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Email	mdejesus@rockefeller.edu
Description	RVBD3870_(-)_4346659_4348902
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Unique Job ID	3434d5200e271830

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4nh0A_	 Alignment		100.0	43	PDB header: cell cycle Chain: A: PDB Molecule: cell divisionftsk/spoiii; PDBTitle: cytoplasmic domain of the thermomonospora curvata type vii secretion2 atpase eccc
2	c4n1aE_	 Alignment		100.0	18	PDB header: protein binding/protein binding Chain: E: PDB Molecule: cell divisionftsk/spoiii; PDBTitle: thermomonospora curvata eccc (atpases 2 and 3) in complex with a2 signal sequence peptide
3	c2iuuE_	 Alignment		100.0	26	PDB header: membrane protein Chain: E: PDB Molecule: dna translocase ftsk; PDBTitle: p. aeruginosa ftsk motor domain, hexamer
4	c2iutA_	 Alignment		100.0	26	PDB header: membrane protein Chain: A: PDB Molecule: dna translocase ftsk; PDBTitle: p. aeruginosa ftsk motor domain, dimeric
5	c2iusB_	 Alignment		100.0	23	PDB header: membrane protein Chain: B: PDB Molecule: dna translocase ftsk; PDBTitle: e. coli ftsk motor domain
6	c4lyaA_	 Alignment		100.0	16	PDB header: cell cycle Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: essc (atpases 2 and 3) from geobacillus thermodenitrificans (semet)
7	c4kfuC_	 Alignment		99.9	14	PDB header: hydrolase Chain: C: PDB Molecule: genome packaging ntpase b204; PDBTitle: structure of the genome packaging ntpase b204 from sulfolobus turreted2 icosahedral virus 2 in complex with amppcp
8	c4d2iB_	 Alignment		99.8	21	PDB header: hydrolase Chain: B: PDB Molecule: hera; PDBTitle: crystal structure of the hera hexameric dna translocase2 from sulfolobus solfataricus bound to amp-pnp
9	c4ag5A_	 Alignment		99.8	19	PDB header: hydrolase Chain: A: PDB Molecule: type iv secretory pathway virb4 components-like protein; PDBTitle: structure of virb4 of thermoanaerobacter pseudethanolicus
10	d1e9ra_	 Alignment		99.4	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
11	c4ag5D_	 Alignment		98.9	18	PDB header: hydrolase Chain: D: PDB Molecule: type iv secretory pathway virb4 components-like protein; PDBTitle: structure of virb4 of thermoanaerobacter pseudethanolicus

12	c4xgcD_	Alignment		98.1	13	PDB header: dna binding protein Chain: D: PDB Molecule: origin recognition complex subunit 4; PDBTitle: crystal structure of the eukaryotic origin recognition complex
13	c5udbD_	Alignment		97.9	14	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
14	c4xguB_	Alignment		97.9	22	PDB header: atp-binding protein Chain: B: PDB Molecule: putative pachytene checkpoint protein 2; PDBTitle: structure of c. elegans pch-2
15	c4xgcE_	Alignment		97.9	15	PDB header: dna binding protein Chain: E: PDB Molecule: origin recognition complex subunit 5; PDBTitle: crystal structure of the eukaryotic origin recognition complex
16	c5vq9D_	Alignment		97.9	17	PDB header: protein binding Chain: D: PDB Molecule: pachytene checkpoint protein 2 homolog; PDBTitle: structure of human trip13, apo form
17	c2v1uA_	Alignment		97.8	17	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
18	d1w5sa2	Alignment		97.7	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
19	c1xwiA_	Alignment		97.7	20	PDB header: protein transport Chain: A: PDB Molecule: skd1 protein; PDBTitle: crystal structure of vps4b
20	d1fnna2	Alignment		97.6	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
21	c3l0aA_	Alignment	not modelled	97.6	14	PDB header: hydrolase Chain: A: PDB Molecule: transcription termination factor rho; PDBTitle: structure of rna-free rho transcription termination factor from2 thermotoga maritima
22	c2qbyA_	Alignment	not modelled	97.6	11	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)
23	c6matE_	Alignment	not modelled	97.6	17	PDB header: ribosomal protein Chain: E: PDB Molecule: rix7 mutant; PDBTitle: cryo-em structure of the essential ribosome assembly aaa-atpase rix7
24	c5w0tA_	Alignment	not modelled	97.6	19	PDB header: hydrolase Chain: A: PDB Molecule: protein msp1; PDBTitle: crystal structure of monomeric msp1 from s. cerevisiae
25	c3hu2C_	Alignment	not modelled	97.6	15	PDB header: transport protein Chain: C: PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: structure of p97 n-d1 r86a mutant in complex with atpgs
26	c1s3sa_	Alignment	not modelled	97.5	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
27	c5e7pA_	Alignment	not modelled	97.5	21	PDB header: hydrolase Chain: A: PDB Molecule: cell division control protein cdc48; PDBTitle: crystal structure of msmeg_0858 (uniprot a0qqs4), a aaa atpase.
28	c3d8bB_	Alignment	not modelled	97.5	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

29	c3l0oB_	Alignment	not modelled	97.5	16	PDB header: hydrolase Chain: B: PDB Molecule: transcription termination factor rho; PDBTitle: structure of rna-free rho transcription termination factor from2 thermotoga maritima
30	d1xpuA3	Alignment	not modelled	97.5	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
31	c5uj7C_	Alignment	not modelled	97.5	17	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
32	c2zamA_	Alignment	not modelled	97.5	19	PDB header: protein transport Chain: A: PDB Molecule: vacuolar protein sorting-associated protein 4b; PDBTitle: crystal structure of mouse skd1/vps4b apo-form
33	c5g4gF_	Alignment	not modelled	97.4	17	PDB header: hydrolase Chain: F: PDB Molecule: vcp-like atpase; PDBTitle: structure of the atpgs-bound vat complex
34	c6b5cA_	Alignment	not modelled	97.4	16	PDB header: cell cycle Chain: A: PDB Molecule: katanin p60 atpase-containing subunit a-like 1; PDBTitle: structural basis for katanin self-assembly
35	c5ujmE_	Alignment	not modelled	97.4	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
36	c5wc0D_	Alignment	not modelled	97.4	16	PDB header: motor protein Chain: D: PDB Molecule: meiotic spindle formation protein mei-1; PDBTitle: katanin hexamer in spiral conformation
37	d1nfa_	Alignment	not modelled	97.4	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
38	c5ifwB_	Alignment	not modelled	97.4	15	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
39	c5kzjf_	Alignment	not modelled	97.4	20	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
40	c1xpuB_	Alignment	not modelled	97.4	17	PDB header: transcription/rna Chain: B: PDB Molecule: rho transcription termination factor; PDBTitle: structural mechanism of inhibition of the rho transcription2 termination factor by the antibiotic 5a-(3-formylphenylsulfanyl)-3 dihydrobicyclomycin (fpdb)
41	c3b9pA_	Alignment	not modelled	97.4	17	PDB header: hydrolase Chain: A: PDB Molecule: cg5977-pa, isoform a; PDBTitle: spastin
42	c4b4tj_	Alignment	not modelled	97.3	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
43	c1fnnB_	Alignment	not modelled	97.3	17	PDB header: cell cycle Chain: B: PDB Molecule: cell division control protein 6; PDBTitle: crystal structure of cdc6p from pyrobaculum aerophilum
44	c6epcj_	Alignment	not modelled	97.3	17	PDB header: hydrolase Chain: J: PDB Molecule: 26s proteasome regulatory subunit 8; PDBTitle: ground state 26s proteasome (gs2)
45	c3cf1C_	Alignment	not modelled	97.3	15	PDB header: transport protein Chain: C: PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: structure of p97/vcp in complex with adp/adp.alpha
46	c6opcF_	Alignment	not modelled	97.3	13	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)
47	c5udbE_	Alignment	not modelled	97.3	12	PDB header: replication Chain: E: PDB Molecule: origin recognition complex subunit 5; PDBTitle: structural basis of mcm2-7 replicative helicase loading by orc-cdc62 and cdt1
48	c6hecH_	Alignment	not modelled	97.3	20	PDB header: hydrolase Chain: H: PDB Molecule: proteasome-activating nucleotidase; PDBTitle: pan-proteasome in state 4
49	c3te6A_	Alignment	not modelled	97.2	16	PDB header: gene regulation Chain: A: PDB Molecule: regulatory protein sir3; PDBTitle: crystal structure of the s. cerevisiae sir3 aaa+ domain
50	c1u9iA_	Alignment	not modelled	97.2	19	PDB header: circadian clock protein Chain: A: PDB Molecule: kaic; PDBTitle: crystal structure of circadian clock protein kaic with phosphorylation2 sites
51	c2qbyB_	Alignment	not modelled	97.2	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)
52	c3eihB_	Alignment	not modelled	97.2	20	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
53	c2ztsB_	Alignment	not modelled	97.2	15	PDB header: atp-binding protein Chain: B: PDB Molecule: putative uncharacterized protein ph0186; PDBTitle: crystal structure of kaic-like protein ph0186 from hyperthermophilic2 archaea pyrococcus horikoshii ot3
54	d1p9ra_	Alignment	not modelled	97.2	24	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases

						Family: RecA protein-like (ATPase-domain)
55	c4phtC	Alignment	not modelled	97.1	24	PDB header: protein transport Chain: C: PDB Molecule: general secretory pathway protein e; PDBTitle: atpase gspe in complex with the cytoplasmic domain of gspl from the2 vibrio vulnificus type ii secretion system
56	c2hbcC	Alignment	not modelled	97.1	16	PDB header: replication Chain: C: PDB Molecule: chromosomal replication initiator protein dnaa; PDBTitle: structure of amppcp-bound dnaa from aquifex aeolicus
57	c3cf2B	Alignment	not modelled	97.1	16	PDB header: transport protein Chain: B: PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: structure of p97/vcp in complex with adp/amp-pnp
58	c6nyyC	Alignment	not modelled	97.1	14	PDB header: translocase Chain: C: PDB Molecule: afg3-like protein 2; PDBTitle: human m-aaa protease afg3l2, substrate-bound
59	c4b4tH	Alignment	not modelled	97.1	15	PDB header: hydrolase Chain: H: PDB Molecule: 26s protease regulatory subunit 7 homolog; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
60	c4yerB	Alignment	not modelled	97.0	14	PDB header: hydrolase Chain: B: PDB Molecule: abc transporter atp-binding protein; PDBTitle: crystal structure of an abc transporter atp-binding protein (tm_1403)2 from thermotoga maritima msb8 at 2.35 a resolution
61	c6amxA	Alignment	not modelled	97.0	16	PDB header: transport protein Chain: A: PDB Molecule: abc transporter; PDBTitle: crystal structure of nucelotide binding domain of o-antigen2 polysaccharide abc-transporter
62	d1qvra2	Alignment	not modelled	97.0	23	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
63	d1cr2a	Alignment	not modelled	96.9	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
64	c5gjqL	Alignment	not modelled	96.9	19	PDB header: hydrolase Chain: L: PDB Molecule: 26s protease regulatory subunit 10b; PDBTitle: structure of the human 26s proteasome bound to usp14-ubal
65	c5x06G	Alignment	not modelled	96.9	19	PDB header: replication Chain: G: PDB Molecule: dnaa regulatory inactivator hda; PDBTitle: dna replication regulation protein
66	c5uj7B	Alignment	not modelled	96.9	19	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
67	c4i16A	Alignment	not modelled	96.9	15	PDB header: hydrolase Chain: A: PDB Molecule: figetin-like protein 1; PDBTitle: crystal structure of figl-1 aaa domain in complex with adp
68	c3gfoA	Alignment	not modelled	96.9	16	PDB header: atp binding protein Chain: A: PDB Molecule: cobalt import atp-binding protein cbio 1; PDBTitle: structure of cbio1 from clostridium perfringens: part of the abc2 transporter complex cbionq.
69	c6epdM	Alignment	not modelled	96.9	17	PDB header: hydrolase Chain: M: PDB Molecule: 26s proteasome regulatory subunit 6a; PDBTitle: substrate processing state 26s proteasome (sps1)
70	c1q57G	Alignment	not modelled	96.9	13	PDB header: transferase Chain: G: PDB Molecule: dna primase/helicase; PDBTitle: the crystal structure of the bifunctional primase-helicase of2 bacteriophage t7
71	c3vfdA	Alignment	not modelled	96.9	20	PDB header: hydrolase Chain: A: PDB Molecule: spastin; PDBTitle: human spastin aaa domain
72	c5x40A	Alignment	not modelled	96.9	18	PDB header: transport protein Chain: A: PDB Molecule: cobalt abc transporter atp-binding protein; PDBTitle: structure of a cbio dimer bound with amppcp
73	c5jwqA	Alignment	not modelled	96.9	17	PDB header: transcription regulator Chain: A: PDB Molecule: circadian clock protein kinase kaic; PDBTitle: crystal structure of kaic s431e in complex with foldswitch-stabilized2 kaib from thermosynechococcus elongatus
74	c5zr1A	Alignment	not modelled	96.9	14	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
75	c4kxfF	Alignment	not modelled	96.9	17	PDB header: immune system Chain: F: PDB Molecule: nlr family card domain-containing protein 4; PDBTitle: crystal structure of nlrc4 reveals its autoinhibition mechanism
76	c5tshF	Alignment	not modelled	96.8	21	PDB header: atp-binding protein Chain: F: PDB Molecule: type iv pilus biogenesis atpase pilb; PDBTitle: pilb from geobacter metallireducens bound to amp-pnp
77	c5l3rC	Alignment	not modelled	96.8	17	PDB header: protein transport Chain: C: PDB Molecule: signal recognition particle 54 kda protein, chloroplastic; PDBTitle: structure of the gtpase heterodimer of chloroplast srp54 and ftsy from2 arabidopsis thaliana
78	c1iy2A	Alignment	not modelled	96.8	16	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent metalloprotease ftsh; PDBTitle: crystal structure of the ftsh atpase domain from thermus2 thermophilus
79	c4b4tK	Alignment	not modelled	96.8	20	PDB header: hydrolase Chain: K: PDB Molecule: 26s protease regulatory subunit 6b homolog; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
						PDB header: protein transport

80	c5l3qB_	Alignment	not modelled	96.8	16	Chain: B: PDB Molecule: signal recognition particle receptor subunit alpha; PDBTitle: structure of the gtpase heterodimer of human srp54 and sralpha
81	c4nmmA_	Alignment	not modelled	96.8	14	PDB header: replication Chain: A: PDB Molecule: replicative dna helicase; PDBTitle: aquifex aeolicus replicative helicase (dnab) complexed with adp, at2 3.3 resolution
82	d1tf7a1	Alignment	not modelled	96.8	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
83	d2i1qa2	Alignment	not modelled	96.8	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
84	c6gebK_	Alignment	not modelled	96.7	22	PDB header: hydrolase Chain: K: PDB Molecule: dotb; PDBTitle: x-ray structure of the legionella pneumophila atpase dotb
85	c1szpC_	Alignment	not modelled	96.7	20	PDB header: dna binding protein Chain: C: PDB Molecule: dna repair protein rad51; PDBTitle: a crystal structure of the rad51 filament
86	c4lcbA_	Alignment	not modelled	96.7	15	PDB header: protein transport Chain: A: PDB Molecule: cell division protein cdvc, vps4; PDBTitle: structure of vps4 homolog from acidianus hospitalis
87	c3bgwD_	Alignment	not modelled	96.7	12	PDB header: replication Chain: D: PDB Molecule: dnab-like replicative helicase; PDBTitle: the structure of a dnab-like replicative helicase and its interactions2 with primase
88	c5mpaL_	Alignment	not modelled	96.7	18	PDB header: hydrolase Chain: L: PDB Molecule: 26s protease subunit rpt4; PDBTitle: 26s proteasome in presence of atp (s2)
89	c3sylB_	Alignment	not modelled	96.7	19	PDB header: chaperone Chain: B: PDB Molecule: protein cbbx; PDBTitle: crystal structure of the aaa+ protein cbbx, native structure
90	c2fnaA_	Alignment	not modelled	96.7	12	PDB header: atp-binding protein Chain: A: PDB Molecule: conserved hypothetical protein; PDBTitle: crystal structure of an archaeal aaa+ atpase (sso1545) from sulfobolobus2 solfataricus p2 at 2.00 a resolution
91	c3ldaA_	Alignment	not modelled	96.7	20	PDB header: dna binding protein Chain: A: PDB Molecule: dna repair protein rad51; PDBTitle: yeast rad51 h352y filament interface mutant
92	c3bh0A_	Alignment	not modelled	96.7	13	PDB header: replication Chain: A: PDB Molecule: dnab-like replicative helicase; PDBTitle: atpase domain of g40p
93	c2vyeA_	Alignment	not modelled	96.6	16	PDB header: hydrolase/dna Chain: A: PDB Molecule: replicative dna helicase; PDBTitle: crystal structure of the dnac-ssdna complex
94	c6azyA_	Alignment	not modelled	96.6	21	PDB header: chaperone Chain: A: PDB Molecule: heat shock protein hsp104; PDBTitle: crystal structure of hsp104 r328m/r757m mutant from calcarisporiella2 thermophila
95	c4xgcA_	Alignment	not modelled	96.6	16	PDB header: dna binding protein Chain: A: PDB Molecule: origin recognition complex subunit 1; PDBTitle: crystal structure of the eukaryotic origin recognition complex
96	c4ypnA_	Alignment	not modelled	96.6	18	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
97	d1jbka_	Alignment	not modelled	96.6	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
98	c2j7pA_	Alignment	not modelled	96.6	21	PDB header: signal recognition Chain: A: PDB Molecule: signal recognition particle protein; PDBTitle: gmppnp-stabilized ng domain complex of the srp gtpases ffh2 and ftsy
99	c4b4tl_	Alignment	not modelled	96.6	20	PDB header: hydrolase Chain: I: PDB Molecule: 26s protease regulatory subunit 4 homolog; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
100	c1iqpF_	Alignment	not modelled	96.6	21	PDB header: replication Chain: F: PDB Molecule: rfcs; PDBTitle: crystal structure of the clamp loader small subunit from2 pyrococcus furiosus
101	c1w5sB_	Alignment	not modelled	96.6	20	PDB header: replication Chain: B: PDB Molecule: origin recognition complex subunit 2 orc2; PDBTitle: structure of the aeropyrum pernix orc2 protein (adp form)
102	d1l8qa2	Alignment	not modelled	96.5	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
103	c2d62A_	Alignment	not modelled	96.5	19	PDB header: sugar binding protein Chain: A: PDB Molecule: multiple sugar-binding transport atp-binding PDBTitle: crystal structure of multiple sugar binding transport atp-2 binding protein
104	c4ydsA_	Alignment	not modelled	96.5	15	PDB header: hydrolase Chain: A: PDB Molecule: flagella-related protein h; PDBTitle: flah from sulfobolobus acidocaldarius with atp and mg-ion
105	c2dfIA_	Alignment	not modelled	96.5	16	PDB header: recombination Chain: A: PDB Molecule: dna repair and recombination protein rada; PDBTitle: crystal structure of left-handed rada filament PDB header: dna binding protein

106	c2z4rB_	Alignment	not modelled	96.5	14	Chain: B: PDB Molecule: chromosomal replication initiator protein dnaa; PDBTitle: crystal structure of domain iii from the thermotoga2 maritima replication initiation protein dnaa
107	d1ewqa2	Alignment	not modelled	96.5	23	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
108	c4z8xC_	Alignment	not modelled	96.5	16	PDB header: hydrolase Chain: C: PDB Molecule: atp-dependent zinc metalloprotease ftsh; PDBTitle: truncated ftsh from a. aeolicus
109	c2x8aA_	Alignment	not modelled	96.5	15	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
110	d1iqa2	Alignment	not modelled	96.5	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
111	c6gefB_	Alignment	not modelled	96.5	31	PDB header: hydrolase Chain: B: PDB Molecule: type iv secretion system protein dotb; PDBTitle: x-ray structure of the yersinia pseudotuberculosis atpase dotb
112	d2fnaa2	Alignment	not modelled	96.4	12	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
113	c6qelB_	Alignment	not modelled	96.4	12	PDB header: replication Chain: B: PDB Molecule: replicative dna helicase; PDBTitle: e. coli dnabc apo complex
114	c5b57D_	Alignment	not modelled	96.4	19	PDB header: metal transport Chain: D: PDB Molecule: hemin import atp-binding protein hmuu; PDBTitle: inward-facing conformation of abc heme importer bhuuv from2 burkholderia cenocepacia
115	c3pfiB_	Alignment	not modelled	96.4	18	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
116	c3pvsA_	Alignment	not modelled	96.4	22	PDB header: recombination Chain: A: PDB Molecule: replication-associated recombination protein a; PDBTitle: structure and biochemical activities of escherichia coli mgsa
117	c4b4tM_	Alignment	not modelled	96.4	22	PDB header: hydrolase Chain: M: PDB Molecule: 26s protease regulatory subunit 6a; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
118	c4wiaA_	Alignment	not modelled	96.4	13	PDB header: atp-binding protein Chain: A: PDB Molecule: putative flagella-related protein h; PDBTitle: crystal structure of flagellar accessory protein flah from2 methanocaldococcus jannaschii
119	c2dhrC_	Alignment	not modelled	96.4	19	PDB header: hydrolase Chain: C: PDB Molecule: ftsh; PDBTitle: whole cytosolic region of atp-dependent metalloprotease2 ftsh (g399l)
120	c4rvcA_	Alignment	not modelled	96.4	20	PDB header: transport protein Chain: A: PDB Molecule: abc transporter atp-binding protein; PDBTitle: structure of atp binding subunit of abc transporter