























Phyre2

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Description	RVBD2670c (-)_2985741_2986850
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Unique Job ID	9a4866115623e42c

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2qgzA_	 Alignment		99.9	20	PDB header: hydrolase Chain: A: PDB Molecule: putative primosome component; PDBTitle: crystal structure of a putative primosome component from streptococcus2 pyogenes serotype m3. northeast structural genomics target dr58
2	c2w58B_	 Alignment		99.9	19	PDB header: hydrolase Chain: B: PDB Molecule: primosome component (helicase loader); PDBTitle: crystal structure of the dnaI
3	c5bq5A_	 Alignment		99.8	20	PDB header: atp-binding protein Chain: A: PDB Molecule: insertion sequence is5376 putative atp-binding protein; PDBTitle: crystal structure of the istb aaa+ domain bound to adp-bef3
4	c5he8J_	 Alignment		99.8	20	PDB header: protein binding Chain: J: PDB Molecule: helicase loader; PDBTitle: bacterial initiation protein
5	c6qell_	 Alignment		99.8	19	PDB header: replication Chain: L: PDB Molecule: dna replication protein dnac; PDBTitle: e. coli dnabc apo complex
6	c3ec2A_	 Alignment		99.8	18	PDB header: replication Chain: A: PDB Molecule: dna replication protein dnac; PDBTitle: crystal structure of the dnac helicase loader
7	c5g4gF_	 Alignment		99.8	22	PDB header: hydrolase Chain: F: PDB Molecule: vcvp-like atpase; PDBTitle: structure of the atpgs-bound vat complex
8	c3cf2B_	 Alignment		99.8	17	PDB header: transport protein Chain: B: PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: structure of p97/vcp in complex with adp/amp-pnp
9	c3cf1C_	 Alignment		99.7	16	PDB header: transport protein Chain: C: PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: structure of p97/vcp in complex with adp/adp.alfx
10	c2hcbC_	 Alignment		99.7	16	PDB header: replication Chain: C: PDB Molecule: chromosomal replication initiator protein dnaa; PDBTitle: structure of amppcp-bound dnaa from aquifex aeolicus
11	c5e7pA_	 Alignment		99.7	23	PDB header: hydrolase Chain: A: PDB Molecule: cell division control protein cdc48; PDBTitle: crystal structure of msmeg_0858 (uniprot a0qqs4), a aaa atpase.

12	c4m4wO_	Alignment		99.7	18	PDB header: replication Chain: O: PDB Molecule: primosomal protein dnaI; PDBTitle: mechanistic implications for the bacterial primosome assembly of the 2 structure of a helicase-helicase loader complex
13	c5kzfj_	Alignment		99.7	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
14	c3hu2C_	Alignment		99.6	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
15	c6epdM_	Alignment		99.6	20	PDB header: hydrolase Chain: M: PDB Molecule: 26s proteasome regulatory subunit 6a; PDBTitle: substrate processing state 26s proteasome (sps1)
16	c1xwiA_	Alignment		99.6	18	PDB header: protein transport Chain: A: PDB Molecule: skd1 protein; PDBTitle: crystal structure of vps4b
17	c2zamA_	Alignment		99.6	18	PDB header: protein transport Chain: A: PDB Molecule: vacuolar protein sorting-associating protein 4b; PDBTitle: crystal structure of mouse skd1/vps4b apo-form
18	c5ifwB_	Alignment		99.5	19	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
19	c5mpaL_	Alignment		99.5	16	PDB header: hydrolase Chain: L: PDB Molecule: 26s protease subunit rpt4; PDBTitle: 26s proteasome in presence of atp (s2)
20	c4b4tK_	Alignment		99.5	19	PDB header: hydrolase Chain: K: PDB Molecule: 26s protease regulatory subunit 6b homolog; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
21	c1s3sA_	Alignment	not modelled	99.5	19	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
22	c4b4tH_	Alignment	not modelled	99.5	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
23	c4b4tI_	Alignment	not modelled	99.5	18	PDB header: hydrolase Chain: I: PDB Molecule: 26s protease regulatory subunit 4 homolog; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
24	c4b4tJ_	Alignment	not modelled	99.5	16	PDB header: hydrolase Chain: J: PDB Molecule: 26s protease regulatory subunit 8 homolog; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
25	c6matE_	Alignment	not modelled	99.5	17	PDB header: ribosomal protein Chain: E: PDB Molecule: rix7 mutant; PDBTitle: cryo-em structure of the essential ribosome assembly aaa-atpase rix7
26	c6hecH_	Alignment	not modelled	99.5	22	PDB header: hydrolase Chain: H: PDB Molecule: proteasome-activating nucleotidase; PDBTitle: pan-proteasome in state 4
27	c5w0tA_	Alignment	not modelled	99.5	14	PDB header: hydrolase Chain: A: PDB Molecule: protein msp1; PDBTitle: crystal structure of monomeric msp1 from s. cerevisiae
						PDB header: hydrolase

28	c4b4tL_	Alignment	not modelled	99.5	16	Chain: L; PDB Molecule: 26s protease subunit rpt4; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
29	c6epcJ_	Alignment	not modelled	99.5	16	PDB header: hydrolase Chain: J; PDB Molecule: 26s proteasome regulatory subunit 8; PDBTitle: ground state 26s proteasome (gs2)
30	c5gjqL_	Alignment	not modelled	99.5	18	PDB header: hydrolase Chain: L; PDB Molecule: 26s protease regulatory subunit 10b; PDBTitle: structure of the human 26s proteasome bound to usp14-ubal
31	c6opcF_	Alignment	not modelled	99.5	17	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)
32	c3zw6B_	Alignment	not modelled	99.5	14	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.
33	c3vfdA_	Alignment	not modelled	99.5	20	PDB header: hydrolase Chain: A; PDB Molecule: spastin; PDBTitle: human spastin aaa domain
34	c6b5cA_	Alignment	not modelled	99.4	19	PDB header: cell cycle Chain: A; PDB Molecule: katanin p60 atpase-containing subunit a-like 1; PDBTitle: structural basis for katanin self-assembly
35	c6nyyA_	Alignment	not modelled	99.4	19	PDB header: translocase Chain: A; PDB Molecule: afg3-like protein 2; PDBTitle: human m-aaa protease afg3l2, substrate-bound
36	c3j96F_	Alignment	not modelled	99.4	21	PDB header: hydrolase Chain: F; PDB Molecule: vesicle-fusing atpase; PDBTitle: structure of 20s supercomplex determined by single particle2 cryoelectron microscopy (state i)
37	c4b4tM_	Alignment	not modelled	99.4	18	PDB header: hydrolase Chain: M; PDB Molecule: 26s protease regulatory subunit 6a; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
38	c5t0gA_	Alignment	not modelled	99.4	15	PDB header: hydrolase Chain: A; PDB Molecule: 26s protease regulatory subunit 7; PDBTitle: structural basis for dynamic regulation of the human 26s proteasome
39	c4l16A_	Alignment	not modelled	99.4	19	PDB header: hydrolase Chain: A; PDB Molecule: fidgetin-like protein 1; PDBTitle: crystal structure of figl-1 aaa domain in complex with adp
40	c3d8bB_	Alignment	not modelled	99.4	20	PDB header: hydrolase Chain: B; PDB Molecule: fidgetin-like protein 1; PDBTitle: crystal structure of human fidgetin-like protein 1 in complex with adp
41	c6nyyC_	Alignment	not modelled	99.4	20	PDB header: translocase Chain: C; PDB Molecule: afg3-like protein 2; PDBTitle: human m-aaa protease afg3l2, substrate-bound
42	c3b9pA_	Alignment	not modelled	99.4	21	PDB header: hydrolase Chain: A; PDB Molecule: cg5977-pa, isoform a; PDBTitle: spastin
43	c2kjqA_	Alignment	not modelled	99.4	19	PDB header: replication Chain: A; PDB Molecule: dnaa-related protein; PDBTitle: solution structure of protein nmb1076 from neisseria meningitidis.2 northeast structural genomics consortium target mr101b.
44	d1l8qa2	Alignment	not modelled	99.4	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
45	d2ce7a2	Alignment	not modelled	99.3	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
46	c4lcbA_	Alignment	not modelled	99.3	14	PDB header: protein transport Chain: A; PDB Molecule: cell division protein cdvc, vps4; PDBTitle: structure of vps4 homolog from acidianus hospitalis
47	c3eihB_	Alignment	not modelled	99.3	19	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
48	c5wc0D_	Alignment	not modelled	99.3	16	PDB header: motor protein Chain: D; PDB Molecule: meiotic spindle formation protein mei-1; PDBTitle: katanin hexamer in spiral conformation
49	c5vq9D_	Alignment	not modelled	99.3	18	PDB header: protein binding Chain: D; PDB Molecule: pachytene checkpoint protein 2 homolog; PDBTitle: structure of human trip13, apo form
50	c2x8aA_	Alignment	not modelled	99.3	17	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
51	c2z4rB_	Alignment	not modelled	99.2	21	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
52	c2dhrC_	Alignment	not modelled	99.2	18	PDB header: hydrolase Chain: C; PDB Molecule: ftsh; PDBTitle: whole cytosolic region of atp-dependent metalloprotease2 ftsh (g399l)
53	c6mdnF_	Alignment	not modelled	99.2	19	PDB header: hydrolase Chain: F; PDB Molecule: vesicle-fusing atpase; PDBTitle: the 20s supercomplex engaging the snap-25 n-terminus

					(class 2)
54	c4xguB	Alignment	not modelled	99.2	16 PDB header: atp-binding protein Chain: B: PDB Molecule: putative pachytene checkpoint protein 2; PDBTitle: structure of c. elegans pch-2
55	c1iy2A	Alignment	not modelled	99.2	20 PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent metalloprotease ftsh; PDBTitle: crystal structure of the ftsh atpase domain from thermus2 thermophilus
56	d1r7ra3	Alignment	not modelled	99.2	16 Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
57	c5x06G	Alignment	not modelled	99.2	24 PDB header: replication Chain: G: PDB Molecule: dnaa regulatory inactivator hda; PDBTitle: dna replication regulation protein
58	d1e32a2	Alignment	not modelled	99.2	19 Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
59	d1ixza	Alignment	not modelled	99.2	16 Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
60	c6az0A	Alignment	not modelled	99.2	16 PDB header: hydrolase Chain: A: PDB Molecule: mitochondrial inner membrane i-aaa protease supercomplex PDBTitle: mitochondrial atpase protease yme1
61	c4ypnA	Alignment	not modelled	99.1	17 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
62	c2ce7B	Alignment	not modelled	99.1	18 PDB header: cell division protein Chain: B: PDB Molecule: cell division protein ftsh; PDBTitle: edta treated
63	c1qvrB	Alignment	not modelled	99.1	20 PDB header: chaperone Chain: B: PDB Molecule: clpb protein; PDBTitle: crystal structure analysis of clpb
64	c3h4mC	Alignment	not modelled	99.1	19 PDB header: hydrolase Chain: C: PDB Molecule: proteasome-activating nucleotidase; PDBTitle: aaa atpase domain of the proteasome- activating nucleotidase
65	c2r65A	Alignment	not modelled	99.0	16 PDB header: hydrolase Chain: A: PDB Molecule: cell division protease ftsh homolog; PDBTitle: crystal structure of helicobacter pylori atp dependent protease, ftsh2 adp complex
66	c4z8xC	Alignment	not modelled	99.0	18 PDB header: hydrolase Chain: C: PDB Molecule: atp-dependent zinc metalloprotease ftsh; PDBTitle: truncated ftsh from a. aeolicus
67	c3bosA	Alignment	not modelled	99.0	17 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
68	d1sxja2	Alignment	not modelled	99.0	13 Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
69	c3pxiB	Alignment	not modelled	99.0	21 PDB header: protein binding Chain: B: PDB Molecule: negative regulator of genetic competence clpc/mecc; PDBTitle: structure of meca108:clpc
70	c5ubvB	Alignment	not modelled	98.9	13 PDB header: hydrolase Chain: B: PDB Molecule: atpase domain of i-aaa protease; PDBTitle: atpase domain of i-aaa protease from myceliophthora thermophila
71	c2qz4A	Alignment	not modelled	98.9	18 PDB header: hydrolase Chain: A: PDB Molecule: paraplegin; PDBTitle: human paraplegin, aaa domain in complex with adp
72	c4ciuA	Alignment	not modelled	98.9	19 PDB header: chaperone Chain: A: PDB Molecule: chaperone protein clpb; PDBTitle: crystal structure of e. coli clpb
73	c1sxjA	Alignment	not modelled	98.9	15 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)
74	d1oz4a3	Alignment	not modelled	98.9	14 Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
75	c3pfiB	Alignment	not modelled	98.9	12 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
76	c3u5zM	Alignment	not modelled	98.8	12 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
77	c1nsfA	Alignment	not modelled	98.8	17 PDB header: protein transport Chain: A: PDB Molecule: n-ethylmaleimide sensitive factor; PDBTitle: d2 hexamerization domain of n-ethylmaleimide sensitive factor (nsf)
78	c4d2qC	Alignment	not modelled	98.8	21 PDB header: chaperone Chain: C: PDB Molecule: clpb; PDBTitle: negative-stain electron microscopy of e. coli clpb mutant e432a (bap2 form bound to clpp)
					PDB header: viral protein

79	c5z3qD_	Alignment	not modelled	98.8	14	Chain: D; PDB Molecule: pv-2c; PDBTitle: crystal structure of a soluble fragment of poliovirus 2c atpase (2.552 angstrom)
80	d1ofha_	Alignment	not modelled	98.7	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
81	c5j1sA_	Alignment	not modelled	98.7	16	PDB header: hydrolase Chain: A; PDB Molecule: torsin-1a; PDBTitle: torsina-lull1 complex, h. sapiens, bound to vhh-bs2
82	c3pvsA_	Alignment	not modelled	98.7	17	PDB header: recombination Chain: A; PDB Molecule: replication-associated recombination protein a; PDBTitle: structure and biochemical activities of escherichia coli mgsa
83	d1g41a_	Alignment	not modelled	98.7	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
84	d1in4a2	Alignment	not modelled	98.7	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
85	c3sylB_	Alignment	not modelled	98.7	17	PDB header: chaperone Chain: B; PDB Molecule: protein cbbx; PDBTitle: crystal structure of the aaa+ protein cbbx, native structure
86	c6azyA_	Alignment	not modelled	98.7	17	PDB header: chaperone Chain: A; PDB Molecule: heat shock protein hsp104; PDBTitle: crystal structure of hsp104 r328m/r757m mutant from calcarisporiella2 thermophila
87	d1d2na_	Alignment	not modelled	98.7	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
88	c4xgcA_	Alignment	not modelled	98.6	20	PDB header: dna binding protein Chain: A; PDB Molecule: origin recognition complex subunit 1; PDBTitle: crystal structure of the eukaryotic origin recognition complex
89	c5uj7B_	Alignment	not modelled	98.6	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
90	c2chgB_	Alignment	not modelled	98.6	14	PDB header: dna-binding protein Chain: B; PDB Molecule: replication factor c small subunit; PDBTitle: replication factor c domains 1 and 2
91	c1in8A_	Alignment	not modelled	98.6	16	PDB header: dna binding protein Chain: A; PDB Molecule: holliday junction dna helicase ruvb; PDBTitle: thermotoga maritima ruvb t158v
92	d1um8a_	Alignment	not modelled	98.6	24	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
93	c6em8E_	Alignment	not modelled	98.6	22	PDB header: chaperone Chain: E; PDB Molecule: atp-dependent clp protease atp-binding subunit clpc; PDBTitle: s.aureus clpc resting state, c2 symmetrised
94	c3te6A_	Alignment	not modelled	98.5	8	PDB header: gene regulation Chain: A; PDB Molecule: regulatory protein sir3; PDBTitle: crystal structure of the s. cerevisiae sir3 aaa+ domain
95	c1r6bX_	Alignment	not modelled	98.5	20	PDB header: hydrolase Chain: X; PDB Molecule: clpa protein; PDBTitle: high resolution crystal structure of clpa
96	c5uj7C_	Alignment	not modelled	98.5	19	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
97	d1qvra3	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
98	c5kneD_	Alignment	not modelled	98.5	21	PDB header: chaperone Chain: D; PDB Molecule: heat shock protein 104; PDBTitle: cryoem reconstruction of hsp104 hexamer
99	c6e111_	Alignment	not modelled	98.5	17	PDB header: protein transport Chain: 1; PDB Molecule: heat shock protein 101; PDBTitle: ptex core complex in the resetting (compact) state
100	c5udbD_	Alignment	not modelled	98.5	21	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
101	c5d4wB_	Alignment	not modelled	98.4	14	PDB header: chaperone Chain: B; PDB Molecule: putative heat shock protein; PDBTitle: crystal structure of hsp104
102	d1fnna2	Alignment	not modelled	98.4	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
103	d1jbka_	Alignment	not modelled	98.4	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
104	c3uk6L_	Alignment	not modelled	98.4	17	PDB header: hydrolase Chain: L; PDB Molecule: ruvb-like 2; PDBTitle: crystal structure of the tip48 (tip49b) hexamer
105	d1iqpa2	Alignment	not modelled	98.4	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
						PDB header: hydrolase

106	c3nbxX_	Alignment	not modelled	98.4	23	Chain: X: PDB Molecule: atpase rava; PDBTitle: crystal structure of e. coli rava (regulatory atpase variant a) in2 complex with adp
107	c5zr1A_	Alignment	not modelled	98.4	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
108	d1sxb2_	Alignment	not modelled	98.3	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
109	c1xxhB_	Alignment	not modelled	98.3	20	PDB header: transferase Chain: B: PDB Molecule: dna polymerase iii subunit gamma; PDBTitle: atpgs bound e. coli clamp loader complex
110	c5kneF_	Alignment	not modelled	98.3	21	PDB header: chaperone Chain: F: PDB Molecule: heat shock protein 104; PDBTitle: cryoem reconstruction of hsp104 hexamer
111	c4xgcD_	Alignment	not modelled	98.3	24	PDB header: dna binding protein Chain: D: PDB Molecule: origin recognition complex subunit 4; PDBTitle: crystal structure of the eukaryotic origin recognition complex
112	d1sxic2_	Alignment	not modelled	98.3	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
113	d1ny5a2_	Alignment	not modelled	98.3	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
114	c6em8F_	Alignment	not modelled	98.3	23	PDB header: chaperone Chain: F: PDB Molecule: atp-dependent clp protease atp-binding subunit clpc; PDBTitle: s.aureus clpc resting state, c2 symmetrised
115	c6blbA_	Alignment	not modelled	98.3	14	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
116	c2p65A_	Alignment	not modelled	98.3	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein pf08_0063; PDBTitle: crystal structure of the first nucleotide binding domain of2 chaperone clpb1, putative, (pv089580) from plasmodium vivax
117	c5vy9C_	Alignment	not modelled	98.3	22	PDB header: chaperone Chain: C: PDB Molecule: heat shock protein 104; PDBTitle: s. cerevisiae hsp104:casein complex, middle domain conformation
118	d1r6bx3_	Alignment	not modelled	98.2	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
119	c5kneA_	Alignment	not modelled	98.2	18	PDB header: chaperone Chain: A: PDB Molecule: heat shock protein 104; PDBTitle: cryoem reconstruction of hsp104 hexamer
120	d1lv7a_	Alignment	not modelled	98.2	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain