Phyre2

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Description	RVBD0370c_(-)_447148_448044
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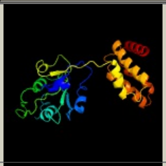
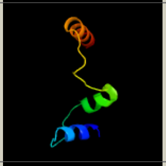
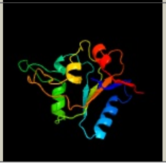
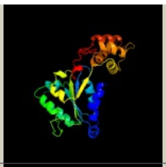
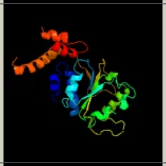
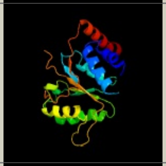
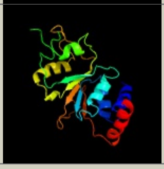
Unique Job ID	e384bc823058054b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6orbA_	Alignment		99.9	22	**PDB header:**motor protein **Chain:** A: **PDB Molecule:**midasin; **PDBTitle:** full-length s. pombe mdn1 in the presence of atp and rbin-1
2	c6i26A_	Alignment		99.9	25	**PDB header:**motor protein **Chain:** A: **PDB Molecule:**midasin,midasin,midasin,midasin; **PDBTitle:** rea1 wild type amppnp state
3	c6edoA_	Alignment		99.9	16	**PDB header:**motor protein **Chain:** A: **PDB Molecule:**midasin; **PDBTitle:** full-length s. pombe mdn1 in the presence of amppnp (ring region)
4	c3nbxX_	Alignment		99.9	15	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**atpase rava; **PDBTitle:** crystal structure of e. coli rava (regulatory atpase variant a) in2 complex with adp
5	c6nyyC_	Alignment		99.9	20	**PDB header:**translocase **Chain:** C: **PDB Molecule:**afg3-like protein 2; **PDBTitle:** human m-aaa protease afg3l2, substrate-bound
6	c2r44A_	Alignment		99.9	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
7	c5g4gF_	Alignment		99.9	22	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**vcp-like atpase; **PDBTitle:** structure of the atpgs-bound vat complex
8	c6i27A_	Alignment		99.9	25	**PDB header:**motor protein **Chain:** A: **PDB Molecule:**midasin,midasin,midasin,midasin,midasin,midasin,midasin; **PDBTitle:** rea1 aaa2l-h2alpha deletion mutant in amppnp state
9	c5c3cB_	Alignment		99.9	23	**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
10	c6nyyA_	Alignment		99.9	19	**PDB header:**translocase **Chain:** A: **PDB Molecule:**afg3-like protein 2; **PDBTitle:** human m-aaa protease afg3l2, substrate-bound
11	c4ypnA_	Alignment		99.9	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

12	c5e7pA_	Alignment		99.9	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cell division control protein cdc48; **PDBTitle:** crystal structure of msmeg_0858 (uniprot a0qqs4), a aaa atpase.
13	c3cf1C_	Alignment		99.8	20	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**transitional endoplasmic reticulum atpase; **PDBTitle:** structure of p97/vcp in complex with adp/adp.alfx
14	c6azyA_	Alignment		99.8	24	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**heat shock protein hsp104; **PDBTitle:** crystal structure of hsp104 r328m/r757m mutant from calcarisporiella2 thermophila
15	c1r6bX_	Alignment		99.8	18	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**clpa protein; **PDBTitle:** high resolution crystal structure of clpa
16	c1qvrB_	Alignment		99.8	28	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**clpb protein; **PDBTitle:** crystal structure analysis of clpb
17	d1g41a_	Alignment		99.8	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
18	c4ciuA_	Alignment		99.8	24	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**chaperone protein clpb; **PDBTitle:** crystal structure of e. coli clpb
19	c6genX_	Alignment		99.8	19	**PDB header:**nuclear protein **Chain:** X: **PDB Molecule:**ruvb-like protein 1; **PDBTitle:** chromatin remodeller-nucleosome complex at 4.5 a resolution.
20	c5kneF_	Alignment		99.8	22	**PDB header:**chaperone **Chain:** F: **PDB Molecule:**heat shock protein 104; **PDBTitle:** cryoem reconstruction of hsp104 hexamer
21	c5kneD_	Alignment	not modelled	99.8	20	**PDB header:**chaperone **Chain:** D: **PDB Molecule:**heat shock protein 104; **PDBTitle:** cryoem reconstruction of hsp104 hexamer
22	c3pfiB_	Alignment	not modelled	99.8	19	**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
23	c2c9oA_	Alignment	not modelled	99.8	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ruvb-like 1; **PDBTitle:** 3d structure of the human ruvb-like helicase ruvbl1
24	d1r6bx3	Alignment	not modelled	99.8	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
25	c4b4tH_	Alignment	not modelled	99.8	21	**PDB header:**hydrolase **Chain:** H: **PDB Molecule:**26s protease regulatory subunit 7 homolog; **PDBTitle:** near-atomic resolution structural model of the yeast 26s proteasome
26	c6em8F_	Alignment	not modelled	99.8	26	**PDB header:**chaperone **Chain:** F: **PDB Molecule:**atp-dependent clp protease atp-binding subunit clpc; **PDBTitle:** s.aureus clpc resting state, c2 symmetrised
27	c4d2qC_	Alignment	not modelled	99.8	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)
28	c6epdM_	Alignment	not modelled	99.8	18	**PDB header:**hydrolase **Chain:** M: **PDB Molecule:**26s proteasome regulatory subunit 6a; **PDBTitle:** substrate processing state 26s proteasome (sps1)

29	c5oafB_	Alignment	not modelled	99.8	21	**PDB header:**gene regulation **Chain:** B: **PDB Molecule:**ruvb-like 2; **PDBTitle:** human rvb1/rvb2 heterohexamer in ino80 complex
30	c5kzfJ_	Alignment	not modelled	99.8	24	**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
31	c6matE_	Alignment	not modelled	99.8	19	**PDB header:**ribosomal protein **Chain:** E: **PDB Molecule:**rix7 mutant; **PDBTitle:** cryo-em structure of the essential ribosome assembly aaa-atpase rix7
32	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)
33	c3vkhB_	Alignment	not modelled	99.8	17	**PDB header:**motor protein **Chain:** B: **PDB Molecule:**dynein heavy chain, cytoplasmic; **PDBTitle:** x-ray structure of a functional full-length dynein motor domain
34	c6e111_	Alignment	not modelled	99.8	21	**PDB header:**protein transport **Chain:** 1: **PDB Molecule:**heat shock protein 101; **PDBTitle:** ptex core complex in the resetting (compact) state
35	c3hu2C_	Alignment	not modelled	99.8	20	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**transitional endoplasmic reticulum atpase; **PDBTitle:** structure of p97 n-d1 r86a mutant in complex with atpgs
36	c5ifwB_	Alignment	not modelled	99.8	26	**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
37	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
38	c6hypA_	Alignment	not modelled	99.8	18	**PDB header:**motor protein **Chain:** A: **PDB Molecule:**midasin,midasin; **PDBTitle:** rea1 wild type adp state (aaa+ ring part)
39	c5vy9C_	Alignment	not modelled	99.8	19	**PDB header:**chaperone **Chain:** C: **PDB Molecule:**heat shock protein 104; **PDBTitle:** s. cerevisiae hsp104:casein complex, middle domain conformation
40	c5d4wB_	Alignment	not modelled	99.8	19	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**putative heat shock protein; **PDBTitle:** crystal structure of hsp104
41	c6epcJ_	Alignment	not modelled	99.8	21	**PDB header:**hydrolase **Chain:** J: **PDB Molecule:**26s proteasome regulatory subunit 8; **PDBTitle:** ground state 26s proteasome (gs2)
42	c4b4tJ_	Alignment	not modelled	99.8	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
43	c3zw6B_	Alignment	not modelled	99.8	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.
44	c3cf2B_	Alignment	not modelled	99.8	26	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**transitional endoplasmic reticulum atpase; **PDBTitle:** structure of p97/vcp in complex with adp/amp-pnp
45	c4b4tL_	Alignment	not modelled	99.8	19	**PDB header:**hydrolase **Chain:** L: **PDB Molecule:**26s protease subunit rpt4; **PDBTitle:** near-atomic resolution structural model of the yeast 26s proteasome
46	c4b4tI_	Alignment	not modelled	99.8	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
47	c3vkhA_	Alignment	not modelled	99.8	17	**PDB header:**motor protein **Chain:** A: **PDB Molecule:**dynein heavy chain, cytoplasmic; **PDBTitle:** x-ray structure of a functional full-length dynein motor domain
48	c4xguB_	Alignment	not modelled	99.8	22	**PDB header:**atp-binding protein **Chain:** B: **PDB Molecule:**putative pachytene checkpoint protein 2; **PDBTitle:** structure of c. elegans pch-2
49	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
50	c3vfdA_	Alignment	not modelled	99.8	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**spastin; **PDBTitle:** human spastin aaa domain
51	c4lcbA_	Alignment	not modelled	99.8	16	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**cell division protein cdvc, vps4; **PDBTitle:** structure of vps4 homolog from acidianus hospitalis
52	c5vq9D_	Alignment	not modelled	99.8	18	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**pachytene checkpoint protein 2 homolog; **PDBTitle:** structure of human trip13, apo form
53	c3hteC_	Alignment	not modelled	99.8	15	**PDB header:**motor protein **Chain:** C: **PDB Molecule:**atp-dependent clp protease atp-binding subunit clpx; **PDBTitle:** crystal structure of nucleotide-free hexameric clpx
54	c2ce7B_	Alignment	not modelled	99.8	19	**PDB header:**cell division protein **Chain:** B: **PDB Molecule:**cell division protein ftsh;

						PDBTitle: edta treated
55	c4ww4A_	Alignment	not modelled	99.8	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ruvb-like 1; **PDBTitle:** double-heterohexameric rings of full-length rvb1(adp)/rvb2(adp)
56	c6hecH_	Alignment	not modelled	99.8	19	**PDB header:**hydrolase **Chain:** H: **PDB Molecule:**proteasome-activating nucleotidase; **PDBTitle:** pan-proteasome in state 4
57	c3d8bB_	Alignment	not modelled	99.7	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**fidgetin-like protein 1; **PDBTitle:** crystal structure of human fidgetin-like protein 1 in complex with adp
58	c3b9pA_	Alignment	not modelled	99.7	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cg5977-pa, isoform a; **PDBTitle:** spastin
59	c2c9oC_	Alignment	not modelled	99.7	15	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**ruvb-like 1; **PDBTitle:** 3d structure of the human ruvb-like helicase ruvbl1
60	c4r7zB_	Alignment	not modelled	99.7	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cell division control protein 21; **PDBTitle:** pfmcm-aaa double-octamer
61	c5wc0D_	Alignment	not modelled	99.7	20	**PDB header:**motor protein **Chain:** D: **PDB Molecule:**meiotic spindle formation protein mei-1; **PDBTitle:** katanin hexamer in spiral conformation
62	d1ofha_	Alignment	not modelled	99.7	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
63	c3pxiB_	Alignment	not modelled	99.7	26	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**negative regulator of genetic competence clpc/mecb; **PDBTitle:** structure of meca108:clpc
64	c5nugB_	Alignment	not modelled	99.7	17	**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
65	c3vkgA_	Alignment	not modelled	99.7	18	**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	c2zamA_	Alignment	not modelled	99.7	23	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**vacuolar protein sorting-associating protein 4b; **PDBTitle:** crystal structure of mouse skd1/vps4b apo-form
67	d1g8pa_	Alignment	not modelled	99.7	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
68	c4b4tM_	Alignment	not modelled	99.7	21	**PDB header:**hydrolase **Chain:** M: **PDB Molecule:**26s protease regulatory subunit 6a; **PDBTitle:** near-atomic resolution structural model of the yeast 26s proteasome
69	c3uk6H_	Alignment	not modelled	99.7	16	**PDB header:**hydrolase **Chain:** H: **PDB Molecule:**ruvb-like 2; **PDBTitle:** crystal structure of the tip48 (tip49b) hexamer
70	c3pvsA_	Alignment	not modelled	99.7	18	**PDB header:**recombination **Chain:** A: **PDB Molecule:**replication-associated recombination protein a; **PDBTitle:** structure and biochemical activities of escherichia coli mgsa
71	c4z8xC_	Alignment	not modelled	99.7	20	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**atp-dependent zinc metalloprotease ftsh; **PDBTitle:** truncated ftsh from a. aeolicus
72	c1in8A_	Alignment	not modelled	99.7	22	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**holliday junction dna helicase ruvb; **PDBTitle:** thermotoga maritima ruvb t158v
73	c4l16A_	Alignment	not modelled	99.7	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**fidgetin-like protein 1; **PDBTitle:** crystal structure of figl-1 aaa domain in complex with adp
74	c5mpaL_	Alignment	not modelled	99.7	23	**PDB header:**hydrolase **Chain:** L: **PDB Molecule:**26s protease subunit rpt4; **PDBTitle:** 26s proteasome in presence of atp (s2)
75	c6eesA_	Alignment	not modelled	99.7	21	**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
76	c6em8E_	Alignment	not modelled	99.7	28	**PDB header:**chaperone **Chain:** E: **PDB Molecule:**atp-dependent clp protease atp-binding subunit clpc; **PDBTitle:** s.aureus clpc resting state, c2 symmetrised
77	d1in4a2	Alignment	not modelled	99.7	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
78	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
79	c1xxhB_	Alignment	not modelled	99.7	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**dna polymerase iii subunit gamma; **PDBTitle:** atpgs bound e. coli clamp loader complex
80	c4ww4B_	Alignment	not modelled	99.7	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**ruvb-like 2; **PDBTitle:** double-heterohexameric rings of full-length rvb1(adp)/rvb2(adp)
						PDB header:hydrolase

81	c5gjqL_	Alignment	not modelled	99.7	23	**Chain:** L: **PDB Molecule:**26s protease regulatory subunit 10b; **PDBTitle:** structure of the human 26s proteasome bound to usp14-ubal
82	d1ixsb2	Alignment	not modelled	99.7	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
83	c1xwiA_	Alignment	not modelled	99.7	23	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**skd1 protein; **PDBTitle:** crystal structure of vps4b
84	c4b4tK_	Alignment	not modelled	99.7	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
85	c3vkgB_	Alignment	not modelled	99.7	17	**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
86	c6djuA_	Alignment	not modelled	99.7	21	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**chaperone protein clpb; **PDBTitle:** mtb clpb in complex with atpgammas and casein, conformer 1
87	c6b5cA_	Alignment	not modelled	99.7	21	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**katanin p60 atpase-containing subunit a-like 1; **PDBTitle:** structural basis for katanin self-assembly
88	c4rh7A_	Alignment	not modelled	99.7	18	**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
89	c4yplE_	Alignment	not modelled	99.7	20	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**lon protease; **PDBTitle:** crystal structure of a hexameric lona protease bound to three adps
90	c6az0A_	Alignment	not modelled	99.7	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mitochondrial inner membrane i-aaa protease supercomplex **PDBTitle:** mitochondrial atpase protease yme1
91	c6em8H_	Alignment	not modelled	99.7	25	**PDB header:**chaperone **Chain:** H: **PDB Molecule:**atp-dependent clp protease atp-binding subunit clpc; **PDBTitle:** s.aureus clpc resting state, c2 symmetrised
92	c1sxjE_	Alignment	not modelled	99.7	14	**PDB header:**replication **Chain:** E: **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)
93	c1s3sA_	Alignment	not modelled	99.7	21	**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
94	c6on2A_	Alignment	not modelled	99.7	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent protease la; **PDBTitle:** lon protease from yersinia pestis with y2853 substrate
95	d1qvra3	Alignment	not modelled	99.7	25	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
96	c4akgB_	Alignment	not modelled	99.7	13	**PDB header:**motor protein **Chain:** B: **PDB Molecule:**glutathione s-transferase class-mu 26 kda isozyme, dynein **PDBTitle:** dynein motor domain - atp complex
97	d1iqpa2	Alignment	not modelled	99.7	22	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
98	c2chgB_	Alignment	not modelled	99.7	17	**PDB header:**dna-binding protein **Chain:** B: **PDB Molecule:**replication factor c small subunit; **PDBTitle:** replication factor c domains 1 and 2
99	c3u5zM_	Alignment	not modelled	99.7	21	**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
100	c6opcF_	Alignment	not modelled	99.7	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)
101	c3j96F_	Alignment	not modelled	99.7	22	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**vesicle-fusing atpase; **PDBTitle:** structure of 20s supercomplex determined by single particle2 cryoelectron microscopy (state i)
102	c5t0gA_	Alignment	not modelled	99.7	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**26s protease regulatory subunit 7; **PDBTitle:** structural basis for dynamic regulation of the human 26s proteasome
103	c3k1jA_	Alignment	not modelled	99.7	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent protease lon; **PDBTitle:** crystal structure of lon protease from thermococcus onnurineus na1
104	c2qz4A_	Alignment	not modelled	99.7	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**paraplegin; **PDBTitle:** human paraplegin, aaa domain in complex with adp
105	c4w8fA_	Alignment	not modelled	99.7	13	**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
106	c3h4mC_	Alignment	not modelled	99.7	18	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**proteasome-activating nucleotidase; **PDBTitle:** aaa atpase domain of the proteasome- activating

						nucleotidase
107	c5w0tA_	Alignment	not modelled	99.7	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein msp1; **PDBTitle:** crystal structure of monomeric msp1 from s. cerevisiae
108	d2ce7a2	Alignment	not modelled	99.7	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
109	d1ny5a2	Alignment	not modelled	99.7	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
110	c6or5A_	Alignment	not modelled	99.7	16	**PDB header:**motor protein **Chain:** A: **PDB Molecule:**midasin; **PDBTitle:** full-length s. pombe mdn1 in the presence of amppnp (ring region)
111	c5ep4A_	Alignment	not modelled	99.7	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative repressor protein luxo; **PDBTitle:** structure, regulation, and inhibition of the quorum-sensing signal2 integrator luxo
112	d1sxje2	Alignment	not modelled	99.7	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
113	c1sxjC_	Alignment	not modelled	99.7	13	**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)
114	c1ojlD_	Alignment	not modelled	99.7	16	**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
115	c1hqcB_	Alignment	not modelled	99.7	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**ruvb; **PDBTitle:** structure of ruvb from thermus thermophilus hb8
116	c1iqpF_	Alignment	not modelled	99.6	22	**PDB header:**replication **Chain:** F: **PDB Molecule:**rfcs; **PDBTitle:** crystal structure of the clamp loader small subunit from2 pyrococcus furiosus
117	c1sxjA_	Alignment	not modelled	99.6	16	**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)
118	c5kneA_	Alignment	not modelled	99.6	19	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**heat shock protein 104; **PDBTitle:** cryoem reconstruction of hsp104 hexamer
119	d1sxjc2	Alignment	not modelled	99.6	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
120	c2chvE_	Alignment	not modelled	99.6	17	**PDB header:**dna-binding protein **Chain:** E: **PDB Molecule:**replication factor c small subunit; **PDBTitle:** replication factor c adpnp complex