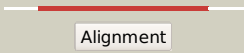
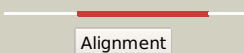
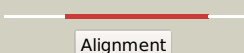
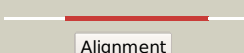

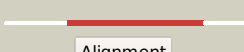
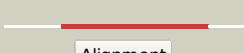

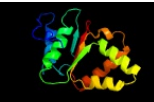






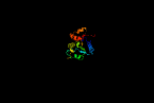



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3427c_(-)_3844065_3844820
Date	Fri Aug 9 18:20:10 BST 2019
Unique Job ID	1f4439350a66a9c7

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5bq5A_</a>	 Alignment		100.0	31	<b>PDB header:</b> atp-binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> insertion sequence is5376 putative atp-binding protein; <b>PDBTitle:</b> crystal structure of the istb aaa+ domain bound to adp-bef3
2	<a href="#">c6qell_</a>	 Alignment		100.0	17	<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
3	<a href="#">c2w58B_</a>	 Alignment		100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> primosome component (helicase loader); <b>PDBTitle:</b> crystal structure of the dnaI
4	<a href="#">c2qqzA_</a>	 Alignment		100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> putative primosome component; <b>PDBTitle:</b> crystal structure of a putative primosome component from streptococcus2 pyogenes serotype m3. northeast structural genomics target dr58
5	<a href="#">c5he8J_</a>	 Alignment		100.0	21	<b>PDB header:</b> protein binding <b>Chain:</b> J; <b>PDB Molecule:</b> helicase loader; <b>PDBTitle:</b> bacterial initiation protein
6	<a href="#">c4m4wO_</a>	 Alignment		100.0	20	<b>PDB header:</b> replication <b>Chain:</b> O; <b>PDB Molecule:</b> primosomal protein dnaI; <b>PDBTitle:</b> mechanistic implications for the bacterial primosome assembly of the2 structure of a helicase-helicase loader complex
7	<a href="#">c3ec2A_</a>	 Alignment		100.0	17	<b>PDB header:</b> replication <b>Chain:</b> A; <b>PDB Molecule:</b> dna replication protein dnac; <b>PDBTitle:</b> crystal structure of the dnac helicase loader
8	<a href="#">c2hcbC_</a>	 Alignment		99.8	18	<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
9	<a href="#">c2kjqA_</a>	 Alignment		99.8	19	<b>PDB header:</b> replication <b>Chain:</b> A; <b>PDB Molecule:</b> dnaa-related protein; <b>PDBTitle:</b> solution structure of protein nmb1076 from neisseria meningitidis.2 northeast structural genomics consortium target mr101b.
10	<a href="#">d1l8qa2</a>	 Alignment		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
11	<a href="#">c5x06G_</a>	 Alignment		99.7	17	<b>PDB header:</b> replication <b>Chain:</b> G; <b>PDB Molecule:</b> dnaa regulatory inactivator hda; <b>PDBTitle:</b> dna replication regulation protein

12	<a href="#">c2z4rB_</a>	Alignment		99.6	20	<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
13	<a href="#">c3bosA_</a>	Alignment		99.5	14	<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
14	<a href="#">c3zw6B_</a>	Alignment		99.1	13	<b>PDB header:</b> photosynthesis <b>Chain:</b> B: <b>PDB Molecule:</b> ribulose biphosphate carboxylase/oxygenase activase 1, <b>PDBTitle:</b> model of hexameric aaa domain arrangement of green-type rubisco2 activase from tobacco.
15	<a href="#">c3cf2B_</a>	Alignment		99.1	19	<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
16	<a href="#">c4xguB_</a>	Alignment		99.1	19	<b>PDB header:</b> atp-binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> putative pachyten checkpoint protein 2; <b>PDBTitle:</b> structure of c. elegans pch-2
17	<a href="#">c1qvrB_</a>	Alignment		99.0	19	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> clpb protein; <b>PDBTitle:</b> crystal structure analysis of clpb
18	<a href="#">c4ypnA_</a>	Alignment		99.0	23	<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
19	<a href="#">c6azyA_</a>	Alignment		99.0	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
20	<a href="#">c3pfiB_</a>	Alignment		99.0	17	<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
21	<a href="#">c4ciuA_</a>	Alignment	not modelled	98.9	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
22	<a href="#">c3pxiB_</a>	Alignment	not modelled	98.9	26	<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
23	<a href="#">c6epdM_</a>	Alignment	not modelled	98.9	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)
24	<a href="#">c4b4tj_</a>	Alignment	not modelled	98.9	19	<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
25	<a href="#">c5ifwB_</a>	Alignment	not modelled	98.9	17	<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
26	<a href="#">c5w0tA_</a>	Alignment	not modelled	98.9	19	<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
27	<a href="#">c5g4gF_</a>	Alignment	not modelled	98.9	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
28	<a href="#">c3hu2C_</a>	Alignment	not modelled	98.9	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 n-d1 r86a mutant in complex with atpgs
						<b>PDB header:</b> transport protein

29	<a href="#">c3cf1C</a>	Alignment	not modelled	98.9	20	<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
30	<a href="#">c3vfdA</a>	Alignment	not modelled	98.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> spastin; <b>PDBTitle:</b> human spastin aaa domain
31	<a href="#">c5mpaL</a>	Alignment	not modelled	98.9	23	<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)
32	<a href="#">c4b4tL</a>	Alignment	not modelled	98.9	21	<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
33	<a href="#">c5z3qD</a>	Alignment	not modelled	98.9	16	<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)
34	<a href="#">c3d8bB</a>	Alignment	not modelled	98.8	15	<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
35	<a href="#">c6hecH</a>	Alignment	not modelled	98.8	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
36	<a href="#">c4d2qC</a>	Alignment	not modelled	98.8	21	<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)
37	<a href="#">c5vq9D</a>	Alignment	not modelled	98.8	19	<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
38	<a href="#">d2ce7a2</a>	Alignment	not modelled	98.8	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
39	<a href="#">c1nsfA</a>	Alignment	not modelled	98.8	19	<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)
40	<a href="#">c6b5cA</a>	Alignment	not modelled	98.8	16	<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
41	<a href="#">c4l16A</a>	Alignment	not modelled	98.8	16	<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="#">d1ny5a2</a>	Alignment	not modelled	98.8	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
43	<a href="#">d1jbka</a>	Alignment	not modelled	98.8	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
44	<a href="#">c4b4tM</a>	Alignment	not modelled	98.8	17	<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
45	<a href="#">c5e7pA</a>	Alignment	not modelled	98.8	23	<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.
46	<a href="#">c3b9pA</a>	Alignment	not modelled	98.8	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> cg5977-pa, isoform a; <b>PDBTitle:</b> spastin
47	<a href="#">c5kneD</a>	Alignment	not modelled	98.7	19	<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
48	<a href="#">c4lcbA</a>	Alignment	not modelled	98.7	16	<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
49	<a href="#">d1lixza</a>	Alignment	not modelled	98.7	23	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
50	<a href="#">c5j1sA</a>	Alignment	not modelled	98.7	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
51	<a href="#">c4z8xC</a>	Alignment	not modelled	98.7	14	<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
52	<a href="#">d1d2na</a>	Alignment	not modelled	98.7	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
53	<a href="#">c6epcJ</a>	Alignment	not modelled	98.7	21	<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)
54	<a href="#">c4b4tK</a>	Alignment	not modelled	98.7	24	<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
55	<a href="#">c6opcF</a>	Alignment	not modelled	98.7	20	<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)

56	<a href="#">c2zamA_</a>	Alignment	not modelled	98.7	19	<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
57	<a href="#">c4b4tH_</a>	Alignment	not modelled	98.7	21	<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
58	<a href="#">c5kzfj_</a>	Alignment	not modelled	98.7	23	<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
59	<a href="#">c2dhrC_</a>	Alignment	not modelled	98.7	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)
60	<a href="#">c1in8A_</a>	Alignment	not modelled	98.7	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
61	<a href="#">c4b4tI_</a>	Alignment	not modelled	98.7	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
62	<a href="#">c1iy2A_</a>	Alignment	not modelled	98.7	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
63	<a href="#">c5kneF_</a>	Alignment	not modelled	98.7	19	<b>PDB header:</b> chaperone <b>Chain:</b> F; <b>PDB Molecule:</b> heat shock protein 104; <b>PDBTitle:</b> cryoem reconstruction of hsp104 hexamer
64	<a href="#">c3hteC_</a>	Alignment	not modelled	98.7	15	<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
65	<a href="#">c6em8E_</a>	Alignment	not modelled	98.7	25	<b>PDB header:</b> chaperone <b>Chain:</b> E; <b>PDB Molecule:</b> atp-dependent clp protease atp-binding subunit clpc; <b>PDBTitle:</b> s.aureus clpc resting state, c2 symmetrised
66	<a href="#">c6nyyA_</a>	Alignment	not modelled	98.7	21	<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
67	<a href="#">d1qvra3</a>	Alignment	not modelled	98.7	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
68	<a href="#">c1s3sA_</a>	Alignment	not modelled	98.7	18	<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
69	<a href="#">c2ce7B_</a>	Alignment	not modelled	98.7	19	<b>PDB header:</b> cell division protein <b>Chain:</b> B; <b>PDB Molecule:</b> cell division protein ftsh; <b>PDBTitle:</b> edta treated
70	<a href="#">c2x8aA_</a>	Alignment	not modelled	98.7	22	<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
71	<a href="#">c2p65A_</a>	Alignment	not modelled	98.7	18	<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
72	<a href="#">c1r6bX_</a>	Alignment	not modelled	98.7	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
73	<a href="#">c3eihB_</a>	Alignment	not modelled	98.7	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
74	<a href="#">c3pvsA_</a>	Alignment	not modelled	98.6	23	<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
75	<a href="#">d1lum8a_</a>	Alignment	not modelled	98.6	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
76	<a href="#">c6matE_</a>	Alignment	not modelled	98.6	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
77	<a href="#">c5gjql_</a>	Alignment	not modelled	98.6	20	<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
78	<a href="#">c1sxjA_</a>	Alignment	not modelled	98.6	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)
79	<a href="#">c6nyyC_</a>	Alignment	not modelled	98.6	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
80	<a href="#">c4xgcA_</a>	Alignment	not modelled	98.6	14	<b>PDB header:</b> dna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> origin recognition complex subunit 1; <b>PDBTitle:</b> crystal structure of the eukaryotic origin recognition

						complex
81	<a href="#">c6mdnF_</a>	Alignment	not modelled	98.6	20	<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)
82	<a href="#">c6az0A_</a>	Alignment	not modelled	98.6	24	<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
83	<a href="#">c5wc0D_</a>	Alignment	not modelled	98.6	14	<b>PDB header:</b> motor protein <b>Chain:</b> D: <b>PDB Molecule:</b> meiotic spindle formation protein mei-1; <b>PDBTitle:</b> katanin hexamer in spiral conformation
84	<a href="#">c3te6A_</a>	Alignment	not modelled	98.6	6	<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
85	<a href="#">c2c99A_</a>	Alignment	not modelled	98.6	21	<b>PDB header:</b> transcription regulation <b>Chain:</b> A: <b>PDB Molecule:</b> psp operon transcriptional activator; <b>PDBTitle:</b> structural basis of the nucleotide driven conformational2 changes in the aaa domain of transcription activator pspf
86	<a href="#">d1r6bx3</a>	Alignment	not modelled	98.6	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
87	<a href="#">c5vy9C_</a>	Alignment	not modelled	98.6	21	<b>PDB header:</b> chaperone <b>Chain:</b> C: <b>PDB Molecule:</b> heat shock protein 104; <b>PDBTitle:</b> s. cerevisiae hsp104:casein complex, middle domain conformation
88	<a href="#">c5udbD_</a>	Alignment	not modelled	98.6	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
89	<a href="#">c3j96F_</a>	Alignment	not modelled	98.6	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)
90	<a href="#">c5d4wB_</a>	Alignment	not modelled	98.5	17	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> putative heat shock protein; <b>PDBTitle:</b> crystal structure of hsp104
91	<a href="#">d1iqpa2</a>	Alignment	not modelled	98.5	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
92	<a href="#">d1sxja2</a>	Alignment	not modelled	98.5	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
93	<a href="#">d1in4a2</a>	Alignment	not modelled	98.5	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
94	<a href="#">c5t0gA_</a>	Alignment	not modelled	98.5	19	<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
95	<a href="#">c1ojlD_</a>	Alignment	not modelled	98.5	23	<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
96	<a href="#">c3u5zM_</a>	Alignment	not modelled	98.5	21	<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
97	<a href="#">c5ep4A_</a>	Alignment	not modelled	98.5	18	<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
98	<a href="#">c5uj7C_</a>	Alignment	not modelled	98.5	17	<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
99	<a href="#">c3nbxX_</a>	Alignment	not modelled	98.5	24	<b>PDB header:</b> hydrolase <b>Chain:</b> X: <b>PDB Molecule:</b> atpase rava; <b>PDBTitle:</b> crystal structure of e. coli rava (regulatory atpase variant a) in2 complex with adp
100	<a href="#">c4xgcD_</a>	Alignment	not modelled	98.5	15	<b>PDB header:</b> dna binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> origin recognition complex subunit 4; <b>PDBTitle:</b> crystal structure of the eukaryotic origin recognition complex
101	<a href="#">c5grbF_</a>	Alignment	not modelled	98.5	18	<b>PDB header:</b> hydrolase/inhibitor <b>Chain:</b> F: <b>PDB Molecule:</b> ev71 2c atpase; <b>PDBTitle:</b> crystal structure of 2c helicase from enterovirus 71 (ev71) bound with2 atpgammas
102	<a href="#">d1r7ra3</a>	Alignment	not modelled	98.5	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
103	<a href="#">c5uj7B_</a>	Alignment	not modelled	98.5	14	<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
104	<a href="#">c2px0D_</a>	Alignment	not modelled	98.5	16	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> D: <b>PDB Molecule:</b> flagellar biosynthesis protein flhf; <b>PDBTitle:</b> crystal structure of flhf complexed with gmppnp/mg(2+)
105	<a href="#">d1e32a2</a>	Alignment	not modelled	98.5	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
106	<a href="#">c2chgB_</a>	Alignment	not modelled	98.5	16	<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

107	<a href="#">c3sylvB_</a>	Alignment	not modelled	98.5	18	<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
108	<a href="#">d1lofha_</a>	Alignment	not modelled	98.5	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
109	<a href="#">c6e111_</a>	Alignment	not modelled	98.5	25	<b>PDB header:</b> protein transport <b>Chain:</b> 1: <b>PDB Molecule:</b> heat shock protein 101; <b>PDBTitle:</b> ptx core complex in the resetting (compact) state
110	<a href="#">c5l3sF_</a>	Alignment	not modelled	98.5	17	<b>PDB header:</b> protein transport <b>Chain:</b> F: <b>PDB Molecule:</b> signal recognition particle receptor ftsy; <b>PDBTitle:</b> structure of the gtpase heterodimer of crenarchaeal srp54 and ftsy
111	<a href="#">c5ubvB_</a>	Alignment	not modelled	98.5	21	<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
112	<a href="#">c6em8F_</a>	Alignment	not modelled	98.5	25	<b>PDB header:</b> chaperone <b>Chain:</b> F: <b>PDB Molecule:</b> atp-dependent clp protease atp-binding subunit clpC; <b>PDBTitle:</b> s.aureus clpC resting state, c2 symmetrised
113	<a href="#">c1vmaA_</a>	Alignment	not modelled	98.4	17	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> cell division protein ftsy; <b>PDBTitle:</b> crystal structure of cell division protein ftsy (tm0570) from <i>Thermotoga maritima</i> at 1.60 Å resolution
114	<a href="#">c2cnwF_</a>	Alignment	not modelled	98.4	18	<b>PDB header:</b> signal recognition <b>Chain:</b> F: <b>PDB Molecule:</b> cell division protein ftsy; <b>PDBTitle:</b> gdpalf4 complex of the srp gtpases ffh and ftsy
115	<a href="#">c1xwiA_</a>	Alignment	not modelled	98.4	18	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> skd1 protein; <b>PDBTitle:</b> crystal structure of vps4b
116	<a href="#">c2j7pA_</a>	Alignment	not modelled	98.4	17	<b>PDB header:</b> signal recognition <b>Chain:</b> A: <b>PDB Molecule:</b> signal recognition particle protein; <b>PDBTitle:</b> gmppnp-stabilized ng domain complex of the srp gtpases ffh2 and ftsy
117	<a href="#">c6djuA_</a>	Alignment	not modelled	98.4	13	<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
118	<a href="#">c5exsA_</a>	Alignment	not modelled	98.4	21	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator fleq; <b>PDBTitle:</b> aaa+ atpase fleq from <i>Pseudomonas aeruginosa</i> bound to atp-gamma-s
119	<a href="#">c5kneA_</a>	Alignment	not modelled	98.4	16	<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
120	<a href="#">c2qz4A_</a>	Alignment	not modelled	98.4	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