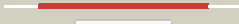



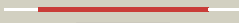



















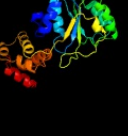



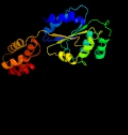

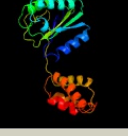


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2813 (-)_3118234_3119046
Date	Wed Aug 7 12:50:47 BST 2019
Unique Job ID	4ceb42febbf1a0c7

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1fnna2	 Alignment		99.9	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
2	d1w5sa2	 Alignment		99.9	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
3	c2z4rB_	 Alignment		99.8	12	PDB header: dna binding protein Chain: B; PDB Molecule: chromosomal replication initiator protein dnaa; PDBTitle: crystal structure of domain iii from the thermotoga2 maritima replication initiation protein dnaa
4	c5zr1A_	 Alignment		99.8	17	PDB header: dna binding protein/dna Chain: A; PDB Molecule: origin recognition complex subunit 1; PDBTitle: saccharomyces cerevisiae origin recognition complex bound to a 72-bp2 origin dna containing acs and b1 element
5	c1fnnB_	 Alignment		99.7	15	PDB header: cell cycle Chain: B; PDB Molecule: cell division control protein 6; PDBTitle: crystal structure of cdc6p from pyrobaculum aerophilum
6	c6blbA_	 Alignment		99.7	18	PDB header: hydrolase Chain: A; PDB Molecule: holliday junction atp-dependent dna helicase ruvb; PDBTitle: 1.88 angstrom resolution crystal structure holliday junction atp-2 dependent dna helicase (ruvb) from pseudomonas aeruginosa in complex3 with adp
7	c1in8A_	 Alignment		99.7	20	PDB header: dna binding protein Chain: A; PDB Molecule: holliday junction dna helicase ruvb; PDBTitle: thermotoga maritima ruvb t158v
8	d1in4a2	 Alignment		99.7	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
9	c3pfiB_	 Alignment		99.7	20	PDB header: hydrolase Chain: B; PDB Molecule: holliday junction atp-dependent dna helicase ruvb; PDBTitle: 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
10	c1w5sB_	 Alignment		99.7	20	PDB header: replication Chain: B; PDB Molecule: origin recognition complex subunit 2 orc2; PDBTitle: structure of the aeropyrum pernix orc2 protein (adp form)
11	c6nyyC_	 Alignment		99.7	17	PDB header: translocase Chain: C; PDB Molecule: afg3-like protein 2; PDBTitle: human m-aaa protease afg3l2, substrate-bound

12	c2c9oA	Alignment		99.7	16	PDB header: hydrolase Chain: A: PDB Molecule: ruvb-like 1; PDBTitle: 3d structure of the human ruvb-like helicase ruvb1
13	c6genX	Alignment		99.7	21	PDB header: nuclear protein Chain: X: PDB Molecule: ruvb-like protein 1; PDBTitle: chromatin remodeller-nucleosome complex at 4.5 a resolution.
14	d1ixsb2	Alignment		99.7	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
15	c4b4tL	Alignment		99.7	15	PDB header: hydrolase Chain: L: PDB Molecule: 26s protease subunit rpt4; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
16	d1njfa	Alignment		99.7	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
17	c2c9oC	Alignment		99.7	14	PDB header: hydrolase Chain: C: PDB Molecule: ruvb-like 1; PDBTitle: 3d structure of the human ruvb-like helicase ruvb1
18	c3te6A	Alignment		99.7	12	PDB header: gene regulation Chain: A: PDB Molecule: regulatory protein sir3; PDBTitle: crystal structure of the s. cerevisiae sir3 aaa+ domain
19	c3uk6H	Alignment		99.7	12	PDB header: hydrolase Chain: H: PDB Molecule: ruvb-like 2; PDBTitle: crystal structure of the tip48 (tip49b) hexamer
20	c4b4tL	Alignment		99.7	15	PDB header: hydrolase Chain: I: PDB Molecule: 26s protease regulatory subunit 4 homolog; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
21	c6epdM	Alignment	not modelled	99.7	12	PDB header: hydrolase Chain: M: PDB Molecule: 26s proteasome regulatory subunit 6a; PDBTitle: substrate processing state 26s proteasome (sps1)
22	d1sxd2	Alignment	not modelled	99.7	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
23	c5oafB	Alignment	not modelled	99.7	17	PDB header: gene regulation Chain: B: PDB Molecule: ruvb-like 2; PDBTitle: human rvb1/rvb2 heterohexamer in ino80 complex
24	c2qbyA	Alignment	not modelled	99.7	14	PDB header: replication/dna Chain: A: PDB Molecule: cell division control protein 6 homolog 1; PDBTitle: crystal structure of a heterodimer of cdc6/orc1 initiators2 bound to origin dna (from s. solfataricus)
25	c6epcJ	Alignment	not modelled	99.6	16	PDB header: hydrolase Chain: J: PDB Molecule: 26s proteasome regulatory subunit 8; PDBTitle: ground state 26s proteasome (gs2)
26	c5gjqL	Alignment	not modelled	99.6	17	PDB header: hydrolase Chain: L: PDB Molecule: 26s protease regulatory subunit 10b; PDBTitle: structure of the human 26s proteasome bound to usp14-ubal
27	c2v1uA	Alignment	not modelled	99.6	16	PDB header: replication Chain: A: PDB Molecule: cell division control protein 6 homolog; PDBTitle: structure of the aeropyrum pernix orc1 protein in complex2 with dna
28	c4b4tJ	Alignment	not modelled	99.6	15	PDB header: hydrolase Chain: J: PDB Molecule: 26s protease regulatory subunit 8 homolog; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome

29	c4b4tH_	Alignment	not modelled	99.6	16	PDB header: hydrolase Chain: H: PDB Molecule: 26s protease regulatory subunit 7 homolog; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
30	c2dhrC_	Alignment	not modelled	99.6	17	PDB header: hydrolase Chain: C: PDB Molecule: ftsh; PDBTitle: whole cytosolic region of atp-dependent metalloprotease2 ftsh (g399l)
31	c4b4tM_	Alignment	not modelled	99.6	17	PDB header: hydrolase Chain: M: PDB Molecule: 26s protease regulatory subunit 6a; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
32	c3bosA_	Alignment	not modelled	99.6	15	PDB header: hydrolase regulator,dna binding protein Chain: A: PDB Molecule: putative dna replication factor; PDBTitle: crystal structure of a putative dna replication regulator hda2 (sama_1916) from shewanella amazonensis sb2b at 1.75 a resolution
33	c5mpaL_	Alignment	not modelled	99.6	14	PDB header: hydrolase Chain: L: PDB Molecule: 26s protease subunit rpt4; PDBTitle: 26s proteasome in presence of atp (s2)
34	d1ny5a2	Alignment	not modelled	99.6	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
35	c6hecH_	Alignment	not modelled	99.6	15	PDB header: hydrolase Chain: H: PDB Molecule: proteasome-activating nucleotidase; PDBTitle: pan-proteasome in state 4
36	c3h4mC_	Alignment	not modelled	99.6	13	PDB header: hydrolase Chain: C: PDB Molecule: proteasome-activating nucleotidase; PDBTitle: aaa atpase domain of the proteasome- activating nucleotidase
37	c4ww4A_	Alignment	not modelled	99.6	18	PDB header: hydrolase Chain: A: PDB Molecule: ruvb-like 1; PDBTitle: double-heterohexameric rings of full-length rvb1(adp)/rvb2(adp)
38	d2ce7a2	Alignment	not modelled	99.6	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
39	c4b4tK_	Alignment	not modelled	99.6	13	PDB header: hydrolase Chain: K: PDB Molecule: 26s protease regulatory subunit 6b homolog; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
40	c1hqcB_	Alignment	not modelled	99.6	18	PDB header: hydrolase Chain: B: PDB Molecule: ruvb; PDBTitle: structure of ruvb from thermus thermophilus hb8
41	c6nyyA_	Alignment	not modelled	99.6	16	PDB header: translocase Chain: A: PDB Molecule: afg3-like protein 2; PDBTitle: human m-aaa protease afg3l2, substrate-bound
42	c5t0gA_	Alignment	not modelled	99.6	15	PDB header: hydrolase Chain: A: PDB Molecule: 26s protease regulatory subunit 7; PDBTitle: structural basis for dynamic regulation of the human 26s proteasome
43	c2ce7B_	Alignment	not modelled	99.6	18	PDB header: cell division protein Chain: B: PDB Molecule: cell division protein ftsh; PDBTitle: edta treated
44	c3pvsA_	Alignment	not modelled	99.6	14	PDB header: recombination Chain: A: PDB Molecule: replication-associated recombination protein a; PDBTitle: structure and biochemical activities of escherichia coli mgsa
45	c5e7pA_	Alignment	not modelled	99.6	19	PDB header: hydrolase Chain: A: PDB Molecule: cell division control protein cdc48; PDBTitle: crystal structure of msmeg_0858 (uniprot a0qqs4), a aaa atpase.
46	d1sxc2	Alignment	not modelled	99.6	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
47	c2chgB_	Alignment	not modelled	99.6	19	PDB header: dna-binding protein Chain: B: PDB Molecule: replication factor c small subunit; PDBTitle: replication factor c domains 1 and 2
48	d1iqpa2	Alignment	not modelled	99.6	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
49	c1iy2A_	Alignment	not modelled	99.6	16	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent metalloprotease ftsh; PDBTitle: crystal structure of the ftsh atpase domain from thermus2 thermophilus
50	c5udb9_	Alignment	not modelled	99.6	14	PDB header: replication Chain: 9: PDB Molecule: cell division control protein 6; PDBTitle: structural basis of mcm2-7 replicative helicase loading by orc-cdc62 and cdt1
51	c6qi8E_	Alignment	not modelled	99.6	14	PDB header: chaperone Chain: E: PDB Molecule: ruvb-like 2; PDBTitle: truncated human r2tp complex, structure 3 (adp-filled)
52	c1xxhB_	Alignment	not modelled	99.6	18	PDB header: transferase Chain: B: PDB Molecule: dna polymerase iii subunit gamma; PDBTitle: atpgs bound e. coli clamp loader complex
53	c5ubvB_	Alignment	not modelled	99.6	16	PDB header: hydrolase Chain: B: PDB Molecule: atpase domain of i-aaa protease; PDBTitle: atpase domain of i-aaa protease from myceliophthora thermophila
54	d2fnaa2	Alignment	not modelled	99.6	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases

						Family:Extended AAA-ATPase domain
55	c4z8xC_	Alignment	not modelled	99.6	16	PDB header: hydrolase Chain: C: PDB Molecule: atp-dependent zinc metalloprotease ftsh; PDBTitle: truncated ftsh from a. aeolicus
56	d1ixza_	Alignment	not modelled	99.6	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
57	d1sxja2	Alignment	not modelled	99.6	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
58	d1sxb2	Alignment	not modelled	99.6	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
59	c6az0A_	Alignment	not modelled	99.5	20	PDB header: hydrolase Chain: A: PDB Molecule: mitochondrial inner membrane i-aaa protease supercomplex PDBTitle: mitochondrial atpase protease yme1
60	c5ep4A_	Alignment	not modelled	99.5	16	PDB header: transcription Chain: A: PDB Molecule: putative repressor protein luxo; PDBTitle: structure, regulation, and inhibition of the quorum-sensing signal2 integrator luxo
61	c5g4gF_	Alignment	not modelled	99.5	20	PDB header: hydrolase Chain: F: PDB Molecule: vcp-like atpase; PDBTitle: structure of the atpgs-bound vat complex
62	d1lv7a_	Alignment	not modelled	99.5	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
63	c1ojfF_	Alignment	not modelled	99.5	15	PDB header: response regulator Chain: F: PDB Molecule: transcriptional regulatory protein zrar; PDBTitle: crystal structure of a sigma54-activator suggests the mechanism for2 the conformational switch necessary for sigma54 binding
64	d1r6bx2	Alignment	not modelled	99.5	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
65	d1a5ta2	Alignment	not modelled	99.5	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
66	c3b9pA_	Alignment	not modelled	99.5	14	PDB header: hydrolase Chain: A: PDB Molecule: cg5977-pa, isoform a; PDBTitle: spastin
67	c5uj7C_	Alignment	not modelled	99.5	12	PDB header: dna binding protein Chain: C: PDB Molecule: origin recognition complex subunit 4; PDBTitle: structure of the active form of human origin recognition complex2 atpase motor module, complex subunits 1, 4, 5
68	c3hu2C_	Alignment	not modelled	99.5	18	PDB header: transport protein Chain: C: PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: structure of p97 n-d1 r86a mutant in complex with atpgs
69	c1xwiA_	Alignment	not modelled	99.5	15	PDB header: protein transport Chain: A: PDB Molecule: skd1 protein; PDBTitle: crystal structure of vps4b
70	c1sxaA_	Alignment	not modelled	99.5	18	PDB header: replication Chain: A: PDB Molecule: activator 1 95 kda subunit; PDBTitle: crystal structure of the eukaryotic clamp loader (replication factor2 c, rfc) bound to the dna sliding clamp (proliferating cell nuclear3 antigen, pcna)
71	c2qbyB_	Alignment	not modelled	99.5	13	PDB header: replication/dna Chain: B: PDB Molecule: cell division control protein 6 homolog 3; PDBTitle: crystal structure of a heterodimer of cdc6/orc1 initiators2 bound to origin dna (from s. solfataricus)
72	c5exsA_	Alignment	not modelled	99.5	13	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator fleq; PDBTitle: aaa+ atpase fleq from pseudomonas aeruginosa bound to atp-gamma-s
73	c4l16A_	Alignment	not modelled	99.5	20	PDB header: hydrolase Chain: A: PDB Molecule: fidgetin-like protein 1; PDBTitle: crystal structure of figl-1 aaa domain in complex with adp
74	c2qenA_	Alignment	not modelled	99.5	14	PDB header: unknown function Chain: A: PDB Molecule: walker-type atpase; PDBTitle: the walker-type atpase paby2304 of pyrococcus abyssi
75	c2x8aA_	Alignment	not modelled	99.5	16	PDB header: nuclear protein Chain: A: PDB Molecule: nuclear valosin-containing protein-like; PDBTitle: human nuclear valosin containing protein like (nvl), c-2 terminal aaa-atpase domain
76	c3cf1C_	Alignment	not modelled	99.5	14	PDB header: transport protein Chain: C: PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: structure of p97/vcp in complex with adp/adp.alfx
77	c2zamA_	Alignment	not modelled	99.5	14	PDB header: protein transport Chain: A: PDB Molecule: vacuolar protein sorting-associating protein 4b; PDBTitle: crystal structure of mouse skd1/vps4b apo-form
78	c3vfdA_	Alignment	not modelled	99.5	16	PDB header: hydrolase Chain: A: PDB Molecule: spastin; PDBTitle: human spastin aaa domain
79	c4ww4B_	Alignment	not modelled	99.5	18	PDB header: hydrolase Chain: B: PDB Molecule: rvb-like 2; PDBTitle: double-heterohexameric rings of full-length rvb1(adp)/rvb2(adp)
80	c1s3sA_	Alignment	not modelled	99.5	15	PDB header: protein binding Chain: A: PDB Molecule: transitional endoplasmic reticulum atpase (ter) PDBTitle: crystal structure of aaa atpase p97/vcp nd1 in complex

						with2 p47 c
81	c2r65A_	Alignment	not modelled	99.4	15	PDB header: hydrolase Chain: A: PDB Molecule: cell division protease ftsH homolog; PDBTitle: crystal structure of helicobacter pylori atp dependent protease, ftsH2 adp complex
82	c6matE_	Alignment	not modelled	99.4	13	PDB header: ribosomal protein Chain: E: PDB Molecule: rix7 mutant; PDBTitle: cryo-em structure of the essential ribosome assembly aaa-atpase rix7
83	c3d8bB_	Alignment	not modelled	99.4	17	PDB header: hydrolase Chain: B: PDB Molecule: fidgetin-like protein 1; PDBTitle: crystal structure of human fidgetin-like protein 1 in complex with adp
84	c5udbA_	Alignment	not modelled	99.4	16	PDB header: replication Chain: A: PDB Molecule: origin recognition complex subunit 1; PDBTitle: structural basis of mcm2-7 replicative helicase loading by orc-cdc62 and cdt1
85	c2c99A_	Alignment	not modelled	99.4	11	PDB header: transcription regulation Chain: A: PDB Molecule: psp operon transcriptional activator; PDBTitle: structural basis of the nucleotide driven conformational2 changes in the aaa domain of transcription activator pspf
86	c4lcbA_	Alignment	not modelled	99.4	12	PDB header: protein transport Chain: A: PDB Molecule: cell division protein cdvc, vps4; PDBTitle: structure of vps4 homolog from acidianus hospitalis
87	d1g8pa_	Alignment	not modelled	99.4	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
88	c4xgcD_	Alignment	not modelled	99.4	13	PDB header: dna binding protein Chain: D: PDB Molecule: origin recognition complex subunit 4; PDBTitle: crystal structure of the eukaryotic origin recognition complex
89	c1ny5A_	Alignment	not modelled	99.4	15	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigm54 activator (aaa+ atpase) in the inactive2 state
90	c5vq9D_	Alignment	not modelled	99.4	16	PDB header: protein binding Chain: D: PDB Molecule: pachytene checkpoint protein 2 homolog; PDBTitle: structure of human trip13, apo form
91	c1sxjC_	Alignment	not modelled	99.4	16	PDB header: replication Chain: C: PDB Molecule: activator 1 40 kda subunit; PDBTitle: crystal structure of the eukaryotic clamp loader (replication factor2 c, rfc) bound to the dna sliding clamp (proliferating cell nuclear3 antigen, pcna)
92	c3k1jA_	Alignment	not modelled	99.4	15	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent protease lon; PDBTitle: crystal structure of lon protease from thermococcus onnurineus na1
93	c2fnaA_	Alignment	not modelled	99.4	15	PDB header: atp-binding protein Chain: A: PDB Molecule: conserved hypothetical protein; PDBTitle: crystal structure of an archaeal aaa+ atpase (sso1545) from sulfobolbus2 solfataricus p2 at 2.00 a resolution
94	c1iqpF_	Alignment	not modelled	99.4	21	PDB header: replication Chain: F: PDB Molecule: rfcs; PDBTitle: crystal structure of the clamp loader small subunit from2 pyrococcus furiosus
95	c5ifwB_	Alignment	not modelled	99.4	14	PDB header: signaling protein Chain: B: PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: quantitative interaction mapping reveals an extended ubiquitin2 regulatory domain in aspl that disrupts functional p97 hexamers and3 induces cell death
96	c1ojjD_	Alignment	not modelled	99.4	13	PDB header: response regulator Chain: D: PDB Molecule: transcriptional regulatory protein zrar; PDBTitle: crystal structure of a sigma54-activator suggests the mechanism for2 the conformational switch necessary for sigma54 binding
97	c4xgcA_	Alignment	not modelled	99.4	20	PDB header: dna binding protein Chain: A: PDB Molecule: origin recognition complex subunit 1; PDBTitle: crystal structure of the eukaryotic origin recognition complex
98	d1l8qa2	Alignment	not modelled	99.4	10	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
99	d1sxje2	Alignment	not modelled	99.4	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
100	c3eihB_	Alignment	not modelled	99.4	15	PDB header: protein transport Chain: B: PDB Molecule: vacuolar protein sorting-associated protein 4; PDBTitle: crystal structure of s.cerevisiae vps4 in the presence of atpgammas
101	c5udbD_	Alignment	not modelled	99.4	12	PDB header: replication Chain: D: PDB Molecule: origin recognition complex subunit 4; PDBTitle: structural basis of mcm2-7 replicative helicase loading by orc-cdc62 and cdt1
102	c3u5zM_	Alignment	not modelled	99.3	11	PDB header: dna binding protein/dna Chain: M: PDB Molecule: dna polymerase accessory protein 44; PDBTitle: structure of t4 bacteriophage clamp loader bound to the t4 clamp,2 primer-template dna, and atp analog
103	c5w0tA_	Alignment	not modelled	99.3	13	PDB header: hydrolase Chain: A: PDB Molecule: protein msp1; PDBTitle: crystal structure of monomeric msp1 from s. cerevisiae
104	c2chvE_	Alignment	not modelled	99.3	19	PDB header: dna-binding protein Chain: E: PDB Molecule: replication factor c small subunit; PDBTitle: replication factor c adpnp complex
105	c6b5cA_	Alignment	not modelled	99.3	19	PDB header: cell cycle Chain: A: PDB Molecule: katanin p60 atpase-containing subunit a-like 1; PDBTitle: structural basis for katanin self-assembly

106	c5kzfl_	Alignment	not modelled	99.3	14	PDB header: hydrolase Chain: J: PDB Molecule: proteasome-associated atpase; PDBTitle: crystal structure of near full-length hexameric mycobacterium2 tuberculosis proteasomal atpase mpa in apo form
107	c5ujmE_	Alignment	not modelled	99.3	12	PDB header: replication Chain: E: PDB Molecule: origin recognition complex subunit 5; PDBTitle: structure of the active form of human origin recognition complex and2 its atpase motor module
108	c5ep0A_	Alignment	not modelled	99.3	15	PDB header: transcription Chain: A: PDB Molecule: putative repressor protein luxo; PDBTitle: quorum-sensing signal integrator luxo - receiver+catalytic domains
109	c5uj7B_	Alignment	not modelled	99.3	20	PDB header: dna binding protein Chain: B: PDB Molecule: origin recognition complex subunit 1; PDBTitle: structure of the active form of human origin recognition complex2 atpase motor module, complex subunits 1, 4, 5
110	c1sxE_	Alignment	not modelled	99.3	18	PDB header: replication Chain: E: PDB Molecule: activator 1 40 kda subunit; PDBTitle: crystal structure of the eukaryotic clamp loader (replication factor2 c, rfc) bound to the dna sliding clamp (proliferating cell nuclear3 antigen, pcna)
111	c1jr3E_	Alignment	not modelled	99.3	20	PDB header: transferase Chain: E: PDB Molecule: dna polymerase iii, delta' subunit; PDBTitle: crystal structure of the processivity clamp loader gamma complex of e.2 coli dna polymerase iii
112	c2r44A_	Alignment	not modelled	99.3	15	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative atpase (chu_0153) from cytophaga2 hutchinsonii atcc 33406 at 2.00 a resolution
113	c1sxD_	Alignment	not modelled	99.3	15	PDB header: replication Chain: D: PDB Molecule: activator 1 41 kda subunit; PDBTitle: crystal structure of the eukaryotic clamp loader (replication factor2 c, rfc) bound to the dna sliding clamp (proliferating cell nuclear3 antigen, pcna)
114	c3j96F_	Alignment	not modelled	99.3	15	PDB header: hydrolase Chain: F: PDB Molecule: vesicle-fusing atpase; PDBTitle: structure of 20s supercomplex determined by single particle2 cryoelectron microscopy (state i)
115	c2qz4A_	Alignment	not modelled	99.3	15	PDB header: hydrolase Chain: A: PDB Molecule: paraplegin; PDBTitle: human paraplegin, aaa domain in complex with adp
116	c1sxB_	Alignment	not modelled	99.3	19	PDB header: replication Chain: B: PDB Molecule: activator 1 37 kda subunit; PDBTitle: crystal structure of the eukaryotic clamp loader (replication factor2 c, rfc) bound to the dna sliding clamp (proliferating cell nuclear3 antigen, pcna)
117	c3sylB_	Alignment	not modelled	99.3	17	PDB header: chaperone Chain: B: PDB Molecule: protein cbbx; PDBTitle: crystal structure of the aaa+ protein cbbx, native structure
118	c5wc0D_	Alignment	not modelled	99.3	15	PDB header: motor protein Chain: D: PDB Molecule: meiotic spindle formation protein mei-1; PDBTitle: katanin hexamer in spiral conformation
119	d1e32a2	Alignment	not modelled	99.3	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
120	c5d4wB_	Alignment	not modelled	99.3	15	PDB header: chaperone Chain: B: PDB Molecule: putative heat shock protein; PDBTitle: crystal structure of hsp104