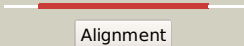

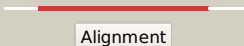

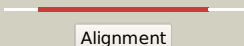







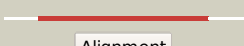











Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3659c_(-)_4097114_4098277
Date	Fri Aug 9 18:20:34 BST 2019
Unique Job ID	40ebd35bf76d7c6a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4ii7D_	 Alignment		100.0	25	PDB header: hydrolase Chain: D: PDB Molecule: flai atpase; PDBTitle: archaeallum assembly atpase flai
2	c2oaq1_	 Alignment		100.0	24	PDB header: hydrolase Chain: 1: PDB Molecule: type ii secretion system protein; PDBTitle: crystal structure of the archaeal secretion atpase gspe in complex2 with phosphate
3	c2gzaB_	 Alignment		100.0	25	PDB header: hydrolase Chain: B: PDB Molecule: type iv secretion system protein virb11; PDBTitle: crystal structure of the virb11 atpase from the brucella suis type iv2 secretion system in complex with sulphate
4	d1g6oa_	 Alignment		100.0	24	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
5	c4phtC_	 Alignment		100.0	23	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
6	c5fl3A_	 Alignment		100.0	25	PDB header: transport protein Chain: A: PDB Molecule: pili retraction protein pilt; PDBTitle: pilt2 from thermus thermophilus
7	c3jvvA_	 Alignment		100.0	23	PDB header: atp binding protein Chain: A: PDB Molecule: twitching motility protein; PDBTitle: crystal structure of p. aeruginosa pilt with bound amp-ppc
8	c5zfqA_	 Alignment		100.0	21	PDB header: transport protein Chain: A: PDB Molecule: twitching motility pilus retraction protein; PDBTitle: crystal structure of pilt-4, a retraction atpase motor of type iv2 pilus , from geobacter sulfurreducens
9	c6gebK_	 Alignment		100.0	17	PDB header: hydrolase Chain: K: PDB Molecule: dotb; PDBTitle: x-ray structure of the legionella pneumophila atpase dotb
10	c5tshF_	 Alignment		100.0	23	PDB header: atp-binding protein Chain: F: PDB Molecule: type iv pilus biogenesis atpase pilb; PDBTitle: pilb from geobacter metallireducens bound to amp-pnp
11	c4kssC_	 Alignment		100.0	24	PDB header: protein transport Chain: C: PDB Molecule: type ii secretion system protein e, hemolysin-coregulated PDBTitle: crystal structure of vibrio cholerae atpase gspse hexamer

12	c5it5B_	Alignment		100.0	22	PDB header: transport protein Chain: B: PDB Molecule: atp binding motif-containing protein pilf; PDBTitle: thermus thermophilus pilb core atpase region
13	c2gszE_	Alignment		100.0	23	PDB header: protein transport Chain: E: PDB Molecule: twitching motility protein pilt; PDBTitle: structure of a. aeolicus pilt with 6 monomers per asymmetric unit
14	d1p9ra_	Alignment		100.0	23	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
15	c6gefB_	Alignment		100.0	19	PDB header: hydrolase Chain: B: PDB Molecule: type iv secretion system protein dotb; PDBTitle: x-ray structure of the yersinia pseudotuberculosis atpase dotb
16	c5f4hF_	Alignment		100.0	15	PDB header: hydrolase Chain: F: PDB Molecule: nucleotide binding protein pinc; PDBTitle: archael ruvb-like holiday junction helicase
17	c5ywwA_	Alignment		100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: nucleotide binding protein pinc; PDBTitle: archael ruvb-like holiday junction helicase
18	c2eyuA_	Alignment		100.0	26	PDB header: protein transport Chain: A: PDB Molecule: twitching motility protein pilt; PDBTitle: the crystal structure of the c-terminal domain of aquifex2 aeolicus pilt
19	c2ja1A_	Alignment		99.6	14	PDB header: transferase Chain: A: PDB Molecule: thymidine kinase; PDBTitle: thymidine kinase from b. cereus with ttp bound as phosphate2 donor.
20	c1xx6B_	Alignment		99.2	18	PDB header: transferase Chain: B: PDB Molecule: thymidine kinase; PDBTitle: x-ray structure of clostridium acetobutylicum thymidine kinase with2 adp. northeast structural genomics target car26.
21	c2qq0B_	Alignment	not modelled	99.0	19	PDB header: transferase Chain: B: PDB Molecule: thymidine kinase; PDBTitle: thymidine kinase from thermotoga maritima in complex with2 thymidine + appnhp
22	c5mvrA_	Alignment	not modelled	98.8	20	PDB header: transferase Chain: A: PDB Molecule: trna threonylcarbamoyladenine biosynthesis protein tsae; PDBTitle: crystal structure of bacillus subtilus ydib
23	d1nija1	Alignment	not modelled	98.7	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
24	d1ye8a1	Alignment	not modelled	98.4	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
25	c6hz4B_	Alignment	not modelled	98.4	11	PDB header: dna binding protein Chain: B: PDB Molecule: 5-methylcytosine-specific restriction enzyme b; PDBTitle: structure of mcrcbc without dna binding domains (one half of the full2 complex)
26	c4nkrB_	Alignment	not modelled	98.4	14	PDB header: unknown function Chain: B: PDB Molecule: molybdopterin-guanine dinucleotide biosynthesis protein b; PDBTitle: the crystal structure of bacillus subtilis mobb
27	d2i3ba1	Alignment	not modelled	98.2	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
28	c6matE_	Alignment	not modelled	98.0	23	PDB header: ribosomal protein Chain: E: PDB Molecule: rix7 mutant; PDBTitle: cryo-em structure of the essential ribosome assembly aaa-atpase rix7

29	c5ftbA_	Alignment	not modelled	98.0	18	PDB header: hydrolase Chain: A: PDB Molecule: tptr domain protein; PDBTitle: crystal structure of pif1 helicase from bacteroides in2 complex with amppnp
30	c4ww4B_	Alignment	not modelled	98.0	23	PDB header: hydrolase Chain: B: PDB Molecule: ruvb-like 2; PDBTitle: double-heterohexameric rings of full-length rvb1(adp)/rvb2(adp)
31	c5x06G_	Alignment	not modelled	98.0	16	PDB header: replication Chain: G: PDB Molecule: dnaa regulatory inactivator hda; PDBTitle: dna replication regulation protein
32	d1cr2a_	Alignment	not modelled	98.0	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
33	c3uk6H_	Alignment	not modelled	98.0	28	PDB header: hydrolase Chain: H: PDB Molecule: ruvb-like 2; PDBTitle: crystal structure of the tip48 (tip49b) hexamer
34	c1nijA_	Alignment	not modelled	98.0	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein yjia; PDBTitle: yjia protein
35	c2r65A_	Alignment	not modelled	97.9	24	PDB header: hydrolase Chain: A: PDB Molecule: cell division protease ftsh homolog; PDBTitle: crystal structure of helicobacter pylori atp dependent protease, ftsh2 adp complex
36	c2f1rA_	Alignment	not modelled	97.9	15	PDB header: biosynthetic protein Chain: A: PDB Molecule: molybdopterin-guanine dinucleotide biosynthesis PDBTitle: crystal structure of molybdopterin-guanine biosynthesis2 protein b (mobb)
37	c5c3cB_	Alignment	not modelled	97.9	24	PDB header: protein binding Chain: B: PDB Molecule: cbbq/nirq/norq domain protein; PDBTitle: structural characterization of a newly identified component of alpha-2 carboxysomes: the aaa+ domain protein cso-cbbq
38	c3b9pA_	Alignment	not modelled	97.9	31	PDB header: hydrolase Chain: A: PDB Molecule: cg5977-pa, isoform a; PDBTitle: spastin
39	c1xwiA_	Alignment	not modelled	97.9	20	PDB header: protein transport Chain: A: PDB Molecule: skd1 protein; PDBTitle: crystal structure of vps4b
40	c5fhhA_	Alignment	not modelled	97.8	23	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent dna helicase pif1; PDBTitle: structure of human pif1 helicase domain residues 200-641
41	d1d2na_	Alignment	not modelled	97.8	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
42	c5t0gA_	Alignment	not modelled	97.8	21	PDB header: hydrolase Chain: A: PDB Molecule: 26s protease regulatory subunit 7; PDBTitle: structural basis for dynamic regulation of the human 26s proteasome
43	c5o6dB_	Alignment	not modelled	97.8	17	PDB header: hydrolase Chain: B: PDB Molecule: atp-dependent dna helicase pif1; PDBTitle: structure of scpif1 in complex with polydt and atpgs
44	c6epdM_	Alignment	not modelled	97.8	22	PDB header: hydrolase Chain: M: PDB Molecule: 26s proteasome regulatory subunit 6a; PDBTitle: substrate processing state 26s proteasome (sps1)
45	d1tq4a_	Alignment	not modelled	97.8	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
46	c6nyyC_	Alignment	not modelled	97.8	22	PDB header: translocase Chain: C: PDB Molecule: afg3-like protein 2; PDBTitle: human m-aaa protease afg3l2, substrate-bound
47	c5xktA_	Alignment	not modelled	97.8	31	PDB header: hydrolase Chain: A: PDB Molecule: urease accessory protein ureg; PDBTitle: klebsiella pneumoniae ureg in complex with gmppnp and nickel
48	c2c9oA_	Alignment	not modelled	97.8	18	PDB header: hydrolase Chain: A: PDB Molecule: ruvb-like 1; PDBTitle: 3d structure of the human ruvb-like helicase ruvb1l
49	c4ww4A_	Alignment	not modelled	97.8	27	PDB header: hydrolase Chain: A: PDB Molecule: ruvb-like 1; PDBTitle: double-heterohexameric rings of full-length rvb1(adp)/rvb2(adp)
50	c6epcJ_	Alignment	not modelled	97.8	24	PDB header: hydrolase Chain: J: PDB Molecule: 26s proteasome regulatory subunit 8; PDBTitle: ground state 26s proteasome (gs2)
51	c3eihB_	Alignment	not modelled	97.8	22	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
52	c1nsfA_	Alignment	not modelled	97.8	18	PDB header: protein transport Chain: A: PDB Molecule: n-ethylmaleimide sensitive factor; PDBTitle: d2 hexamerization domain of n-ethylmaleimide sensitive factor (nsf)
53	c6hypA_	Alignment	not modelled	97.8	17	PDB header: motor protein Chain: A: PDB Molecule: midasin,midasin; PDBTitle: rea1 wild type adp state (aaa+ ring part)
54	d1lixz_	Alignment	not modelled	97.8	26	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
						PDB header: replication

55	c1sxC_	Alignment	not modelled	97.8	22	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)
56	c4wiaA_	Alignment	not modelled	97.8	16	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
57	c5g4gF_	Alignment	not modelled	97.8	23	PDB header: hydrolase Chain: F; PDB Molecule: vcp-like atpase; PDBTitle: structure of the atpgs-bound vat complex
58	d1ixsb2	Alignment	not modelled	97.8	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
59	d2qy9a2	Alignment	not modelled	97.8	24	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
60	c2dhrC_	Alignment	not modelled	97.7	27	PDB header: hydrolase Chain: C; PDB Molecule: ftsh; PDBTitle: whole cytosolic region of atp-dependent metalloprotease2 ftsh (g399l)
61	c2zamA_	Alignment	not modelled	97.7	27	PDB header: protein transport Chain: A; PDB Molecule: vacuolar protein sorting-associated protein 4b; PDBTitle: crystal structure of mouse skd1/vps4b apo-form
62	d2awna2	Alignment	not modelled	97.7	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
63	c4xgcA_	Alignment	not modelled	97.7	19	PDB header: dna binding protein Chain: A; PDB Molecule: origin recognition complex subunit 1; PDBTitle: crystal structure of the eukaryotic origin recognition complex
64	c6e111_	Alignment	not modelled	97.7	15	PDB header: protein transport Chain: 1; PDB Molecule: heat shock protein 101; PDBTitle: ptex core complex in the resetting (compact) state
65	d1fnna2	Alignment	not modelled	97.7	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
66	d1yrba1	Alignment	not modelled	97.7	26	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
67	c5exsA_	Alignment	not modelled	97.7	11	PDB header: transcription Chain: A; PDB Molecule: transcriptional regulator fleq; PDBTitle: aaa+ atpase fleq from pseudomonas aeruginosa bound to atp-gamma-s
68	d1r6bx2	Alignment	not modelled	97.7	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
69	c5kneF_	Alignment	not modelled	97.7	14	PDB header: chaperone Chain: F; PDB Molecule: heat shock protein 104; PDBTitle: cryoem reconstruction of hsp104 hexamer
70	d2ce7a2	Alignment	not modelled	97.7	23	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
71	c3pxiB_	Alignment	not modelled	97.7	26	PDB header: protein binding Chain: B; PDB Molecule: negative regulator of genetic competence clpc/mecb; PDBTitle: structure of meca108:clpc
72	c1in8A_	Alignment	not modelled	97.7	15	PDB header: dna binding protein Chain: A; PDB Molecule: holliday junction dna helicase ruvb; PDBTitle: thermotoga maritima ruvb t158v
73	c3a4mB_	Alignment	not modelled	97.7	20	PDB header: transferase Chain: B; PDB Molecule: l-seryl-trna(sec) kinase; PDBTitle: crystal structure of archaeal o-phosphoseryl-trna(sec)2 kinase
74	d1xjca_	Alignment	not modelled	97.7	25	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
75	c5oafB_	Alignment	not modelled	97.7	24	PDB header: gene regulation Chain: B; PDB Molecule: ruvb-like 2; PDBTitle: human rvb1/rvb2 heterohexamer in ino80 complex
76	d1r7ra3	Alignment	not modelled	97.7	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
77	d1e32a2	Alignment	not modelled	97.7	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
78	c4ydsA_	Alignment	not modelled	97.7	19	PDB header: hydrolase Chain: A; PDB Molecule: flagella-related protein h; PDBTitle: flah from sulfolobus acidocaldarius with atp and mg-ion
79	c4z8xC_	Alignment	not modelled	97.7	26	PDB header: hydrolase Chain: C; PDB Molecule: atp-dependent zinc metalloprotease ftsh; PDBTitle: truncated ftsh from a. aeolicus
80	c2z4rB_	Alignment	not modelled	97.7	20	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
81	c5mpaL_	Alignment	not modelled	97.7	21	PDB header: hydrolase Chain: L; PDB Molecule: 26s protease subunit rpt4; PDBTitle: 26s proteasome in presence of atp (s2)

82	c3pvsA	Alignment	not modelled	97.7	23	PDB header: recombination Chain: A: PDB Molecule: replication-associated recombination protein a; PDBTitle: structure and biochemical activities of escherichia coli mgsa
83	c1zu4A	Alignment	not modelled	97.7	21	PDB header: protein transport Chain: A: PDB Molecule: ftsy; PDBTitle: crystal structure of ftsy from mycoplasma mycoides-space2 group p21212
84	c1ojfF	Alignment	not modelled	97.7	19	PDB header: response regulator Chain: F: PDB Molecule: transcriptional regulatory protein zrar; PDBTitle: crystal structure of a sigma54-activator suggests the mechanism for the conformational switch necessary for sigma54 binding
85	c2r44A	Alignment	not modelled	97.6	13	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
86	c2c9oC	Alignment	not modelled	97.6	26	PDB header: hydrolase Chain: C: PDB Molecule: ruvb-like 1; PDBTitle: 3d structure of the human ruvb-like helicase ruvb1
87	c3b85A	Alignment	not modelled	97.6	25	PDB header: hydrolase Chain: A: PDB Molecule: phosphate starvation-inducible protein; PDBTitle: crystal structure of predicted phosphate starvation-induced atpase2 pho2 from corynebacterium glutamicum
88	c3upuC	Alignment	not modelled	97.6	19	PDB header: hydrolase/dna Chain: C: PDB Molecule: atp-dependent dna helicase dda; PDBTitle: crystal structure of the t4 phage sf1b helicase dda
89	d1ls1a2	Alignment	not modelled	97.6	24	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
90	c5owvC	Alignment	not modelled	97.6	16	PDB header: lipid binding protein Chain: C: PDB Molecule: gtp-binding protein; PDBTitle: an oligomerised bacterial dynamin pair provides a mechanism for the long-range sensing and tethering of membranes
91	d1okkd2	Alignment	not modelled	97.6	26	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
92	c4xrpA	Alignment	not modelled	97.6	16	PDB header: protein binding Chain: A: PDB Molecule: pnkp1; PDBTitle: structure of the pnkp1/rnl/hen1 rna repair complex
93	d1ny5a2	Alignment	not modelled	97.6	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
94	c5b57D	Alignment	not modelled	97.6	26	PDB header: metal transport Chain: D: PDB Molecule: hemin import atp-binding protein hmuV; PDBTitle: inward-facing conformation of abc heme importer bhuv from burkholderia cenocepacia
95	c1sxB	Alignment	not modelled	97.6	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 nuclear antigen, pcna)
96	d1qzxa3	Alignment	not modelled	97.6	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
97	c5kneA	Alignment	not modelled	97.6	13	PDB header: chaperone Chain: A: PDB Molecule: heat shock protein 104; PDBTitle: cryoem reconstruction of hsp104 hexamer
98	c6opcF	Alignment	not modelled	97.6	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)
99	c6hecH	Alignment	not modelled	97.6	24	PDB header: hydrolase Chain: H: PDB Molecule: proteasome-activating nucleotidase; PDBTitle: pan-proteasome in state 4
100	c6qi8E	Alignment	not modelled	97.6	26	PDB header: chaperone Chain: E: PDB Molecule: ruvb-like 2; PDBTitle: truncated human r2tp complex, structure 3 (adp-filled)
101	d1njfa	Alignment	not modelled	97.6	24	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
102	c1hv8B	Alignment	not modelled	97.6	17	PDB header: rna binding protein Chain: B: PDB Molecule: putative atp-dependent rna helicase mj0669; PDBTitle: crystal structure of a dead box protein from the hyperthermophile methanococcus jannaschii
103	c6em8E	Alignment	not modelled	97.6	27	PDB header: chaperone Chain: E: PDB Molecule: atp-dependent clp protease atp-binding subunit clpC; PDBTitle: s.aureus clpC resting state, c2 symmetrised
104	c2qz4A	Alignment	not modelled	97.6	18	PDB header: hydrolase Chain: A: PDB Molecule: paraplegin; PDBTitle: human paraplegin, aaa domain in complex with adp
105	d1vmaa2	Alignment	not modelled	97.6	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
106	d1sxb2	Alignment	not modelled	97.6	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
107	c4b4H	Alignment	not modelled	97.6	10	PDB header: hydrolase Chain: L: PDB Molecule: 26s protease subunit rpt4;

107	c4u4L_	Alignment	not modelled	97.6	19	PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome PDB header: hydrolase
108	c4b4tH_	Alignment	not modelled	97.6	25	Chain: H; PDB Molecule: 26s protease regulatory subunit 7 homolog; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
109	c2q9cA_	Alignment	not modelled	97.6	19	PDB header: signaling protein Chain: A; PDB Molecule: cell division protein ftsy; PDBTitle: structure of ftsy:gmpnp with mgcl complex
110	c4g1uD_	Alignment	not modelled	97.6	28	PDB header: transport protein/hydrolase Chain: D; PDB Molecule: hemin import atp-binding protein hmuV; PDBTitle: x-ray structure of the bacterial heme transporter hmuV from yersinia2 pestis
111	c6blbA_	Alignment	not modelled	97.6	17	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
112	c4l16A_	Alignment	not modelled	97.6	24	PDB header: hydrolase Chain: A; PDB Molecule: fidgetin-like protein 1; PDBTitle: crystal structure of figl-1 aaa domain in complex with adp
113	c2yz2B_	Alignment	not modelled	97.6	35	PDB header: hydrolase Chain: B; PDB Molecule: putative abc transporter atp-binding protein tm_0222; PDBTitle: crystal structure of the abc transporter in the cobalt transport2 system
114	c5l3qB_	Alignment	not modelled	97.6	22	PDB header: protein transport Chain: B; PDB Molecule: signal recognition particle receptor subunit alpha; PDBTitle: structure of the gtpase heterodimer of human srp54 and sralpha
115	c5owvA_	Alignment	not modelled	97.6	17	PDB header: lipid binding protein Chain: A; PDB Molecule: gtp-binding protein; PDBTitle: an oligomerised bacterial dynamin pair provides a mechanism for the2 long-range sensing and tethering of membranes
116	d1in4a2	Alignment	not modelled	97.6	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
117	c5ep4A_	Alignment	not modelled	97.6	17	PDB header: transcription Chain: A; PDB Molecule: putative repressor protein luxO; PDBTitle: structure, regulation, and inhibition of the quorum-sensing signal2 integrator luxO
118	c2ce7B_	Alignment	not modelled	97.6	24	PDB header: cell division protein Chain: B; PDB Molecule: cell division protein ftsh; PDBTitle: edta treated
119	c5gjqL_	Alignment	not modelled	97.6	21	PDB header: hydrolase Chain: L; PDB Molecule: 26s protease regulatory subunit 10b; PDBTitle: structure of the human 26s proteasome bound to usp14-ubal
120	d1sxja2	Alignment	not modelled	97.6	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain