Phyre2

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Description	RVBD0958_(-)_1069887_1071266
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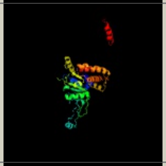
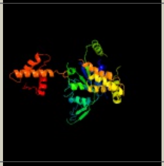
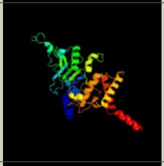
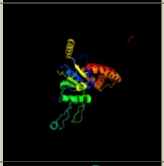
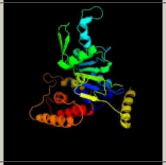
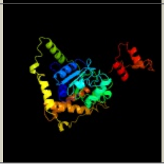
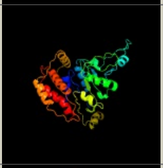
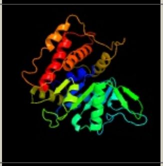
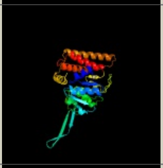
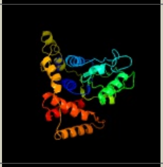
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5udb7_	Alignment		100.0	18	**PDB header:**replication **Chain:** 7: **PDB Molecule:**dna replication licensing factor mcm7; **PDBTitle:** structural basis of mcm2-7 replicative helicase loading by orc-cdc62 and cdt1
2	c3jc76_	Alignment		100.0	18	**PDB header:**hydrolase **Chain:** 6: **PDB Molecule:**dna replication licensing factor mcm6; **PDBTitle:** structure of the eukaryotic replicative cmg helicase and pumpjack2 motion
3	c5udb3_	Alignment		100.0	18	**PDB header:**replication **Chain:** 3: **PDB Molecule:**dna replication licensing factor mcm3; **PDBTitle:** structural basis of mcm2-7 replicative helicase loading by orc-cdc62 and cdt1
4	c5u8s4_	Alignment		100.0	16	**PDB header:**replication **Chain:** 4: **PDB Molecule:**dna replication licensing factor mcm4; **PDBTitle:** structure of eukaryotic cmg helicase at a replication fork
5	c3nbxX_	Alignment		100.0	20	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**atpase rava; **PDBTitle:** crystal structure of e. coli rava (regulatory atpase variant a) in2 complex with adp
6	c5h7i7_	Alignment		100.0	19	**PDB header:**hydrolase **Chain:** 7: **PDB Molecule:**dna replication licensing factor mcm7; **PDBTitle:** cryo-em structure of the cdt1-mcm2-7 complex in amppnp state
7	c4r7zB_	Alignment		100.0	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cell division control protein 21; **PDBTitle:** pfmcm-aaa double-octamer
8	c5v8f3_	Alignment		100.0	19	**PDB header:**replication **Chain:** 3: **PDB Molecule:**dna replication licensing factor mcm3; **PDBTitle:** structural basis of mcm2-7 replicative helicase loading by orc-cdc62 and cdt1
9	c3ja82_	Alignment		100.0	19	**PDB header:**hydrolase **Chain:** 2: **PDB Molecule:**minichromosome maintenance 2; **PDBTitle:** cryo-em structure of the mcm2-7 double hexamer
10	c3ja87_	Alignment		100.0	18	**PDB header:**hydrolase **Chain:** 7: **PDB Molecule:**minichromosome maintenance 7; **PDBTitle:** cryo-em structure of the mcm2-7 double hexamer
11	c3jc55_	Alignment		100.0	18	**PDB header:**hydrolase **Chain:** 5: **PDB Molecule:**minichromosome maintenance protein 5; **PDBTitle:** structure of the eukaryotic replicative cmg helicase and pumpjack2 motion

12	c3ja85_	Alignment		100.0	22	**PDB header:**hydrolase **Chain:** 5: **PDB Molecule:**minichromosome maintenance 5; **PDBTitle:** cryo-em structure of the mcm2-7 double hexamer
13	c3ja84_	Alignment		100.0	16	**PDB header:**hydrolase **Chain:** 4: **PDB Molecule:**minichromosome maintenance 4; **PDBTitle:** cryo-em structure of the mcm2-7 double hexamer
14	c3ja83_	Alignment		100.0	20	**PDB header:**hydrolase **Chain:** 3: **PDB Molecule:**minichromosome maintenance 3; **PDBTitle:** cryo-em structure of the mcm2-7 double hexamer
15	c5udb5_	Alignment		100.0	22	**PDB header:**replication **Chain:** 5: **PDB Molecule:**minichromosome maintenance protein 5; **PDBTitle:** structural basis of mcm2-7 replicative helicase loading by orc-cdc62 and cdt1
16	c3jc72_	Alignment		100.0	19	**PDB header:**hydrolase **Chain:** 2: **PDB Molecule:**dna replication licensing factor mcm2; **PDBTitle:** structure of the eukaryotic replicative cmg helicase and pumpjack2 motion
17	c3ja86_	Alignment		100.0	19	**PDB header:**hydrolase **Chain:** 6: **PDB Molecule:**minichromosome maintenance 6; **PDBTitle:** cryo-em structure of the mcm2-7 double hexamer
18	c3f8tA_	Alignment		100.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**predicted atpase involved in replication control, cdc46/mcm **PDBTitle:** crystal structure analysis of a full-length mcm homolog from2 methanopyrus kandleri
19	c6hv92_	Alignment		100.0	18	**PDB header:**dna binding protein **Chain:** 2: **PDB Molecule:**dna replication licensing factor mcm2; **PDBTitle:** s. cerevisiae cmg-pol epsilon-dna
20	c6hv93_	Alignment		100.0	19	**PDB header:**dna binding protein **Chain:** 3: **PDB Molecule:**dna replication licensing factor mcm3; **PDBTitle:** s. cerevisiae cmg-pol epsilon-dna
21	c3jc57_	Alignment	not modelled	100.0	18	**PDB header:**hydrolase **Chain:** 7: **PDB Molecule:**dna replication licensing factor mcm7; **PDBTitle:** structure of the eukaryotic replicative cmg helicase and pumpjack2 motion
22	c6hv96_	Alignment	not modelled	100.0	18	**PDB header:**dna binding protein **Chain:** 6: **PDB Molecule:**dna replication licensing factor mcm6; **PDBTitle:** s. cerevisiae cmg-pol epsilon-dna
23	c3jc73_	Alignment	not modelled	100.0	20	**PDB header:**hydrolase **Chain:** 3: **PDB Molecule:**dna replication licensing factor mcm3; **PDBTitle:** structure of the eukaryotic replicative cmg helicase and pumpjack2 motion
24	d1g8pa_	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
25	c3f9vA_	Alignment	not modelled	100.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**minichromosome maintenance protein mcm; **PDBTitle:** crystal structure of a near full-length archaeal mcm: functional2 insights for an aaa+ hexameric helicase
26	c2r44A_	Alignment	not modelled	100.0	20	**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
27	c3k1jA_	Alignment	not modelled	100.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent protease lon; **PDBTitle:** crystal structure of lon protease from thermococcus onnurineus na1
28	c1ny5A_	Alignment	not modelled	100.0	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** crystal structure of sigm54 activator (aaa+ atpase) in the inactive2 state

29	c6hv97_	Alignment	not modelled	100.0	18	**PDB header:**dna binding protein **Chain:** 7: **PDB Molecule:**dna replication licensing factor mcm7; **PDBTitle:** s. cerevisiae cmg-pol epsilon-dna
30	c3dzdA_	Alignment	not modelled	100.0	18	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** crystal structure of sigma54 activator ntrc4 in the inactive2 state
31	c5ep0A_	Alignment	not modelled	100.0	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative repressor protein luxo; **PDBTitle:** quorum-sensing signal integrator luxo - receiver+catalytic domains
32	c5m7nA_	Alignment	not modelled	99.9	18	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**nitrogen assimilation regulatory protein; **PDBTitle:** crystal structure of ntrx from brucella abortus in complex with atp2 processed with the crystaldirect automated mounting and cryo-cooling3 technology
33	c3jc54_	Alignment	not modelled	99.9	21	**PDB header:**hydrolase **Chain:** 4: **PDB Molecule:**dna replication licensing factor mcm4; **PDBTitle:** structure of the eukaryotic replicative cmg helicase and pumpjack2 motion
34	c1ojlD_	Alignment	not modelled	99.9	21	**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
35	c5ep4A_	Alignment	not modelled	99.9	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative repressor protein luxo; **PDBTitle:** structure, regulation, and inhibition of the quorum-sensing signal2 integrator luxo
36	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
37	c5exsA_	Alignment	not modelled	99.9	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator fleq; **PDBTitle:** aaa+ atpase fleq from pseudomonas aeruginosa bound to atp-gamma-s
38	c4fw9A_	Alignment	not modelled	99.9	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ttc1975 peptidase; **PDBTitle:** crystal structure of the lon-like protease mtalonc
39	c5oafB_	Alignment	not modelled	99.9	18	**PDB header:**gene regulation **Chain:** B: **PDB Molecule:**ruvb-like 2; **PDBTitle:** human rvb1/rvb2 heterohexamer in ino80 complex
40	c2c99A_	Alignment	not modelled	99.9	20	**PDB header:**transcription regulation **Chain:** A: **PDB Molecule:**psp operon transcriptional activator; **PDBTitle:** structural basis of the nucleotide driven conformational2 changes in the aaa domain of transcription activator pspf
41	c4ww4A_	Alignment	not modelled	99.9	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ruvb-like 1; **PDBTitle:** double-heterohexameric rings of full-length rvb1(adp)/rvb2(adp)
42	c1ojlF_	Alignment	not modelled	99.9	19	**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
43	c5g4gF_	Alignment	not modelled	99.9	25	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**vcp-like atpase; **PDBTitle:** structure of the atpgs-bound vat complex
44	c4ww4B_	Alignment	not modelled	99.9	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**ruvb-like 2; **PDBTitle:** double-heterohexameric rings of full-length rvb1(adp)/rvb2(adp)
45	c2c9oA_	Alignment	not modelled	99.9	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ruvb-like 1; **PDBTitle:** 3d structure of the human ruvb-like helicase ruvbl1
46	c6genX_	Alignment	not modelled	99.9	19	**PDB header:**nuclear protein **Chain:** X: **PDB Molecule:**ruvb-like protein 1; **PDBTitle:** chromatin remodeller-nucleosome complex at 4.5 a resolution.
47	d1um8a_	Alignment	not modelled	99.8	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
48	d1g41a_	Alignment	not modelled	99.8	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
49	c6blbA_	Alignment	not modelled	99.8	23	**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
50	c6nyyC_	Alignment	not modelled	99.8	17	**PDB header:**translocase **Chain:** C: **PDB Molecule:**afg3-like protein 2; **PDBTitle:** human m-aaa protease afg3l2, substrate-bound
51	c1xxhB_	Alignment	not modelled	99.8	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**dna polymerase iii subunit gamma; **PDBTitle:** atpgs bound e. coli clamp loader complex
52	c5e7pA_	Alignment	not modelled	99.8	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cell division control protein cdc48; **PDBTitle:** crystal structure of msmeg_0858 (uniprot a0qqs4), a aaa atpase.
53	c3pfiB_	Alignment	not modelled	99.8	22	**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
54	d1r6bx3	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
55	c3cf1C_	Alignment	not modelled	99.8	18	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**transitional endoplasmic reticulum atpase; **PDBTitle:** structure of p97/vcp in complex with adp/adp.alfx
56	c3cf2B_	Alignment	not modelled	99.8	22	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**transitional endoplasmic reticulum atpase; **PDBTitle:** structure of p97/vcp in complex with adp/amp-pnp
57	d1qvra3	Alignment	not modelled	99.8	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
58	c5ifwB_	Alignment	not modelled	99.8	20	**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
59	d1ofha_	Alignment	not modelled	99.8	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
60	c2dhrC_	Alignment	not modelled	99.8	21	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**ftsh; **PDBTitle:** whole cytosolic region of atp-dependent metalloprotease2 ftsh (g399l)
61	c6epdM_	Alignment	not modelled	99.8	24	**PDB header:**hydrolase **Chain:** M: **PDB Molecule:**26s proteasome regulatory subunit 6a; **PDBTitle:** substrate processing state 26s proteasome (sps1)
62	c1qvrB_	Alignment	not modelled	99.8	20	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**clpb protein; **PDBTitle:** crystal structure analysis of clpb
63	c3b9pA_	Alignment	not modelled	99.8	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cg5977-pa, isoform a; **PDBTitle:** spastin
64	c5kzfJ_	Alignment	not modelled	99.8	22	**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
65	c3hteC_	Alignment	not modelled	99.8	21	**PDB header:**motor protein **Chain:** C: **PDB Molecule:**atp-dependent clp protease atp-binding subunit clpx; **PDBTitle:** crystal structure of nucleotide-free hexameric clpx
66	c1r6bX_	Alignment	not modelled	99.8	20	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**clpa protein; **PDBTitle:** high resolution crystal structure of clpa
67	c3hu2C_	Alignment	not modelled	99.8	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
68	c3uk6H_	Alignment	not modelled	99.8	15	**PDB header:**hydrolase **Chain:** H: **PDB Molecule:**ruvb-like 2; **PDBTitle:** crystal structure of the tip48 (tip49b) hexamer
69	c6em8F_	Alignment	not modelled	99.8	16	**PDB header:**chaperone **Chain:** F: **PDB Molecule:**atp-dependent clp protease atp-binding subunit clpc; **PDBTitle:** s.aureus clpc resting state, c2 symmetrised
70	c6azyA_	Alignment	not modelled	99.7	21	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**heat shock protein hsp104; **PDBTitle:** crystal structure of hsp104 r328m/r757m mutant from calcarisporiella2 thermophila
71	c5kneD_	Alignment	not modelled	99.7	19	**PDB header:**chaperone **Chain:** D: **PDB Molecule:**heat shock protein 104; **PDBTitle:** cryoem reconstruction of hsp104 hexamer
72	c6em8E_	Alignment	not modelled	99.7	22	**PDB header:**chaperone **Chain:** E: **PDB Molecule:**atp-dependent clp protease atp-binding subunit clpc; **PDBTitle:** s.aureus clpc resting state, c2 symmetrised
73	c6matE_	Alignment	not modelled	99.7	19	**PDB header:**ribosomal protein **Chain:** E: **PDB Molecule:**rix7 mutant; **PDBTitle:** cryo-em structure of the essential ribosome assembly aaa-atpase rix7
74	c6epcJ_	Alignment	not modelled	99.7	21	**PDB header:**hydrolase **Chain:** J: **PDB Molecule:**26s proteasome regulatory subunit 8; **PDBTitle:** ground state 26s proteasome (gs2)
75	c3eihB_	Alignment	not modelled	99.7	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
76	c6qi8E_	Alignment	not modelled	99.7	16	**PDB header:**chaperone **Chain:** E: **PDB Molecule:**ruvb-like 2; **PDBTitle:** truncated human r2tp complex, structure 3 (adp-filled)
77	c1in8A_	Alignment	not modelled	99.7	23	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**holliday junction dna helicase ruvb; **PDBTitle:** thermotoga maritima ruvb t158v
78	c4b4tI_	Alignment	not modelled	99.7	22	**PDB header:**hydrolase **Chain:** I: **PDB Molecule:**26s protease regulatory subunit 4 homolog; **PDBTitle:** near-atomic resolution structural model of the yeast 26s proteasome
79	c2qz4A_	Alignment	not modelled	99.7	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**paraplegin; **PDBTitle:** human paraplegin, aaa domain in complex with adp

80	c5vy9C_	Alignment	not modelled	99.7	22	**PDB header:**chaperone **Chain:** C: **PDB Molecule:**heat shock protein 104; **PDBTitle:** s. cerevisiae hsp104:casein complex, middle domain conformation
81	c1xwiA_	Alignment	not modelled	99.7	18	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**skd1 protein; **PDBTitle:** crystal structure of vps4b
82	c5wc0D_	Alignment	not modelled	99.7	24	**PDB header:**motor protein **Chain:** D: **PDB Molecule:**meiotic spindle formation protein mei-1; **PDBTitle:** katanin hexamer in spiral conformation
83	c4b4tL_	Alignment	not modelled	99.7	16	**PDB header:**hydrolase **Chain:** L: **PDB Molecule:**26s protease subunit rpt4; **PDBTitle:** near-atomic resolution structural model of the yeast 26s proteasome
84	c2c9oC_	Alignment	not modelled	99.7	17	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**ruvb-like 1; **PDBTitle:** 3d structure of the human ruvb-like helicase ruvbl1
85	c5kneF_	Alignment	not modelled	99.7	22	**PDB header:**chaperone **Chain:** F: **PDB Molecule:**heat shock protein 104; **PDBTitle:** cryoem reconstruction of hsp104 hexamer
86	c4xguB_	Alignment	not modelled	99.7	23	**PDB header:**atp-binding protein **Chain:** B: **PDB Molecule:**putative pachytene checkpoint protein 2; **PDBTitle:** structure of c. elegans pch-2
87	c4b4tH_	Alignment	not modelled	99.7	17	**PDB header:**hydrolase **Chain:** H: **PDB Molecule:**26s protease regulatory subunit 7 homolog; **PDBTitle:** near-atomic resolution structural model of the yeast 26s proteasome
88	c4d2qC_	Alignment	not modelled	99.7	19	**PDB header:**chaperone **Chain:** C: **PDB Molecule:**clpb; **PDBTitle:** negative-stain electron microscopy of e. coli clpb mutant e432a (bap2 form bound to clpp)
89	c4b4tJ_	Alignment	not modelled	99.7	20	**PDB header:**hydrolase **Chain:** J: **PDB Molecule:**26s protease regulatory subunit 8 homolog; **PDBTitle:** near-atomic resolution structural model of the yeast 26s proteasome
90	c3j96F_	Alignment	not modelled	99.7	17	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**vesicle-fusing atpase; **PDBTitle:** structure of 20s supercomplex determined by single particle2 cryoelectron microscopy (state i)
91	c5mpaL_	Alignment	not modelled	99.7	15	**PDB header:**hydrolase **Chain:** L: **PDB Molecule:**26s protease subunit rpt4; **PDBTitle:** 26s proteasome in presence of atp (s2)
92	c4l16A_	Alignment	not modelled	99.7	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**fidgetin-like protein 1; **PDBTitle:** crystal structure of figl-1 aaa domain in complex with adp
93	c2chvE_	Alignment	not modelled	99.7	24	**PDB header:**dna-binding protein **Chain:** E: **PDB Molecule:**replication factor c small subunit; **PDBTitle:** replication factor c adpnp complex
94	c5d4wB_	Alignment	not modelled	99.7	20	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**putative heat shock protein; **PDBTitle:** crystal structure of hsp104
95	c6hecH_	Alignment	not modelled	99.7	23	**PDB header:**hydrolase **Chain:** H: **PDB Molecule:**proteasome-activating nucleotidase; **PDBTitle:** pan-proteasome in state 4
96	c4ypnA_	Alignment	not modelled	99.7	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lon protease; **PDBTitle:** crystal structure of a lona fragment containing the 3-helix bundle and2 the aaa-alpha/beta domain
97	c3pvsA_	Alignment	not modelled	99.7	20	**PDB header:**recombination **Chain:** A: **PDB Molecule:**replication-associated recombination protein a; **PDBTitle:** structure and biochemical activities of escherichia coli mgsa
98	c1hqcB_	Alignment	not modelled	99.7	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**ruvb; **PDBTitle:** structure of ruvb from thermus thermophilus hb8
99	c3sylB_	Alignment	not modelled	99.7	19	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**protein cbbx; **PDBTitle:** crystal structure of the aaa+ protein cbbx, native structure
100	d1in4a2	Alignment	not modelled	99.7	23	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
101	c4ciuA_	Alignment	not modelled	99.7	17	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**chaperone protein clpb; **PDBTitle:** crystal structure of e. coli clpb
102	c4z8xC_	Alignment	not modelled	99.7	21	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**atp-dependent zinc metalloprotease ftsh; **PDBTitle:** truncated ftsh from a. aeolicus
103	d1ixsb2	Alignment	not modelled	99.7	23	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
104	c4b4tK_	Alignment	not modelled	99.7	16	**PDB header:**hydrolase **Chain:** K: **PDB Molecule:**26s protease regulatory subunit 6b homolog; **PDBTitle:** near-atomic resolution structural model of the yeast 26s proteasome
105	c2zamA_	Alignment	not modelled	99.7	20	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**vacuolar protein sorting-associating protein 4b; **PDBTitle:** crystal structure of mouse skd1/vps4b apo-form

106	c6e111_	Alignment	not modelled	99.7	19	**PDB header:**protein transport **Chain:** 1: **PDB Molecule:**heat shock protein 101; **PDBTitle:** ptex core complex in the resetting (compact) state
107	c6nyyA_	Alignment	not modelled	99.7	12	**PDB header:**translocase **Chain:** A: **PDB Molecule:**afg3-like protein 2; **PDBTitle:** human m-aaa protease afg3l2, substrate-bound
108	c2p65A_	Alignment	not modelled	99.7	11	**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
109	c3pxiB_	Alignment	not modelled	99.7	20	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**negative regulator of genetic competence clpc/mecb; **PDBTitle:** structure of meca108:clpc
110	c3d8bB_	Alignment	not modelled	99.7	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**fidgetin-like protein 1; **PDBTitle:** crystal structure of human fidgetin-like protein 1 in complex with adp
111	c2ce7B_	Alignment	not modelled	99.7	17	**PDB header:**cell division protein **Chain:** B: **PDB Molecule:**cell division protein ftsh; **PDBTitle:** edta treated
112	c6i26A_	Alignment	not modelled	99.7	19	**PDB header:**motor protein **Chain:** A: **PDB Molecule:**midasin,midasin,midasin,midasin; **PDBTitle:** rea1 wild type amppnp state
113	c1sxjD_	Alignment	not modelled	99.7	15	**PDB header:**replication **Chain:** D: **PDB Molecule:**activator 1 41 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)
114	c1sxjC_	Alignment	not modelled	99.7	18	**PDB header:**replication **Chain:** C: **PDB Molecule:**activator 1 40 kda subunit; **PDBTitle:** crystal structure of the eukaryotic clamp loader (replication factor2 c, rfc) bound to the dna sliding clamp (proliferating cell nuclear3 antigen, pcna)
115	c6az0A_	Alignment	not modelled	99.7	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mitochondrial inner membrane i-aaa protease supercomplex **PDBTitle:** mitochondrial atpase protease yme1
116	c4lcbA_	Alignment	not modelled	99.7	23	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**cell division protein cdvc, vps4; **PDBTitle:** structure of vps4 homolog from acidianus hospitalis
117	c5c3cB_	Alignment	not modelled	99.7	25	**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
118	c4b4tM_	Alignment	not modelled	99.7	19	**PDB header:**hydrolase **Chain:** M: **PDB Molecule:**26s protease regulatory subunit 6a; **PDBTitle:** near-atomic resolution structural model of the yeast 26s proteasome
119	c5gjqL_	Alignment	not modelled	99.7	18	**PDB header:**hydrolase **Chain:** L: **PDB Molecule:**26s protease regulatory subunit 10b; **PDBTitle:** structure of the human 26s proteasome bound to usp14-ubal
120	c5j1sA_	Alignment	not modelled	99.7	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**torsin-1a; **PDBTitle:** torsina-lull1 complex, h. sapiens, bound to vhh-bs2