitle:</b> structure of ruvb from thermus thermophilus hb8
110	<a href="#">c6mdnF</a>	Alignment	not modelled	99.7	14	<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)
111	<a href="#">c5kneA</a>	Alignment	not modelled	99.7	15	<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
112	<a href="#">c6em8F</a>	Alignment	not modelled	99.7	14	<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
113	<a href="#">d1r6bx2</a>	Alignment	not modelled	99.7	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
114	<a href="#">d1lofha</a>	Alignment	not modelled	99.7	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
115	<a href="#">c5vy9C</a>	Alignment	not modelled	99.7	13	<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
116	<a href="#">c3uk6L</a>	Alignment	not modelled	99.7	18	<b>PDB header:</b> hydrolase <b>Chain:</b> L: <b>PDB Molecule:</b> ruvb-like 2; <b>PDBTitle:</b> crystal structure of the tip48 (tip49b) hexamer
117	<a href="#">d1jbka</a>	Alignment	not modelled	99.7	14	<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
118	<a href="#">c2x8aA</a>	Alignment	not modelled	99.7	17	<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 (nvl), c-2 terminal aaa-atpase domain
119	<a href="#">c5kneF</a>	Alignment	not modelled	99.7	13	<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
120	<a href="#">c4ypnA</a>	Alignment	not modelled	99.7	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lon protease; <b>PDBTitle:</b> crystal structure of a lon fragment containing the 3-helix bundle and2 the aaa-alpha/beta domain