



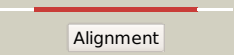

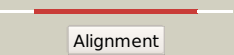

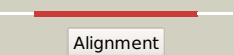

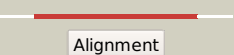



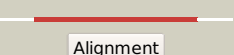





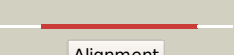





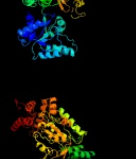
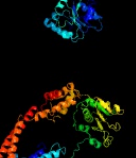


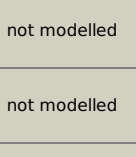


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3596c_clpC1_4038337_4040883
Date	Fri Aug 9 18:20:28 BST 2019
Unique Job ID	e84ef38490dc226f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1qvrB_	 Alignment		100.0	51	PDB header: chaperone Chain: B; PDB Molecule: clpb protein; PDBTitle: crystal structure analysis of clpb
2	c5kneD_	 Alignment		100.0	41	PDB header: chaperone Chain: D; PDB Molecule: heat shock protein 104; PDBTitle: cryoem reconstruction of hsp104 hexamer
3	c6azyA_	 Alignment		100.0	46	PDB header: chaperone Chain: A; PDB Molecule: heat shock protein hsp104; PDBTitle: crystal structure of hsp104 r328m/r757m mutant from calcarisporiella2 thermophila
4	c4d2qC_	 Alignment		100.0	50	PDB header: chaperone Chain: C; PDB Molecule: clpb; PDBTitle: negative-stain electron microscopy of e. coli clpb mutant e432a (bap2 form bound to clpb)
5	c6em8F_	 Alignment		100.0	59	PDB header: chaperone Chain: F; PDB Molecule: atp-dependent clp protease atp-binding subunit clpc; PDBTitle: s.aureus clpc resting state, c2 symmetrised
6	c5vy9C_	 Alignment		100.0	45	PDB header: chaperone Chain: C; PDB Molecule: heat shock protein 104; PDBTitle: s. cerevisiae hsp104:casein complex, middle domain conformation
7	c3pxiB_	 Alignment		100.0	62	PDB header: protein binding Chain: B; PDB Molecule: negative regulator of genetic competence clpc/mechb; PDBTitle: structure of meca108:clpc
8	c1r6bX_	 Alignment		100.0	44	PDB header: hydrolase Chain: X; PDB Molecule: clpa protein; PDBTitle: high resolution crystal structure of clpa
9	c6em8E_	 Alignment		100.0	59	PDB header: chaperone Chain: E; PDB Molecule: atp-dependent clp protease atp-binding subunit clpc; PDBTitle: s.aureus clpc resting state, c2 symmetrised
10	c6e111_	 Alignment		100.0	39	PDB header: protein transport Chain: 1; PDB Molecule: heat shock protein 101; PDBTitle: ptex core complex in the resetting (compact) state
11	c5d4wB_	 Alignment		100.0	51	PDB header: chaperone Chain: B; PDB Molecule: putative heat shock protein; PDBTitle: crystal structure of hsp104

12	c6djuA_	Alignment		100.0	58	PDB header: chaperone Chain: A; PDB Molecule: chaperone protein clpb; PDBTitle: mtb clpb in complex with atpgammas and casein, conformer 1
13	c4ciuA_	Alignment		100.0	55	PDB header: chaperone Chain: A; PDB Molecule: chaperone protein clpb; PDBTitle: crystal structure of e. coli clpb
14	c5kneF_	Alignment		100.0	47	PDB header: chaperone Chain: F; PDB Molecule: heat shock protein 104; PDBTitle: cryoem reconstruction of hsp104 hexamer
15	c6em8H_	Alignment		100.0	60	PDB header: chaperone Chain: H; PDB Molecule: atp-dependent clp protease atp-binding subunit clpc; PDBTitle: s.aureus clpc resting state, c2 symmetrised
16	c5kneA_	Alignment		100.0	49	PDB header: chaperone Chain: A; PDB Molecule: heat shock protein 104; PDBTitle: cryoem reconstruction of hsp104 hexamer
17	c6divE_	Alignment		100.0	64	PDB header: chaperone Chain: E; PDB Molecule: chaperone protein clpb; PDBTitle: mtb clpb in complex with atpgammas and casein, conformer 2
18	c3pxgA_	Alignment		100.0	64	PDB header: protein binding Chain: A; PDB Molecule: negative regulator of genetic competence clpc/mechb; PDBTitle: structure of meca121 and clpc1-485 complex
19	c5g4gF_	Alignment		100.0	23	PDB header: hydrolase Chain: F; PDB Molecule: vcp-like atpase; PDBTitle: structure of the atpgs-bound vat complex
20	c6matE_	Alignment		100.0	19	PDB header: ribosomal protein Chain: E; PDB Molecule: rix7 mutant; PDBTitle: cryo-em structure of the essential ribosome assembly aaa-atpase rix7
21	d1r6bx3	Alignment	not modelled	100.0	42	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
22	d1qvra3	Alignment	not modelled	100.0	58	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
23	d1qvra2	Alignment	not modelled	100.0	49	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
24	c3cf1C_	Alignment	not modelled	100.0	25	PDB header: transport protein Chain: C; PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: structure of p97/vcp in complex with adp/adp.alfx
25	c3cf2B_	Alignment	not modelled	100.0	25	PDB header: transport protein Chain: B; PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: structure of p97/vcp in complex with adp/amp-pnp
26	c5e7pA_	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: A; PDB Molecule: cell division control protein cdc48; PDBTitle: crystal structure of msmeg_0858 (uniprot a0qqs4), a aaa atpase.
27	c5ifwB_	Alignment	not modelled	100.0	24	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
28	d1um8a_	Alignment	not modelled	100.0	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
						PDB header: hydrolase

29	c3j96F_	Alignment	not modelled	100.0	19	Chain: F; PDB Molecule: vesicle-fusing atpase; PDBTitle: structure of 20s supercomplex determined by single particle2 cryoelectron microscopy (state i)
30	c6i26A_	Alignment	not modelled	100.0	21	PDB header: motor protein Chain: A; PDB Molecule: midasin,midasin,midasin,midasin; PDBTitle: rea1 wild type amppnp state
31	c6opcF_	Alignment	not modelled	100.0	19	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	c6mdnF_	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: F; PDB Molecule: vesicle-fusing atpase; PDBTitle: the 20s supercomplex engaging the snap-25 n-terminus (class 2)
33	d1r6bx2	Alignment	not modelled	100.0	54	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
34	d1e94e_	Alignment	not modelled	100.0	23	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
35	c6orbA_	Alignment	not modelled	100.0	21	PDB header: motor protein Chain: A; PDB Molecule: midasin; PDBTitle: full-length s. pombe mdn1 in the presence of atp and rbin-1
36	c6i27A_	Alignment	not modelled	100.0	22	PDB header: motor protein Chain: A; PDB Molecule: midasin,midasin,midasin,midasin,midasin,midasin; PDBTitle: rea1 aaa2l-h2alpha deletion mutant in amppnp state
37	d1g41a_	Alignment	not modelled	100.0	23	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
38	c2p65A_	Alignment	not modelled	100.0	65	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
39	c5j1sA_	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: A; PDB Molecule: torsin-1a; PDBTitle: torsina-lull1 complex, h. sapiens, bound to vhh-bs2
40	d1jbka_	Alignment	not modelled	100.0	68	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
41	d1ofha_	Alignment	not modelled	100.0	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
42	c6on2A_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: A; PDB Molecule: atp-dependent protease la; PDBTitle: lon protease from yersinia pestis with y2853 substrate
43	c3hteC_	Alignment	not modelled	100.0	23	PDB header: motor protein Chain: C; PDB Molecule: atp-dependent clp protease atp-binding subunit clpx; PDBTitle: crystal structure of nucleotide-free hexameric clpx
44	c4yp1E_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: E; PDB Molecule: lon protease; PDBTitle: crystal structure of a hexameric lona protease bound to three adps
45	c6edoA_	Alignment	not modelled	99.9	19	PDB header: motor protein Chain: A; PDB Molecule: midasin; PDBTitle: full-length s. pombe mdn1 in the presence of amppnp (ring region)
46	c1ny5A_	Alignment	not modelled	99.9	23	PDB header: transcription Chain: A; PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigm54 activator (aaa+ atpase) in the inactive2 state
47	c5ep0A_	Alignment	not modelled	99.9	18	PDB header: transcription Chain: A; PDB Molecule: putative repressor protein luxo; PDBTitle: quorum-sensing signal integrator luxo - receiver+catalytic domains
48	c5m7nA_	Alignment	not modelled	99.9	22	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 crystal direct automated mounting and cryo-cooling3 technology
49	c5kzfj_	Alignment	not modelled	99.9	19	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
50	d1ny5a2	Alignment	not modelled	99.9	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
51	c5ep4A_	Alignment	not modelled	99.9	17	PDB header: transcription Chain: A; PDB Molecule: putative repressor protein luxo; PDBTitle: structure, regulation, and inhibition of the quorum-sensing signal2 integrator luxo
52	c4xgcD_	Alignment	not modelled	99.9	18	PDB header: dna binding protein Chain: D; PDB Molecule: origin recognition complex subunit 4; PDBTitle: crystal structure of the eukaryotic origin recognition complex
53	c5guiA_	Alignment	not modelled	99.9	62	PDB header: chaperone Chain: A; PDB Molecule: chaperone protein clp1, chloroplastic; PDBTitle: crystal structure of the n-terminal domain of caseinolytic protease2 associated chaperone clpc1 from arabidopsis thaliana
54	c3hu2C_	Alignment	not modelled	99.9	24	PDB header: transport protein Chain: C; PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: structure of p97 n-d1 r86a mutant in complex with atpgs
55	c2c99A_	Alignment	not modelled	99.9	21	PDB header: transcription regulation Chain: A; PDB Molecule: psp operon transcriptional activator;

55	c2c92A	Alignment	not modelled	99.9	41	PDBTitle: structural basis of the nucleotide driven conformational2 changes in the aaa domain of transcription activator pspf PDB header: transcription
56	c5exsA	Alignment	not modelled	99.9	18	Chain: A; PDB Molecule: transcriptional regulator fleq; PDBTitle: aaa+ atpase fleq from pseudomonas aeruginosa bound to atp-gamma-s
57	c4ypnA	Alignment	not modelled	99.9	20	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
58	c3vkhB	Alignment	not modelled	99.9	15	PDB header: motor protein Chain: B; PDB Molecule: dynein heavy chain, cytoplasmic; PDBTitle: x-ray structure of a functional full-length dynein motor domain
59	c3fh2A	Alignment	not modelled	99.9	88	PDB header: hydrolase Chain: A; PDB Molecule: probable atp-dependent protease (heat shock protein); PDBTitle: the crystal structure of the probable atp-dependent protease (heat2 shock protein) from corynebacterium glutamicum
60	c4rh7A	Alignment	not modelled	99.9	12	PDB header: motor protein Chain: A; PDB Molecule: green fluorescent protein/cytoplasmic dynein 2 heavy chain PDBTitle: crystal structure of human cytoplasmic dynein 2 motor domain in2 complex with adp.vi
61	c5nugB	Alignment	not modelled	99.9	16	PDB header: motor protein Chain: B; PDB Molecule: cytoplasmic dynein 1 heavy chain 1; PDBTitle: motor domains from human cytoplasmic dynein-1 in the phi-particle2 conformation
62	c4xbiA	Alignment	not modelled	99.9	22	PDB header: chaperone Chain: A; PDB Molecule: clpb protein, putative,green fluorescent protein; PDBTitle: structure of a malarial protein involved in proteostasis
63	c1xwiA	Alignment	not modelled	99.9	26	PDB header: protein transport Chain: A; PDB Molecule: skd1 protein; PDBTitle: crystal structure of vps4b
64	c3vkhA	Alignment	not modelled	99.9	15	PDB header: motor protein Chain: A; PDB Molecule: dynein heavy chain, cytoplasmic; PDBTitle: x-ray structure of a functional full-length dynein motor domain
65	c3vkgA	Alignment	not modelled	99.9	16	PDB header: motor protein Chain: A; PDB Molecule: dynein heavy chain, cytoplasmic; PDBTitle: x-ray structure of an mtbd truncation mutant of dynein motor domain
66	c3dzdA	Alignment	not modelled	99.9	23	PDB header: transcription regulator Chain: A; PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigma54 activator ntrc4 in the inactive2 state
67	c1ojlD	Alignment	not modelled	99.9	20	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
68	c6epdM	Alignment	not modelled	99.9	21	PDB header: hydrolase Chain: M; PDB Molecule: 26s proteasome regulatory subunit 6a; PDBTitle: substrate processing state 26s proteasome (sps1)
69	c1s3sA	Alignment	not modelled	99.9	27	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
70	c2k77A	Alignment	not modelled	99.9	64	PDB header: chaperone, protein binding Chain: A; PDB Molecule: negative regulator of genetic competence PDBTitle: nmr solution structure of the bacillus subtilis clpc n-2 domain
71	c4b4tH	Alignment	not modelled	99.9	22	PDB header: hydrolase Chain: H; PDB Molecule: 26s protease regulatory subunit 7 homolog; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
72	c6az0A	Alignment	not modelled	99.9	22	PDB header: hydrolase Chain: A; PDB Molecule: mitochondrial inner membrane i-aaa protease supercomplex PDBTitle: mitochondrial atpase protease yme1
73	c1ojlF	Alignment	not modelled	99.9	20	PDB header: response regulator Chain: F; PDB Molecule: transcriptional regulatory protein zrar; PDBTitle: crystal structure of a sigma54-activator suggests the mechanism for2 the conformational switch necessary for sigma54 binding
74	c6epcJ	Alignment	not modelled	99.9	22	PDB header: hydrolase Chain: J; PDB Molecule: 26s proteasome regulatory subunit 8; PDBTitle: ground state 26s proteasome (gs2)
75	c4b4tJ	Alignment	not modelled	99.9	23	PDB header: hydrolase Chain: J; PDB Molecule: 26s protease regulatory subunit 8 homolog; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
76	c3fesB	Alignment	not modelled	99.9	44	PDB header: atp binding protein Chain: B; PDB Molecule: atp-dependent clp endopeptidase; PDBTitle: crystal structure of the atp-dependent clp protease clpc from2 clostridium difficile
77	c6hecH	Alignment	not modelled	99.9	23	PDB header: hydrolase Chain: H; PDB Molecule: proteasome-activating nucleotidase; PDBTitle: pan-proteasome in state 4
78	c4w8fA	Alignment	not modelled	99.9	12	PDB header: motor protein Chain: A; PDB Molecule: dynein heavy chain lysozyme chimera; PDBTitle: crystal structure of the dynein motor domain in the amppnp-bound state
79	c6nyyC	Alignment	not modelled	99.9	22	PDB header: translocase Chain: C; PDB Molecule: afg3-like protein 2; PDBTitle: human m-aaa protease afg3l2, substrate-bound PDB header: motor protein

80	c4akgB	Alignment	not modelled	99.9	13	Chain: B; PDB Molecule: glutathione s-transferase class-mu 26 kda isozyme, dynein PDBTitle: dynein motor domain - atp complex
81	c4uqwA	Alignment	not modelled	99.9	10	PDB header: chaperone Chain: A; PDB Molecule: protein clpv1; PDBTitle: coevolution of the atpase clpv, the tssb-tssc sheath and2 the accessory hsie protein distinguishes two type vi3 secretion classes
82	c3eihB	Alignment	not modelled	99.9	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
83	c3sylB	Alignment	not modelled	99.9	26	PDB header: chaperone Chain: B; PDB Molecule: protein cbbx; PDBTitle: crystal structure of the aaa+ protein cbbx, native structure
84	c6or5A	Alignment	not modelled	99.9	19	PDB header: motor protein Chain: A; PDB Molecule: midasin; PDBTitle: full-length s. pombe mdn1 in the presence of amppnp (ring region)
85	d1khya	Alignment	not modelled	99.9	23	Fold: Double Clp-N motif Superfamily: Double Clp-N motif Family: Double Clp-N motif
86	c4b4tI	Alignment	not modelled	99.9	19	PDB header: hydrolase Chain: I; PDB Molecule: 26s protease regulatory subunit 4 homolog; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
87	c2ce7B	Alignment	not modelled	99.9	17	PDB header: cell division protein Chain: B; PDB Molecule: cell division protein ftsh; PDBTitle: edta treated
88	c3zriA	Alignment	not modelled	99.9	15	PDB header: chaperone Chain: A; PDB Molecule: clpb protein; PDBTitle: n-domain of clpv from vibrio cholerae
89	c2dhrC	Alignment	not modelled	99.9	21	PDB header: hydrolase Chain: C; PDB Molecule: ftsh; PDBTitle: whole cytosolic region of atp-dependent metalloprotease2 ftsh (g399l)
90	c4b4tK	Alignment	not modelled	99.9	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
91	c4b4tM	Alignment	not modelled	99.9	22	PDB header: hydrolase Chain: M; PDB Molecule: 26s protease regulatory subunit 6a; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
92	c4l16A	Alignment	not modelled	99.9	25	PDB header: hydrolase Chain: A; PDB Molecule: fidgetin-like protein 1; PDBTitle: crystal structure of figl-1 aaa domain in complex with adp
93	c5mpaL	Alignment	not modelled	99.9	24	PDB header: hydrolase Chain: L; PDB Molecule: 26s protease subunit rpt4; PDBTitle: 26s proteasome in presence of atp (s2)
94	c4b4tL	Alignment	not modelled	99.9	22	PDB header: hydrolase Chain: L; PDB Molecule: 26s protease subunit rpt4; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
95	c5gjqL	Alignment	not modelled	99.9	23	PDB header: hydrolase Chain: L; PDB Molecule: 26s protease regulatory subunit 10b; PDBTitle: structure of the human 26s proteasome bound to usp14-ubal
96	c3b9pA	Alignment	not modelled	99.9	22	PDB header: hydrolase Chain: A; PDB Molecule: cg5977-pa, isoform a; PDBTitle: spastin
97	c3vkgB	Alignment	not modelled	99.9	15	PDB header: motor protein Chain: B; PDB Molecule: dynein heavy chain, cytoplasmic; PDBTitle: x-ray structure of an mtbd truncation mutant of dynein motor domain
98	c3pfiB	Alignment	not modelled	99.9	20	PDB header: hydrolase Chain: B; PDB Molecule: holliday junction atp-dependent dna helicase ruvb; PDBTitle: 2.7 angstrom resolution crystal structure of a probable holliday2 junction dna helicase (ruvb) from campylobacter jejuni subsp. jejuni3 nctc 11168 in complex with adenosine-5'-diphosphate
99	c5u2IA	Alignment	not modelled	99.9	20	PDB header: protein binding Chain: A; PDB Molecule: heat shock protein 104; PDBTitle: crystal structure of the hsp104 n-terminal domain from candida2 albicans
100	c6eesA	Alignment	not modelled	99.9	17	PDB header: motor protein Chain: A; PDB Molecule: midasin; PDBTitle: fitted model of s. pombe mdn1 into the cryo-em map obtained in the2 presence of atp and rbin-1
101	c4y0bA	Alignment	not modelled	99.9	27	PDB header: protein binding Chain: A; PDB Molecule: double clp-n motif protein; PDBTitle: the structure of arabidopsis clpt1
102	c5gkmA	Alignment	not modelled	99.9	33	PDB header: chaperone Chain: A; PDB Molecule: at5g51070/k3k7_27; PDBTitle: crystal structure of the n-terminal domain of caseinolytic protease2 associated chaperone clpd from arabidopsis thaliana
103	c5w0tA	Alignment	not modelled	99.9	20	PDB header: hydrolase Chain: A; PDB Molecule: protein msp1; PDBTitle: crystal structure of monomeric msp1 from s. cerevisiae
104	c4hh5A	Alignment	not modelled	99.9	17	PDB header: protein binding Chain: A; PDB Molecule: putative type vi secretion protein; PDBTitle: n-terminal domain (1-163) of clpv1 atpase from e.coli eaec sci1 t6ss.
105	c3m6aC	Alignment	not modelled	99.9	21	PDB header: hydrolase Chain: C; PDB Molecule: atp-dependent protease la 1; PDBTitle: crystal structure of bacillus subtilis lon c-terminal domain

106	c5t0gA_	Alignment	not modelled	99.9	21	PDB header: hydrolase Chain: A; PDB Molecule: 26s protease regulatory subunit 7; PDBTitle: structural basis for dynamic regulation of the human 26s proteasome
107	c4y0cB_	Alignment	not modelled	99.8	28	PDB header: protein binding Chain: B; PDB Molecule: clp protease-related protein at4g12060, chloroplastic; PDBTitle: the structure of arabidopsis clpt2
108	c6nyyA_	Alignment	not modelled	99.8	20	PDB header: translocase Chain: A; PDB Molecule: afg3-like protein 2; PDBTitle: human m-aaa protease afg3l2, substrate-bound
109	c2r44A_	Alignment	not modelled	99.8	18	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
110	c4z8xC_	Alignment	not modelled	99.8	21	PDB header: hydrolase Chain: C; PDB Molecule: atp-dependent zinc metalloprotease ftsh; PDBTitle: truncated ftsh from a. aeolicus
111	d1k6ka_	Alignment	not modelled	99.8	22	Fold: Double Clp-N motif Superfamily: Double Clp-N motif Family: Double Clp-N motif
112	c4irfA_	Alignment	not modelled	99.8	14	PDB header: chaperone Chain: A; PDB Molecule: malarial clpb2 atpase/hsp101 protein; PDBTitle: preliminary structural investigations of a malarial protein secretion2 system
113	c6blbA_	Alignment	not modelled	99.8	20	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
114	c2zamA_	Alignment	not modelled	99.8	24	PDB header: protein transport Chain: A; PDB Molecule: vacuolar protein sorting-associating protein 4b; PDBTitle: crystal structure of mouse skd1/vps4b apo-form
115	c3pvsA_	Alignment	not modelled	99.8	26	PDB header: recombination Chain: A; PDB Molecule: replication-associated recombination protein a; PDBTitle: structure and biochemical activities of escherichia coli mgsa
116	c3vfdA_	Alignment	not modelled	99.8	17	PDB header: hydrolase Chain: A; PDB Molecule: spastin; PDBTitle: human spastin aaa domain
117	d1qvra1	Alignment	not modelled	99.8	20	Fold: Double Clp-N motif Superfamily: Double Clp-N motif Family: Double Clp-N motif
118	c5oafB_	Alignment	not modelled	99.8	26	PDB header: gene regulation Chain: B; PDB Molecule: ruvb-like 2; PDBTitle: human rvb1/rvb2 heterohexamer in ino80 complex
119	d2ce7a2	Alignment	not modelled	99.8	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
120	c5wc0D_	Alignment	not modelled	99.8	24	PDB header: motor protein Chain: D; PDB Molecule: meiotic spindle formation protein mei-1; PDBTitle: katanin hexamer in spiral conformation