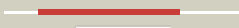











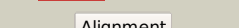

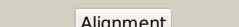

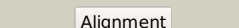

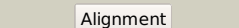





Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3179 (-) _3547615_3548904
Date	Thu Aug 8 16:20:36 BST 2019
Unique Job ID	b640e234e69198b6

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2fnaA_	 Alignment		99.7	17	PDB header: atp-binding protein Chain: A: PDB Molecule: conserved hypothetical protein; PDBTitle: crystal structure of an archaeal aaa+ atpase (sso1545) from <i>sulfolobus2 solfataricus</i> p2 at 2.00 a resolution
2	c2qenA_	 Alignment		99.5	18	PDB header: unknown function Chain: A: PDB Molecule: walker-type atpase; PDBTitle: the walker-type atpase paby2304 of <i>pyrococcus abyssi</i>
3	c3pfiB_	 Alignment		99.4	15	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 <i>campylobacter jejuni</i> subsp. <i>jejuni</i> 3 nctc 11168 in complex with adenosine-5'-diphosphate
4	c1in8A_	 Alignment		99.3	17	PDB header: dna binding protein Chain: A: PDB Molecule: holliday junction dna helicase ruvb; PDBTitle: <i>thermotoga maritima</i> ruvb t158v
5	c6blbA_	 Alignment		99.3	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 <i>pseudomonas aeruginosa</i> in complex3 with adp
6	d2fnaa2	 Alignment		99.2	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
7	c3pvsA_	 Alignment		99.1	21	PDB header: recombination Chain: A: PDB Molecule: replication-associated recombination protein a; PDBTitle: structure and biochemical activities of <i>escherichia coli</i> mgsa
8	c1ojlD_	 Alignment		99.1	18	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
9	c2v1uA_	 Alignment		99.0	14	PDB header: replication Chain: A: PDB Molecule: cell division control protein 6 homolog; PDBTitle: structure of the <i>aeropyrum pernix</i> orc1 protein in complex2 with dna
10	c4b4tl_	 Alignment		99.0	17	PDB header: hydrolase Chain: I: PDB Molecule: 26s protease regulatory subunit 4 homolog; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
11	c4xgcA_	 Alignment		98.9	9	PDB header: dna binding protein Chain: A: PDB Molecule: origin recognition complex subunit 1; PDBTitle: crystal structure of the eukaryotic origin recognition complex

12	c2qbyB_	Alignment		98.9	11	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)
13	c5g4gF_	Alignment		98.9	23	PDB header: hydrolase Chain: F; PDB Molecule: vcp-like atpase; PDBTitle: structure of the atpgs-bound vat complex
14	c5m7nA_	Alignment		98.9	15	PDB header: signaling protein Chain: A; PDB Molecule: nitrogen assimilation regulatory protein; PDBTitle: crystal structure of ntrx from brucella abortus in complex with atp2 processed with the crystaldirect automated mounting and cryo-cooling3 technology
15	c3u5zM_	Alignment		98.9	8	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
16	c3hu2C_	Alignment		98.8	17	PDB header: transport protein Chain: C; PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: structure of p97 n-d1 r86a mutant in complex with atpgs
17	c6az0A_	Alignment		98.8	18	PDB header: hydrolase Chain: A; PDB Molecule: mitochondrial inner membrane i-aaa protease supercomplex PDBTitle: mitochondrial atpase protease yme1
18	c1s3sA_	Alignment		98.8	17	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
19	c6azyA_	Alignment		98.8	15	PDB header: chaperone Chain: A; PDB Molecule: heat shock protein hsp104; PDBTitle: crystal structure of hsp104 r328m/r757m mutant from calcarisporiella2 thermophila
20	c3cf2B_	Alignment		98.8	25	PDB header: transport protein Chain: B; PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: structure of p97/vcp in complex with adp/amp-pnp
21	c4z8xC_	Alignment	not modelled	98.8	19	PDB header: hydrolase Chain: C; PDB Molecule: atp-dependent zinc metalloprotease ftsh; PDBTitle: truncated ftsh from a. aeolicus
22	c1fnnB_	Alignment	not modelled	98.8	14	PDB header: cell cycle Chain: B; PDB Molecule: cell division control protein 6; PDBTitle: crystal structure of cdc6p from pyrobaculum aerophilum
23	c5e7pA_	Alignment	not modelled	98.8	24	PDB header: hydrolase Chain: A; PDB Molecule: cell division control protein cdc48; PDBTitle: crystal structure of msmeg_0858 (uniprot a0qqs4), a aaa atpase.
24	c6epdM_	Alignment	not modelled	98.8	19	PDB header: hydrolase Chain: M; PDB Molecule: 26s proteasome regulatory subunit 6a; PDBTitle: substrate processing state 26s proteasome (sps1)
25	c6nyyC_	Alignment	not modelled	98.8	19	PDB header: translocase Chain: C; PDB Molecule: afg3-like protein 2; PDBTitle: human m-aaa protease afg3l2, substrate-bound
26	c1sxiA_	Alignment	not modelled	98.8	13	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)
27	c4b4tL_	Alignment	not modelled	98.8	22	PDB header: hydrolase Chain: L; PDB Molecule: 26s protease subunit rpt4; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
28	c5mpaL_	Alignment	not modelled	98.8	23	PDB header: hydrolase Chain: L; PDB Molecule: 26s protease subunit rpt4; PDBTitle: 26s proteasome in presence of atp (s2)
						PDB header: hydrolase

29	c2dhrC_	Alignment	not modelled	98.8	23	Chain: C: PDB Molecule: ftsh; PDBTitle: whole cytosolic region of atp-dependent metalloprotease2 ftsh (g399l)
30	d1e32a2	Alignment	not modelled	98.8	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
31	c5ifwB_	Alignment	not modelled	98.8	18	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
32	c6b5cA_	Alignment	not modelled	98.7	14	PDB header: cell cycle Chain: A: PDB Molecule: katanin p60 atpase-containing subunit a-like 1; PDBTitle: structural basis for katanin self-assembly
33	c1r6bX_	Alignment	not modelled	98.7	22	PDB header: hydrolase Chain: X: PDB Molecule: clpa protein; PDBTitle: high resolution crystal structure of clpa
34	c5uj7B_	Alignment	not modelled	98.7	12	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
35	c6mfvc_	Alignment	not modelled	98.7	18	PDB header: signaling protein Chain: C: PDB Molecule: tetratricopeptide repeat sensor ph0952; PDBTitle: crystal structure of the signal transduction atpase with numerous2 domains (stand) protein with a tetratricopeptide repeat sensor ph09523 from pyrococcus horikoshii
36	d1in4a2	Alignment	not modelled	98.7	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
37	c3cf1C_	Alignment	not modelled	98.7	18	PDB header: transport protein Chain: C: PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: structure of p97/vcp in complex with adp/adp.alfx
38	c2x8aA_	Alignment	not modelled	98.7	20	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
39	c6hecH_	Alignment	not modelled	98.7	18	PDB header: hydrolase Chain: H: PDB Molecule: proteasome-activating nucleotidase; PDBTitle: pan-proteasome in state 4
40	c4b4tj_	Alignment	not modelled	98.7	19	PDB header: hydrolase Chain: J: PDB Molecule: 26s protease regulatory subunit 8 homolog; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
41	d2ce7a2	Alignment	not modelled	98.7	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
42	c4ciuA_	Alignment	not modelled	98.7	16	PDB header: chaperone Chain: A: PDB Molecule: chaperone protein clpb; PDBTitle: crystal structure of e. coli clpb
43	c3zw6B_	Alignment	not modelled	98.7	12	PDB header: photosynthesis Chain: B: PDB Molecule: ribulose bisphosphate carboxylase/oxygenase activase 1, PDBTitle: model of hexameric aaa domain arrangement of green-type rubisco2 activase from tobacco.
44	c2qz4A_	Alignment	not modelled	98.7	17	PDB header: hydrolase Chain: A: PDB Molecule: paraplegin; PDBTitle: human paraplegin, aaa domain in complex with adp
45	c5w0tA_	Alignment	not modelled	98.7	19	PDB header: hydrolase Chain: A: PDB Molecule: protein msp1; PDBTitle: crystal structure of monomeric msp1 from s. cerevisiae
46	c2ce7B_	Alignment	not modelled	98.7	18	PDB header: cell division protein Chain: B: PDB Molecule: cell division protein ftsh; PDBTitle: edta treated
47	c6epcJ_	Alignment	not modelled	98.7	22	PDB header: hydrolase Chain: J: PDB Molecule: 26s proteasome regulatory subunit 8; PDBTitle: ground state 26s proteasome (gs2)
48	d1ixza_	Alignment	not modelled	98.7	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
49	c4b4tK_	Alignment	not modelled	98.7	22	PDB header: hydrolase Chain: K: PDB Molecule: 26s protease regulatory subunit 6b homolog; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
50	c1qvrB_	Alignment	not modelled	98.7	19	PDB header: chaperone Chain: B: PDB Molecule: clpb protein; PDBTitle: crystal structure analysis of clpb
51	c4b4tH_	Alignment	not modelled	98.7	18	PDB header: hydrolase Chain: H: PDB Molecule: 26s protease regulatory subunit 7 homolog; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
52	c5wc0D_	Alignment	not modelled	98.7	14	PDB header: motor protein Chain: D: PDB Molecule: meiotic spindle formation protein mei-1; PDBTitle: katanin hexamer in spiral conformation
53	c5d4wB_	Alignment	not modelled	98.7	16	PDB header: chaperone Chain: B: PDB Molecule: putative heat shock protein; PDBTitle: crystal structure of hsp104
54	c3pxiB_	Alignment	not modelled	98.7	13	PDB header: protein binding Chain: B: PDB Molecule: negative regulator of genetic competence clpC/meC;

						PDBTitle: structure of meca108:clpc
55	c2c9oA_	Alignment	not modelled	98.7	21	PDB header: hydrolase Chain: A: PDB Molecule: ruvb-like 1; PDBTitle: 3d structure of the human ruvb-like helicase ruvb1l
56	c1sxB_	Alignment	not modelled	98.7	20	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)
57	c4xgcE_	Alignment	not modelled	98.6	12	PDB header: dna binding protein Chain: E: PDB Molecule: origin recognition complex subunit 5; PDBTitle: crystal structure of the eukaryotic origin recognition complex
58	c1jr3E_	Alignment	not modelled	98.6	19	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
59	d1r7ra3	Alignment	not modelled	98.6	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
60	c5ubvB_	Alignment	not modelled	98.6	20	PDB header: hydrolase Chain: B: PDB Molecule: atpase domain of i-aaa protease; PDBTitle: atpase domain of i-aaa protease from myceliophthora thermophila
61	c1hqCB_	Alignment	not modelled	98.6	16	PDB header: hydrolase Chain: B: PDB Molecule: ruvb; PDBTitle: structure of ruvb from thermus thermophilus hb8
62	c4i16A_	Alignment	not modelled	98.6	15	PDB header: hydrolase Chain: A: PDB Molecule: fidgetin-like protein 1; PDBTitle: crystal structure of figl-1 aaa domain in complex with adp
63	c5vy9C_	Alignment	not modelled	98.6	16	PDB header: chaperone Chain: C: PDB Molecule: heat shock protein 104; PDBTitle: s. cerevisiae hsp104:casein complex, middle domain conformation
64	c5udb9_	Alignment	not modelled	98.6	15	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
65	c5ujmE_	Alignment	not modelled	98.6	16	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
66	c3vfdA_	Alignment	not modelled	98.6	17	PDB header: hydrolase Chain: A: PDB Molecule: spastin; PDBTitle: human spastin aaa domain
67	d1g41a_	Alignment	not modelled	98.6	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
68	c1sxC_	Alignment	not modelled	98.6	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)
69	c1xxhB_	Alignment	not modelled	98.6	22	PDB header: transferase Chain: B: PDB Molecule: dna polymerase iii subunit gamma; PDBTitle: atpgs bound e. coli clamp loader complex
70	c5uj7C_	Alignment	not modelled	98.6	24	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
71	c4ypnA_	Alignment	not modelled	98.6	19	PDB header: hydrolase Chain: A: PDB Molecule: lon protease; PDBTitle: crystal structure of a lon fragment containing the 3-helix bundle and2 the aaa-alpha/beta domain
72	c4b4tM_	Alignment	not modelled	98.6	16	PDB header: hydrolase Chain: M: PDB Molecule: 26s protease regulatory subunit 6a; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
73	c3d8bB_	Alignment	not modelled	98.6	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
74	c5kzfl_	Alignment	not modelled	98.6	16	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
75	d1jbka_	Alignment	not modelled	98.6	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
76	c3b9pA_	Alignment	not modelled	98.6	16	PDB header: hydrolase Chain: A: PDB Molecule: cg5977-pa, isoform a; PDBTitle: spastin
77	c5gjql_	Alignment	not modelled	98.6	17	PDB header: hydrolase Chain: L: PDB Molecule: 26s protease regulatory subunit 10b; PDBTitle: structure of the human 26s proteasome bound to usp14-ubal
78	c1nsfA_	Alignment	not modelled	98.6	12	PDB header: protein transport Chain: A: PDB Molecule: n-ethylmaleimide sensitive factor; PDBTitle: d2 hexamerization domain of n-ethylmaleimide sensitive factor (nsf)
79	d1qvra2	Alignment	not modelled	98.6	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
80	c6matE_	Alignment	not modelled	98.6	16	PDB header: ribosomal protein Chain: E: PDB Molecule: rix7 mutant; PDBTitle: cryo-em structure of the essential ribosome assembly

						aaa-atpase rix7
81	c5kneD	Alignment	not modelled	98.6	16	PDB header: chaperone Chain: D: PDB Molecule: heat shock protein 104; PDBTitle: cryoem reconstruction of hsp104 hexamer
82	c5kneF	Alignment	not modelled	98.6	15	PDB header: chaperone Chain: F: PDB Molecule: heat shock protein 104; PDBTitle: cryoem reconstruction of hsp104 hexamer
83	c6opcF	Alignment	not modelled	98.6	20	PDB header: motor protein Chain: F: PDB Molecule: cell division control protein 48; PDBTitle: cdc48 hexamer in a complex with substrate and shp1(ubx domain)
84	c2zamA	Alignment	not modelled	98.6	17	PDB header: protein transport Chain: A: PDB Molecule: vacuolar protein sorting-associated protein 4b; PDBTitle: crystal structure of mouse skd1/vps4b apo-form
85	d1d2na	Alignment	not modelled	98.6	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
86	c1iy2A	Alignment	not modelled	98.6	22	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent metalloprotease ftsh; PDBTitle: crystal structure of the ftsh atpase domain from thermus2 thermophilus
87	c6em8F	Alignment	not modelled	98.6	16	PDB header: chaperone Chain: F: PDB Molecule: atp-dependent clp protease atp-binding subunit clpC; PDBTitle: s.aureus clpC resting state, c2 symmetrised
88	d1xbta1	Alignment	not modelled	98.6	12	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Type II thymidine kinase
89	d1r6bx3	Alignment	not modelled	98.6	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
90	c5kneA	Alignment	not modelled	98.5	13	PDB header: chaperone Chain: A: PDB Molecule: heat shock protein 104; PDBTitle: cryoem reconstruction of hsp104 hexamer
91	d1lum8a	Alignment	not modelled	98.5	24	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
92	c4lcbA	Alignment	not modelled	98.5	16	PDB header: protein transport Chain: A: PDB Molecule: cell division protein cdvc, vps4; PDBTitle: structure of vps4 homolog from acidianus hospitalis
93	c5oafB	Alignment	not modelled	98.5	20	PDB header: gene regulation Chain: B: PDB Molecule: rvvb-like 2; PDBTitle: human rvb1/rvb2 heterohexamer in ino80 complex
94	c5jl5A	Alignment	not modelled	98.5	15	PDB header: hydrolase Chain: A: PDB Molecule: torsin-1a; PDBTitle: torsina-lull1 complex, h. sapiens, bound to vhh-bs2
95	c1sxE	Alignment	not modelled	98.5	11	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)
96	c2chgB	Alignment	not modelled	98.5	18	PDB header: dna-binding protein Chain: B: PDB Molecule: replication factor c small subunit; PDBTitle: replication factor c domains 1 and 2
97	c1xwiA	Alignment	not modelled	98.5	18	PDB header: protein transport Chain: A: PDB Molecule: skd1 protein; PDBTitle: crystal structure of vps4b
98	c2chvE	Alignment	not modelled	98.5	17	PDB header: dna-binding protein Chain: E: PDB Molecule: replication factor c small subunit; PDBTitle: replication factor c adnp complex
99	c3iz8F	Alignment	not modelled	98.5	13	PDB header: apoptosis Chain: F: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
100	c1vt4L	Alignment	not modelled	98.5	13	PDB header: apoptosis Chain: L: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
101	c1vt4K	Alignment	not modelled	98.5	13	PDB header: apoptosis Chain: K: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
102	c3iz8D	Alignment	not modelled	98.5	13	PDB header: apoptosis Chain: D: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
103	c1vt4O	Alignment	not modelled	98.5	13	PDB header: apoptosis Chain: O: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
104	c3iz8G	Alignment	not modelled	98.5	13	PDB header: apoptosis Chain: G: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
105	c3iz8E	Alignment	not modelled	98.5	13	PDB header: apoptosis Chain: E: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
106	c1vt4N	Alignment	not modelled	98.5	13	PDB header: apoptosis Chain: N: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
107	c1vt4J	Alignment	not modelled	98.5	13	PDB header: apoptosis Chain: J: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome

108	c3iz8B_	Alignment	not modelled	98.5	13	PDB header: apoptosis Chain: B; PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
109	c1vt4P_	Alignment	not modelled	98.5	13	PDB header: apoptosis Chain: P; PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
110	c1vt4I_	Alignment	not modelled	98.5	13	PDB header: apoptosis Chain: I; PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
111	c3iz8A_	Alignment	not modelled	98.5	13	PDB header: apoptosis Chain: A; PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
112	c3iz8H_	Alignment	not modelled	98.5	13	PDB header: apoptosis Chain: H; PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
113	c1vt4M_	Alignment	not modelled	98.5	13	PDB header: apoptosis Chain: M; PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
114	c3iz8C_	Alignment	not modelled	98.5	13	PDB header: apoptosis Chain: C; PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
115	c4xgcD_	Alignment	not modelled	98.5	23	PDB header: dna binding protein Chain: D; PDB Molecule: origin recognition complex subunit 4; PDBTitle: crystal structure of the eukaryotic origin recognition complex
116	c6genX_	Alignment	not modelled	98.5	24	PDB header: nuclear protein Chain: X; PDB Molecule: ruvb-like protein 1; PDBTitle: chromatin remodeller-nucleosome complex at 4.5 a resolution.
117	d1ofha_	Alignment	not modelled	98.5	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
118	d1ny5a2	Alignment	not modelled	98.5	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
119	c5t0gA_	Alignment	not modelled	98.5	17	PDB header: hydrolase Chain: A; PDB Molecule: 26s protease regulatory subunit 7; PDBTitle: structural basis for dynamic regulation of the human 26s proteasome
120	c3h4mC_	Alignment	not modelled	98.5	17	PDB header: hydrolase Chain: C; PDB Molecule: proteasome-activating nucleotidase; PDBTitle: aaa atpase domain of the proteasome- activating nucleotidase