























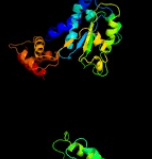
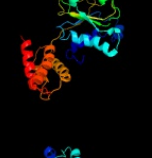
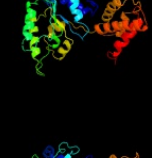

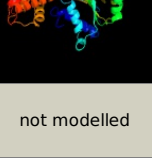


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3884c_(-)_4365157_4367016
Date	Sat Aug 10 22:05:07 BST 2019
Unique Job ID	fe69eccc2083fdd6

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3sylB_</a>	 Alignment		100.0	31	<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
2	<a href="#">c5e7pA_</a>	 Alignment		100.0	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.
3	<a href="#">c6matE_</a>	 Alignment		100.0	22	<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
4	<a href="#">c5g4gF_</a>	 Alignment		100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> F; <b>PDB Molecule:</b> vcpl-like atpase; <b>PDBTitle:</b> structure of the atpgs-bound vat complex
5	<a href="#">c3cf1C_</a>	 Alignment		100.0	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
6	<a href="#">c3hu2C_</a>	 Alignment		100.0	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
7	<a href="#">c6nyyC_</a>	 Alignment		100.0	20	<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
8	<a href="#">c2dhrC_</a>	 Alignment		100.0	22	<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)
9	<a href="#">c6epdM_</a>	 Alignment		100.0	21	<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)
10	<a href="#">c5kzfj_</a>	 Alignment		100.0	22	<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
11	<a href="#">c1s3sA_</a>	 Alignment		100.0	20	<b>PDB header:</b> protein binding <b>Chain:</b> A; <b>PDB Molecule:</b> transitional endoplasmic reticulum atpase (ter) <b>PDBTitle:</b> crystal structure of aaa atpase p97/vcp nd1 in complex with2 p47 c

12	<a href="#">c6genX_</a>	Alignment		100.0	30	<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.
13	<a href="#">c4b4tH_</a>	Alignment		100.0	24	<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
14	<a href="#">c4l16A_</a>	Alignment		100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> fig1-like protein 1; <b>PDBTitle:</b> crystal structure of figl-1 aaa domain in complex with adp
15	<a href="#">c4b4tJ_</a>	Alignment		100.0	24	<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
16	<a href="#">c6epcJ_</a>	Alignment		100.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> J: <b>PDB Molecule:</b> 26s proteasome regulatory subunit 8; <b>PDBTitle:</b> ground state 26s proteasome (gs2)
17	<a href="#">c4b4tI_</a>	Alignment		100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> I: <b>PDB Molecule:</b> 26s protease regulatory subunit 4 homolog; <b>PDBTitle:</b> near-atomic resolution structural model of the yeast 26s proteasome
18	<a href="#">c6hecH_</a>	Alignment		100.0	25	<b>PDB header:</b> hydrolase <b>Chain:</b> H: <b>PDB Molecule:</b> proteasome-activating nucleotidase; <b>PDBTitle:</b> pan-proteasome in state 4
19	<a href="#">c4b4tL_</a>	Alignment		100.0	24	<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
20	<a href="#">c6az0A_</a>	Alignment		100.0	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
21	<a href="#">c1xwiA_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> skd1 protein; <b>PDBTitle:</b> crystal structure of vps4b
22	<a href="#">c4z8xC_</a>	Alignment	not modelled	100.0	23	<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
23	<a href="#">c3b9pA_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cg5977-pa, isoform a; <b>PDBTitle:</b> spastin
24	<a href="#">c3cf2B_</a>	Alignment	not modelled	100.0	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
25	<a href="#">c5ifwB_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> transitional endoplasmic reticulum atpase; <b>PDBTitle:</b> quantitative interaction mapping reveals an extended ubiquitin2 regulatory domain in aspl that disrupts functional p97 hexamers and3 induces cell death
26	<a href="#">c5w0tA_</a>	Alignment	not modelled	100.0	18	<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="#">c4b4tM_</a>	Alignment	not modelled	100.0	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
28	<a href="#">c6nyyA_</a>	Alignment	not modelled	100.0	19	<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
						<b>PDB header:</b> hydrolase

29	<a href="#">c4b4tK_</a>	Alignment	not modelled	100.0	24	<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
30	<a href="#">c3eihB_</a>	Alignment	not modelled	100.0	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
31	<a href="#">c5mpaL_</a>	Alignment	not modelled	100.0	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="#">c2ce7B_</a>	Alignment	not modelled	100.0	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
33	<a href="#">c5gjql_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> L: <b>PDB Molecule:</b> 26s protease regulatory subunit 10b; <b>PDBTitle:</b> structure of the human 26s proteasome bound to usp14-ubal
34	<a href="#">c5t0gA_</a>	Alignment	not modelled	100.0	23	<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
35	<a href="#">d1g41a_</a>	Alignment	not modelled	100.0	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
36	<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
37	<a href="#">d2ce7a2</a>	Alignment	not modelled	99.9	20	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
38	<a href="#">c1iy2A_</a>	Alignment	not modelled	99.9	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
39	<a href="#">d1e32a2</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
40	<a href="#">c6b5cA_</a>	Alignment	not modelled	99.9	15	<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="#">c2zamA_</a>	Alignment	not modelled	99.9	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
42	<a href="#">d1ixza_</a>	Alignment	not modelled	99.9	21	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
43	<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
44	<a href="#">c3vfdA_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> spastin; <b>PDBTitle:</b> human spastin aaa domain
45	<a href="#">c4xguB_</a>	Alignment	not modelled	99.9	16	<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="#">c5nnrD_</a>	Alignment	not modelled	99.9	11	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> n-terminal acetyltransferase-like protein; <b>PDBTitle:</b> structure of naa15/naa10 bound to hypk-thb
47	<a href="#">c3pvsA_</a>	Alignment	not modelled	99.9	26	<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
48	<a href="#">c6c95A_</a>	Alignment	not modelled	99.9	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> n-alpha-acetyltransferase 15, nata auxiliary subunit; <b>PDBTitle:</b> the human nata (naa10/naa15) amino-terminal acetyltransferase complex2 bound to hypk
49	<a href="#">c3j96F_</a>	Alignment	not modelled	99.9	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)
50	<a href="#">c5ubvB_</a>	Alignment	not modelled	99.9	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
51	<a href="#">c3pfiB_</a>	Alignment	not modelled	99.9	23	<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
52	<a href="#">c5oafB_</a>	Alignment	not modelled	99.9	26	<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
53	<a href="#">c2r65A_</a>	Alignment	not modelled	99.9	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cell division protease ftsh homolog; <b>PDBTitle:</b> crystal structure of helicobacter pylori atp dependent protease, ftsh2 adp complex
						<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases

54	<a href="#">d1ofha_</a>	Alignment	not modelled	99.9	20	<b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
55	<a href="#">c4bujF_</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> superkiller protein 3; <b>PDBTitle:</b> crystal structure of the s. cerevisiae ski2-3-8 complex
56	<a href="#">c2c9oA_</a>	Alignment	not modelled	99.9	25	<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
57	<a href="#">c5vy9C_</a>	Alignment	not modelled	99.9	16	<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
58	<a href="#">c6azyA_</a>	Alignment	not modelled	99.9	13	<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
59	<a href="#">c3pxiB_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> negative regulator of genetic competence clpc/meccb; <b>PDBTitle:</b> structure of meca108:clpc
60	<a href="#">c3h4mC_</a>	Alignment	not modelled	99.9	20	<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
61	<a href="#">c5vq9D_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> protein binding <b>Chain:</b> D: <b>PDB Molecule:</b> pachytene checkpoint protein 2 homolog; <b>PDBTitle:</b> structure of human trip13, apo form
62	<a href="#">c4hnxA_</a>	Alignment	not modelled	99.9	9	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> n-terminal acetyltransferase a complex subunit nat1; <b>PDBTitle:</b> the nata acetyltransferase complex bound to ppppp
63	<a href="#">c6mdnF_</a>	Alignment	not modelled	99.9	15	<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)
64	<a href="#">c4kvmA_</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> n-terminal acetyltransferase a complex subunit nat1; <b>PDBTitle:</b> the nata (naa10p/naa15p) amino-terminal acetyltransferase complex2 bound to a bisubstrate analog
65	<a href="#">c5kneA_</a>	Alignment	not modelled	99.9	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
66	<a href="#">c3iegB_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> dnaj homolog subfamily c member 3; <b>PDBTitle:</b> crystal structure of p58(ipk) tpr domain at 2.5 a
67	<a href="#">c6opcF_</a>	Alignment	not modelled	99.9	16	<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)
68	<a href="#">c4ciuA_</a>	Alignment	not modelled	99.9	16	<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
69	<a href="#">c2xpiA_</a>	Alignment	not modelled	99.9	10	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> anaphase-promoting complex subunit cut9; <b>PDBTitle:</b> crystal structure of apc/c hetero-tetramer cut9-hcn1
70	<a href="#">c4ww4B_</a>	Alignment	not modelled	99.9	26	<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 ruvb1(adp)/ruvb2(adp)
71	<a href="#">c5kneF_</a>	Alignment	not modelled	99.9	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
72	<a href="#">c1r6bX_</a>	Alignment	not modelled	99.9	21	<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="#">c4ui9C_</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> cell cycle <b>Chain:</b> C: <b>PDB Molecule:</b> cell division cycle protein 23 homolog; <b>PDBTitle:</b> atomic structure of the human anaphase-promoting complex
74	<a href="#">d1w3ba_</a>	Alignment	not modelled	99.9	11	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> TPR-like <b>Family:</b> Tetratricopeptide repeat (TPR)
75	<a href="#">c6e111_</a>	Alignment	not modelled	99.9	25	<b>PDB header:</b> protein transport <b>Chain:</b> 1: <b>PDB Molecule:</b> heat shock protein 101; <b>PDBTitle:</b> ptex core complex in the resetting (compact) state
76	<a href="#">c4r7sA_</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> tetratricopeptide repeat protein; <b>PDBTitle:</b> crystal structure of a tetratricopeptide repeat protein (parmer_03812)2 from parabacteroides merdae atcc 43184 at 2.39 a resolution
77	<a href="#">c6blbA_</a>	Alignment	not modelled	99.9	21	<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
78	<a href="#">c2y4tA_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> dnaj homolog subfamily c member 3; <b>PDBTitle:</b> crystal structure of the human co-chaperone p58(ipk)
79	<a href="#">c5ganJ_</a>	Alignment	not modelled	99.9	11	<b>PDB header:</b> transcription <b>Chain:</b> J: <b>PDB Molecule:</b> pre-mrna-splicing factor 6; <b>PDBTitle:</b> the overall structure of the yeast spliceosomal u4/u6.u5 tri-snrnp at2 3.7 angstrom

80	<a href="#">c6djuA</a>	Alignment	not modelled	99.9	19	<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
81	<a href="#">c4lcbA</a>	Alignment	not modelled	99.9	20	<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
82	<a href="#">c2qz4A</a>	Alignment	not modelled	99.9	19	<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="#">c1qvrB</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> clpb protein; <b>PDBTitle:</b> crystal structure analysis of clpb
84	<a href="#">c5dseC</a>	Alignment	not modelled	99.9	10	<b>PDB header:</b> protein binding <b>Chain:</b> C: <b>PDB Molecule:</b> tetratricopeptide repeat protein 7b; <b>PDBTitle:</b> crystal structure of the ttc7b/hyccin complex
85	<a href="#">c5d4wB</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> putative heat shock protein; <b>PDBTitle:</b> crystal structure of hsp104
86	<a href="#">d1r7ra3</a>	Alignment	not modelled	99.9	24	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
87	<a href="#">c3pxgA</a>	Alignment	not modelled	99.9	22	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> negative regulator of genetic competence clpc/mebc; <b>PDBTitle:</b> structure of meca121 and clpc1-485 complex
88	<a href="#">c4f3vB</a>	Alignment	not modelled	99.9	25	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> esx-1 secretion system protein eccA1; <b>PDBTitle:</b> crystal structure of n-terminal domain of eccA1 atpase from esx-12 secretion system of mycobacterium tuberculosis
89	<a href="#">c2x8aA</a>	Alignment	not modelled	99.9	19	<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
90	<a href="#">d1in4a2</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
91	<a href="#">c1in8A</a>	Alignment	not modelled	99.9	22	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> holliday junction dna helicase ruvb; <b>PDBTitle:</b> thermotoga maritima ruvb t158v
92	<a href="#">c5dseA</a>	Alignment	not modelled	99.9	10	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> tetratricopeptide repeat protein 7b; <b>PDBTitle:</b> crystal structure of the ttc7b/hyccin complex
93	<a href="#">c4ui9K</a>	Alignment	not modelled	99.9	9	<b>PDB header:</b> cell cycle <b>Chain:</b> K: <b>PDB Molecule:</b> cell division cycle protein 16 homolog; <b>PDBTitle:</b> atomic structure of the human anaphase-promoting complex
94	<a href="#">d1um8a</a>	Alignment	not modelled	99.9	23	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
95	<a href="#">d1r6bx2</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
96	<a href="#">c4ww4A</a>	Alignment	not modelled	99.9	29	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ruvb-like 1; <b>PDBTitle:</b> double-heterohexameric rings of full-length rvb1(adp)/rvb2(adp)
97	<a href="#">d1qvra3</a>	Alignment	not modelled	99.9	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
98	<a href="#">d1r6bx3</a>	Alignment	not modelled	99.9	15	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
99	<a href="#">c6djevE</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> chaperone <b>Chain:</b> E: <b>PDB Molecule:</b> chaperone protein clpb; <b>PDBTitle:</b> mtb clpb in complex with atpgammas and casein, conformer 2
100	<a href="#">c6em8F</a>	Alignment	not modelled	99.9	16	<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
101	<a href="#">c3zw6B</a>	Alignment	not modelled	99.9	13	<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.
102	<a href="#">c6af0A</a>	Alignment	not modelled	99.9	10	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> ctr9 protein; <b>PDBTitle:</b> structure of ctr9, paf1 and cdc73 ternary complex from myceliophthora2 thermophila
103	<a href="#">c3hteC</a>	Alignment	not modelled	99.9	19	<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
104	<a href="#">c2ho1B</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> type 4 fimbrial biogenesis protein pilf; <b>PDBTitle:</b> functional characterization of pseudomonas aeruginosa pilf
105	<a href="#">c4uzvA</a>	Alignment	not modelled	99.9	10	<b>PDB header:</b> motor protein <b>Chain:</b> A: <b>PDB Molecule:</b> flagellar associated protein; <b>PDBTitle:</b> crystal structure of the chlamydomonas ift70 and ift52 complex
						<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases

106	<a href="#">d1lv7a_</a>	Alignment	not modelled	99.9	23	<b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
107	<a href="#">c1nsfA_</a>	Alignment	not modelled	99.9	15	<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)
108	<a href="#">c3fp4A_</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> tpr repeat-containing protein yhr117w; <b>PDBTitle:</b> crystal structure of tom71 complexed with ssa1 c-terminal2 fragment
109	<a href="#">c5kneD_</a>	Alignment	not modelled	99.9	16	<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
110	<a href="#">c2c9oC_</a>	Alignment	not modelled	99.9	16	<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
111	<a href="#">d1qvra2</a>	Alignment	not modelled	99.9	21	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
112	<a href="#">c5o9zG_</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> splicing <b>Chain:</b> G: <b>PDB Molecule:</b> pre-mrna-processing factor 6; <b>PDBTitle:</b> cryo-em structure of a pre-catalytic human spliceosome primed for2 activation (b complex)
113	<a href="#">d1jbka_</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
114	<a href="#">d1ixsb2</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
115	<a href="#">c3hymB_</a>	Alignment	not modelled	99.8	10	<b>PDB header:</b> cell cycle, ligase <b>Chain:</b> B: <b>PDB Molecule:</b> cell division cycle protein 16 homolog; <b>PDBTitle:</b> insights into anaphase promoting complex tpr subdomain2 assembly from a cdc26-apc6 structure
116	<a href="#">c5jqyA_</a>	Alignment	not modelled	99.8	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> aspartyl/asparaginyl beta-hydroxylase; <b>PDBTitle:</b> aspartyl/asparaginyl beta-hydroxylase (asph)oxygenase and tpr domains2 in complex with manganese, n-oxalylglycine and factor x substrate3 peptide fragment(39mer-4ser)
117	<a href="#">d1l8qa2</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
118	<a href="#">c4d2qC_</a>	Alignment	not modelled	99.8	17	<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)
119	<a href="#">c6em8H_</a>	Alignment	not modelled	99.8	18	<b>PDB header:</b> chaperone <b>Chain:</b> H: <b>PDB Molecule:</b> atp-dependent clp protease atp-binding subunit clpc; <b>PDBTitle:</b> s.aureus clpc resting state, c2 symmetrised
120	<a href="#">d1iqpa2</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