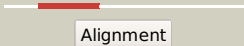

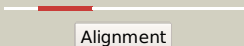

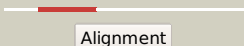

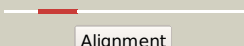
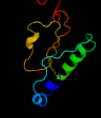
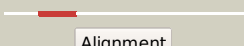

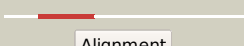

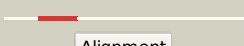
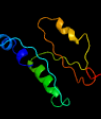







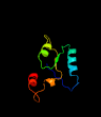
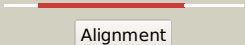

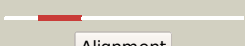











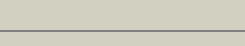

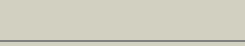


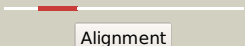
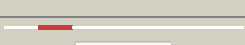
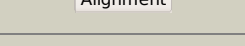
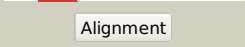
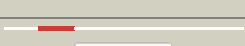
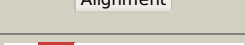
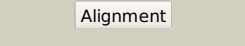


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2655c (- )_2977241_2978668
Date	Wed Aug 7 12:50:30 BST 2019
Unique Job ID	9143870c382e6c9f

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3b9pA_</a>	 Alignment		97.4	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cg5977-pa, isoform a; <b>PDBTitle:</b> spastin
2	<a href="#">c3hu2C_</a>	 Alignment		97.1	19	<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
3	<a href="#">c3hteC_</a>	 Alignment		97.0	14	<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
4	<a href="#">c4b4tl_</a>	 Alignment		96.9	20	<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
5	<a href="#">c6nyyC_</a>	 Alignment		96.9	21	<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
6	<a href="#">d1r6bx3</a>	 Alignment		96.9	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
7	<a href="#">c4b4tH_</a>	 Alignment		96.8	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
8	<a href="#">c5u8s4_</a>	 Alignment		96.8	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
9	<a href="#">c3cf1C_</a>	 Alignment		96.8	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/vcp in complex with adp/adp.alfx
10	<a href="#">c6matE_</a>	 Alignment		96.8	14	<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
11	<a href="#">c1s3sA_</a>	 Alignment		96.7	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

12	<a href="#">c5m7nA_</a>	 Alignment		96.7	17	<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 crystal direct automated mounting and cryo-cooling3 technology
13	<a href="#">c5wc0D_</a>	 Alignment		96.7	17	<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
14	<a href="#">c4ypnA_</a>	 Alignment		96.6	24	<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
15	<a href="#">c6opcF_</a>	 Alignment		96.6	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)
16	<a href="#">d1d2na_</a>	 Alignment		96.6	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
17	<a href="#">d1um8a_</a>	 Alignment		96.5	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
18	<a href="#">c3f8tA_</a>	 Alignment		96.5	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> predicted atpase involved in replication control, cdc46/mcm <b>PDBTitle:</b> crystal structure analysis of a full-length mcm homolog from2 methanopyrus kandleri
19	<a href="#">c2hcbC_</a>	 Alignment		96.5	13	<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
20	<a href="#">c1nsfA_</a>	 Alignment		96.5	16	<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)
21	<a href="#">c4b4tL_</a>	 Alignment	not modelled	96.5	15	<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
22	<a href="#">c5g4gF_</a>	 Alignment	not modelled	96.4	16	<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
23	<a href="#">c4b4tj_</a>	 Alignment	not modelled	96.4	15	<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
24	<a href="#">c6epdM_</a>	 Alignment	not modelled	96.4	13	<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)
25	<a href="#">c4z8xC_</a>	 Alignment	not modelled	96.4	22	<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
26	<a href="#">c3pvsA_</a>	 Alignment	not modelled	96.4	22	<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
27	<a href="#">c3d8bB_</a>	 Alignment	not modelled	96.3	20	<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
28	<a href="#">c3pfiB_</a>	 Alignment	not modelled	96.3	13	<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
29	<a href="#">c6hv92</a>	Alignment	not modelled	96.3	23 <b>PDB header:</b> dna binding protein <b>Chain:</b> 2: <b>PDB Molecule:</b> dna replication licensing factor mcm2; <b>PDBTitle:</b> s. cerevisiae cmg-pol epsilon-dna
30	<a href="#">c4l16A</a>	Alignment	not modelled	96.3	18 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> figetin-like protein 1; <b>PDBTitle:</b> crystal structure of figl-1 aaa domain in complex with adp
31	<a href="#">c4b4tK</a>	Alignment	not modelled	96.3	23 <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
32	<a href="#">c6mdnF</a>	Alignment	not modelled	96.3	19 <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)
33	<a href="#">c6b5cA</a>	Alignment	not modelled	96.3	20 <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
34	<a href="#">d1qvra3</a>	Alignment	not modelled	96.3	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
35	<a href="#">c3dzdA</a>	Alignment	not modelled	96.3	14 <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="#">c3jc76</a>	Alignment	not modelled	96.2	16 <b>PDB header:</b> hydrolase <b>Chain:</b> 6: <b>PDB Molecule:</b> dna replication licensing factor mcm6; <b>PDBTitle:</b> structure of the eukaryotic replicative cmg helicase and pumpjack2 motion
37	<a href="#">c5udb7</a>	Alignment	not modelled	96.2	19 <b>PDB header:</b> replication <b>Chain:</b> 7: <b>PDB Molecule:</b> dna replication licensing factor mcm7; <b>PDBTitle:</b> structural basis of mcm2-7 replicative helicase loading by orc-cdc62 and cdt1
38	<a href="#">c5z3qD</a>	Alignment	not modelled	96.2	14 <b>PDB header:</b> viral protein <b>Chain:</b> D: <b>PDB Molecule:</b> pv-2c; <b>PDBTitle:</b> crystal structure of a soluble fragment of poliovirus 2c atpase (2.552 angstrom)
39	<a href="#">c5ep0A</a>	Alignment	not modelled	96.2	22 <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="#">c3cf2B</a>	Alignment	not modelled	96.2	21 <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
41	<a href="#">c3jc57</a>	Alignment	not modelled	96.2	17 <b>PDB header:</b> hydrolase <b>Chain:</b> 7: <b>PDB Molecule:</b> dna replication licensing factor mcm7; <b>PDBTitle:</b> structure of the eukaryotic replicative cmg helicase and pumpjack2 motion
42	<a href="#">c1sxjA</a>	Alignment	not modelled	96.2	18 <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)
43	<a href="#">d1g41a</a>	Alignment	not modelled	96.2	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
44	<a href="#">c5t0gA</a>	Alignment	not modelled	96.1	16 <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
45	<a href="#">c1ny5A</a>	Alignment	not modelled	96.1	21 <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
46	<a href="#">c5udb3</a>	Alignment	not modelled	96.1	16 <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
47	<a href="#">c5x06G</a>	Alignment	not modelled	96.1	11 <b>PDB header:</b> replication <b>Chain:</b> G: <b>PDB Molecule:</b> dnaa regulatory inactivator hda; <b>PDBTitle:</b> dna replication regulation protein
48	<a href="#">c1ojjD</a>	Alignment	not modelled	96.1	15 <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
49	<a href="#">d2ce7a2</a>	Alignment	not modelled	96.0	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
50	<a href="#">c5ep4A</a>	Alignment	not modelled	96.0	16 <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
51	<a href="#">c1in8A</a>	Alignment	not modelled	96.0	13 <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
52	<a href="#">c3vfdA</a>	Alignment	not modelled	96.0	14 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> spastin; <b>PDBTitle:</b> human spastin aaa domain
53	<a href="#">d1in4a2</a>	Alignment	not modelled	96.0	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
					<b>PDB header:</b> replication <b>Chain:</b> A: <b>PDB Molecule:</b> dnaa-related protein;

54	<a href="#">c2kjqA_</a>	Alignment	not modelled	96.0	15	<b>PDBTitle:</b> solution structure of protein nmb1076 from neisseria meningitidis.2 northeast structural genomics consortium target mr101b.
55	<a href="#">c2r65A_</a>	Alignment	not modelled	96.0	21	<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
56	<a href="#">d1l8qa2</a>	Alignment	not modelled	96.0	11	<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
57	<a href="#">c5h7i7_</a>	Alignment	not modelled	95.9	17	<b>PDB header:</b> hydrolase <b>Chain:</b> 7: <b>PDB Molecule:</b> dna replication licensing factor mcm7; <b>PDBTitle:</b> cryo-em structure of the cdt1-mcm2-7 complex in amppnp state
58	<a href="#">c3eihB_</a>	Alignment	not modelled	95.9	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
59	<a href="#">c5j1sA_</a>	Alignment	not modelled	95.9	14	<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
60	<a href="#">c3j96F_</a>	Alignment	not modelled	95.9	19	<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)
61	<a href="#">c3zw6B_</a>	Alignment	not modelled	95.9	16	<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.
62	<a href="#">c1r6bX_</a>	Alignment	not modelled	95.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> X: <b>PDB Molecule:</b> clpa protein; <b>PDBTitle:</b> high resolution crystal structure of clpa
63	<a href="#">c5kneF_</a>	Alignment	not modelled	95.9	18	<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
64	<a href="#">c1ojfF_</a>	Alignment	not modelled	95.9	14	<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
65	<a href="#">c4b4tM_</a>	Alignment	not modelled	95.8	13	<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
66	<a href="#">c6hecH_</a>	Alignment	not modelled	95.8	17	<b>PDB header:</b> hydrolase <b>Chain:</b> H: <b>PDB Molecule:</b> proteasome-activating nucleotidase; <b>PDBTitle:</b> pan-proteasome in state 4
67	<a href="#">c3jc55_</a>	Alignment	not modelled	95.8	21	<b>PDB header:</b> hydrolase <b>Chain:</b> 5: <b>PDB Molecule:</b> minichromosome maintenance protein 5; <b>PDBTitle:</b> structure of the eukaryotic replicative cmg helicase and pumpjack2 motion
68	<a href="#">c1iy2A_</a>	Alignment	not modelled	95.8	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
69	<a href="#">c6nyyA_</a>	Alignment	not modelled	95.7	22	<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
70	<a href="#">c5mpaL_</a>	Alignment	not modelled	95.7	17	<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)
71	<a href="#">c2zamA_</a>	Alignment	not modelled	95.7	17	<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
72	<a href="#">c2x8aA_</a>	Alignment	not modelled	95.7	16	<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
73	<a href="#">c3ja87_</a>	Alignment	not modelled	95.7	20	<b>PDB header:</b> hydrolase <b>Chain:</b> 7: <b>PDB Molecule:</b> minichromosome maintenance 7; <b>PDBTitle:</b> cryo-em structure of the mcm2-7 double hexamer
74	<a href="#">c3jc72_</a>	Alignment	not modelled	95.6	22	<b>PDB header:</b> hydrolase <b>Chain:</b> 2: <b>PDB Molecule:</b> dna replication licensing factor mcm2; <b>PDBTitle:</b> structure of the eukaryotic replicative cmg helicase and pumpjack2 motion
75	<a href="#">d1lixza_</a>	Alignment	not modelled	95.5	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
76	<a href="#">c5ifwB_</a>	Alignment	not modelled	95.5	16	<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
77	<a href="#">c6az0A_</a>	Alignment	not modelled	95.5	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
78	<a href="#">c5w0tA_</a>	Alignment	not modelled	95.5	16	<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
79	<a href="#">c3ja84_</a>	Alignment	not modelled	95.5	15	<b>PDB header:</b> hydrolase <b>Chain:</b> 4: <b>PDB Molecule:</b> minichromosome maintenance 4; <b>PDBTitle:</b> cryo-em structure of the mcm2-7 double hexamer

80	<a href="#">c5ujmE</a>	Alignment	not modelled	95.5	16	<b>PDB header:</b> replication <b>Chain:</b> E: <b>PDB Molecule:</b> origin recognition complex subunit 5; <b>PDBTitle:</b> structure of the active form of human origin recognition complex and2 its atpase motor module
81	<a href="#">c2dhrC</a>	Alignment	not modelled	95.5	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)
82	<a href="#">c5e7pA</a>	Alignment	not modelled	95.5	27	<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.
83	<a href="#">c2ce7B</a>	Alignment	not modelled	95.5	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
84	<a href="#">c2z4rB</a>	Alignment	not modelled	95.4	16	<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
85	<a href="#">c6epcJ</a>	Alignment	not modelled	95.3	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)
86	<a href="#">d1ny5a2</a>	Alignment	not modelled	95.3	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
87	<a href="#">c6djuA</a>	Alignment	not modelled	95.3	20	<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
88	<a href="#">c6hv96</a>	Alignment	not modelled	95.2	20	<b>PDB header:</b> dna binding protein <b>Chain:</b> 6: <b>PDB Molecule:</b> dna replication licensing factor mcm6; <b>PDBTitle:</b> s. cerevisiae cmg-pol epsilon-dna
89	<a href="#">c3jc73</a>	Alignment	not modelled	95.2	16	<b>PDB header:</b> hydrolase <b>Chain:</b> 3: <b>PDB Molecule:</b> dna replication licensing factor mcm3; <b>PDBTitle:</b> structure of the eukaryotic replicative cmg helicase and pumpjack2 motion
90	<a href="#">c5vq9D</a>	Alignment	not modelled	95.1	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="#">c3ja83</a>	Alignment	not modelled	95.1	16	<b>PDB header:</b> hydrolase <b>Chain:</b> 3: <b>PDB Molecule:</b> minichromosome maintenance 3; <b>PDBTitle:</b> cryo-em structure of the mcm2-7 double hexamer
92	<a href="#">c6hv93</a>	Alignment	not modelled	95.1	16	<b>PDB header:</b> dna binding protein <b>Chain:</b> 3: <b>PDB Molecule:</b> dna replication licensing factor mcm3; <b>PDBTitle:</b> s. cerevisiae cmg-pol epsilon-dna
93	<a href="#">c5d4wB</a>	Alignment	not modelled	95.1	16	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> putative heat shock protein; <b>PDBTitle:</b> crystal structure of hsp104
94	<a href="#">c6blbA</a>	Alignment	not modelled	95.1	14	<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
95	<a href="#">c4r7zB</a>	Alignment	not modelled	95.0	17	<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
96	<a href="#">c3ja82</a>	Alignment	not modelled	94.9	24	<b>PDB header:</b> hydrolase <b>Chain:</b> 2: <b>PDB Molecule:</b> minichromosome maintenance 2; <b>PDBTitle:</b> cryo-em structure of the mcm2-7 double hexamer
97	<a href="#">c3sylB</a>	Alignment	not modelled	94.9	16	<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
98	<a href="#">c5gjqL</a>	Alignment	not modelled	94.9	19	<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
99	<a href="#">c5v8f3</a>	Alignment	not modelled	94.8	16	<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
100	<a href="#">d1r7ra3</a>	Alignment	not modelled	94.7	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
101	<a href="#">c6azyA</a>	Alignment	not modelled	94.7	21	<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
102	<a href="#">c3u5zM</a>	Alignment	not modelled	94.6	18	<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
103	<a href="#">d1ofha</a>	Alignment	not modelled	94.5	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
104	<a href="#">c1sxE</a>	Alignment	not modelled	94.5	13	<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)
105	<a href="#">c5vq9A</a>	Alignment	not modelled	94.4	20	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator fleq;

105	<a href="#">c0c5aA_</a>	Alignment	not modelled	94.4	20	<b>PDBTitle:</b> aaa+ atpase fleq from pseudomonas aeruginosa bound to atp-gamma-s
106	<a href="#">c5he8J_</a>	Alignment	not modelled	94.4	15	<b>PDB header:</b> protein binding <b>Chain:</b> J: <b>PDB Molecule:</b> helicase loader; <b>PDBTitle:</b> bacterial initiation protein
107	<a href="#">c4lcbA_</a>	Alignment	not modelled	94.3	21	<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
108	<a href="#">c5ubvB_</a>	Alignment	not modelled	94.3	20	<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
109	<a href="#">c5c3cB_</a>	Alignment	not modelled	94.3	27	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> cbbq/nirq/norq domain protein; <b>PDBTitle:</b> structural characterization of a newly identified component of alpha-2 carboxysomes: the aaa+ domain protein cso-cbbq
110	<a href="#">c4ciuA_</a>	Alignment	not modelled	94.3	21	<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
111	<a href="#">c4xgcE_</a>	Alignment	not modelled	94.3	14	<b>PDB header:</b> dna binding protein <b>Chain:</b> E: <b>PDB Molecule:</b> origin recognition complex subunit 5; <b>PDBTitle:</b> crystal structure of the eukaryotic origin recognition complex
112	<a href="#">c5kzfl_</a>	Alignment	not modelled	94.2	17	<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
113	<a href="#">c6qeIL_</a>	Alignment	not modelled	94.1	18	<b>PDB header:</b> replication <b>Chain:</b> L: <b>PDB Molecule:</b> dna replication protein dnac; <b>PDBTitle:</b> e. coli dnabc apo complex
114	<a href="#">c5uj7B_</a>	Alignment	not modelled	94.1	19	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> origin recognition complex subunit 1; <b>PDBTitle:</b> structure of the active form of human origin recognition complex2 atpase motor module, complex subunits 1, 4, 5
115	<a href="#">c5vy9C_</a>	Alignment	not modelled	94.1	20	<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="#">d1e32a2</a>	Alignment	not modelled	93.7	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
117	<a href="#">c5udbD_</a>	Alignment	not modelled	93.7	16	<b>PDB header:</b> replication <b>Chain:</b> D: <b>PDB Molecule:</b> origin recognition complex subunit 4; <b>PDBTitle:</b> structural basis of mcm2-7 replicative helicase loading by orc-cdc62 and cdt1
118	<a href="#">c3ja86_</a>	Alignment	not modelled	93.6	21	<b>PDB header:</b> hydrolase <b>Chain:</b> 6: <b>PDB Molecule:</b> minichromosome maintenance 6; <b>PDBTitle:</b> cryo-em structure of the mcm2-7 double hexamer
119	<a href="#">c3pxiB_</a>	Alignment	not modelled	93.5	17	<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
120	<a href="#">c3co5B_</a>	Alignment	not modelled	93.4	13	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> putative two-component system transcriptional response <b>PDBTitle:</b> crystal structure of sigma-54 interaction domain of putative2 transcriptional response regulator from neisseria gonorrhoeae