Phyre^2

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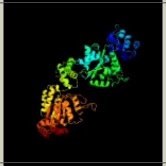
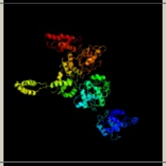
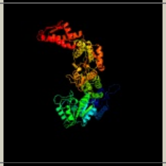
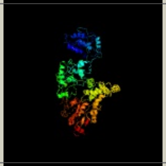
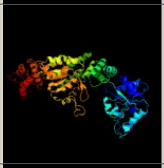
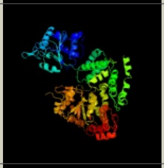
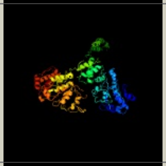
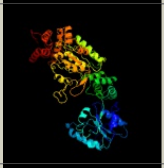
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1qvrB_	Alignment		100.0	56	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**clpb protein; **PDBTitle:** crystal structure analysis of clpb
2	c6azyA_	Alignment		100.0	51	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**heat shock protein hsp104; **PDBTitle:** crystal structure of hsp104 r328m/r757m mutant from calcarisporiella2 thermophila
3	c5kneD_	Alignment		100.0	44	**PDB header:**chaperone **Chain:** D: **PDB Molecule:**heat shock protein 104; **PDBTitle:** cryoem reconstruction of hsp104 hexamer
4	c4d2qC_	Alignment		100.0	54	**PDB header:**chaperone **Chain:** C: **PDB Molecule:**clpb; **PDBTitle:** negative-stain electron microscopy of e. coli clpb mutant e432a (bap2 form bound to clpp)
5	c5vy9C_	Alignment		100.0	46	**PDB header:**chaperone **Chain:** C: **PDB Molecule:**heat shock protein 104; **PDBTitle:** s. cerevisiae hsp104:casein complex, middle domain conformation
6	c3pxiB_	Alignment		100.0	52	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**negative regulator of genetic competence clpc/mecb; **PDBTitle:** structure of meca108:clpc
7	c6em8F_	Alignment		100.0	50	**PDB header:**chaperone **Chain:** F: **PDB Molecule:**atp-dependent clp protease atp-binding subunit clpc; **PDBTitle:** s.aureus clpc resting state, c2 symmetrised
8	c1r6bX_	Alignment		100.0	44	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**clpa protein; **PDBTitle:** high resolution crystal structure of clpa
9	c6e111_	Alignment		100.0	40	**PDB header:**protein transport **Chain:** 1: **PDB Molecule:**heat shock protein 101; **PDBTitle:** ptex core complex in the resetting (compact) state
10	c6em8E_	Alignment		100.0	51	**PDB header:**chaperone **Chain:** E: **PDB Molecule:**atp-dependent clp protease atp-binding subunit clpc; **PDBTitle:** s.aureus clpc resting state, c2 symmetrised
11	c5d4wB_	Alignment		100.0	52	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**putative heat shock protein; **PDBTitle:** crystal structure of hsp104

12	c4ciuA_	Alignment		100.0	59	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**chaperone protein clpb; **PDBTitle:** crystal structure of e. coli clpb
13	c6djuA_	Alignment		100.0	96	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**chaperone protein clpb; **PDBTitle:** mtb clpb in complex with atpgammas and casein, conformer 1
14	c5kneF_	Alignment		100.0	50	**PDB header:**chaperone **Chain:** F: **PDB Molecule:**heat shock protein 104; **PDBTitle:** cryoem reconstruction of hsp104 hexamer
15	c6em8H_	Alignment		100.0	56	**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	53	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**heat shock protein 104; **PDBTitle:** cryoem reconstruction of hsp104 hexamer
17	c6djvE_	Alignment		100.0	100	**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	49	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**negative regulator of genetic competence clpc/mecb; **PDBTitle:** structure of meca121 and clpc1-485 complex
19	d1r6bx3	Alignment		100.0	44	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
20	c5g4gF_	Alignment		100.0	25	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**vcp-like atpase; **PDBTitle:** structure of the atpgs-bound vat complex
21	c6matE_	Alignment	not modelled	100.0	20	**PDB header:**ribosomal protein **Chain:** E: **PDB Molecule:**rix7 mutant; **PDBTitle:** cryo-em structure of the essential ribosome assembly aaa-atpase rix7
22	d1qvra3	Alignment	not modelled	100.0	61	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
23	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
24	d1qvra2	Alignment	not modelled	100.0	62	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
25	c3cf2B_	Alignment	not modelled	100.0	22	**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	22	**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	23	**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	23	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain

29	c6i26A_	Alignment	not modelled	100.0	19	**PDB header:**motor protein **Chain:** A: **PDB Molecule:**midasin,midasin,midasin,midasin; **PDBTitle:** rea1 wild type amppnp state
30	c3j96F_	Alignment	not modelled	100.0	20	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**vesicle-fusing atpase; **PDBTitle:** structure of 20s supercomplex determined by single particle2 cryoelectron microscopy (state i)
31	c6opcF_	Alignment	not modelled	100.0	25	**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	c6orbA_	Alignment	not modelled	100.0	19	**PDB header:**motor protein **Chain:** A: **PDB Molecule:**midasin; **PDBTitle:** full-length s. pombe mdn1 in the presence of atp and rbin-1
34	c6edoA_	Alignment	not modelled	100.0	14	**PDB header:**motor protein **Chain:** A: **PDB Molecule:**midasin; **PDBTitle:** full-length s. pombe mdn1 in the presence of amppnp (ring region)
35	c6i27A_	Alignment	not modelled	100.0	16	**PDB header:**motor protein **Chain:** A: **PDB Molecule:**midasin,midasin,midasin,midasin,midasin,midasin,midasin; **PDBTitle:** rea1 aaa2l-h2alpha deletion mutant in amppnp state
36	d1g41a_	Alignment	not modelled	100.0	22	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
37	c6on2A_	Alignment	not modelled	100.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent protease la; **PDBTitle:** lon protease from yersinia pestis with y2853 substrate
38	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
39	c4yplE_	Alignment	not modelled	100.0	21	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**lon protease; **PDBTitle:** crystal structure of a hexameric lona protease bound to three adps
40	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
41	c2p65A_	Alignment	not modelled	100.0	70	**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
42	c3hteC_	Alignment	not modelled	100.0	25	**PDB header:**motor protein **Chain:** C: **PDB Molecule:**atp-dependent clp protease atp-binding subunit clpx; **PDBTitle:** crystal structure of nucleotide-free hexameric clpx
43	d1e94e_	Alignment	not modelled	100.0	22	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
44	d1jbka_	Alignment	not modelled	100.0	75	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
45	c5j1sA_	Alignment	not modelled	100.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**torsin-1a; **PDBTitle:** torsina-lull1 complex, h. sapiens, bound to vhh-bs2
46	c6or5A_	Alignment	not modelled	100.0	16	**PDB header:**motor protein **Chain:** A: **PDB Molecule:**midasin; **PDBTitle:** full-length s. pombe mdn1 in the presence of amppnp (ring region)
47	c4ypnA_	Alignment	not modelled	99.9	20	**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
48	d1ny5a2	Alignment	not modelled	99.9	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
49	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
50	c6epdM_	Alignment	not modelled	99.9	18	**PDB header:**hydrolase **Chain:** M: **PDB Molecule:**26s proteasome regulatory subunit 6a; **PDBTitle:** substrate processing state 26s proteasome (sps1)
51	c6epcJ_	Alignment	not modelled	99.9	20	**PDB header:**hydrolase **Chain:** J: **PDB Molecule:**26s proteasome regulatory subunit 8; **PDBTitle:** ground state 26s proteasome (gs2)
52	c5exsA_	Alignment	not modelled	99.9	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator fleq; **PDBTitle:** aaa+ atpase fleq from pseudomonas aeruginosa bound to atp-gamma-s
53	c2c99A_	Alignment	not modelled	99.9	18	**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
54	c6nyyC_	Alignment	not modelled	99.9	19	**PDB header:**translocase **Chain:** C: **PDB Molecule:**afg3-like protein 2; **PDBTitle:** human m-aaa protease afg3l2, substrate-bound
55	c3vkhA_	Alignment	not modelled	99.9	14	**PDB header:**motor protein **Chain:** A: **PDB Molecule:**dynein heavy chain, cytoplasmic; **PDBTitle:** x-ray structure of a functional full-length dynein motor

						domain
56	c1ojlD_	Alignment	not modelled	99.9	17	**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
57	c3sylB_	Alignment	not modelled	99.9	25	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**protein cbbx; **PDBTitle:** crystal structure of the aaa+ protein cbbx, native structure
58	c1xwiA_	Alignment	not modelled	99.9	22	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**skd1 protein; **PDBTitle:** crystal structure of vps4b
59	c4b4tJ_	Alignment	not modelled	99.9	21	**PDB header:**hydrolase **Chain:** J: **PDB Molecule:**26s protease regulatory subunit 8 homolog; **PDBTitle:** near-atomic resolution structural model of the yeast 26s proteasome
60	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
61	c4xgcD_	Alignment	not modelled	99.9	15	**PDB header:**dna binding protein **Chain:** D: **PDB Molecule:**origin recognition complex subunit 4; **PDBTitle:** crystal structure of the eukaryotic origin recognition complex
62	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
63	c4rh7A_	Alignment	not modelled	99.9	14	**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
64	c4b4tH_	Alignment	not modelled	99.9	23	**PDB header:**hydrolase **Chain:** H: **PDB Molecule:**26s protease regulatory subunit 7 homolog; **PDBTitle:** near-atomic resolution structural model of the yeast 26s proteasome
65	c4b4tI_	Alignment	not modelled	99.9	23	**PDB header:**hydrolase **Chain:** I: **PDB Molecule:**26s protease regulatory subunit 4 homolog; **PDBTitle:** near-atomic resolution structural model of the yeast 26s proteasome
66	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
67	c3hu2C_	Alignment	not modelled	99.9	19	**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	c5u2lA_	Alignment	not modelled	99.9	19	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**heat shock protein 104; **PDBTitle:** crystal structure of the hsp104 n-terminal domain from candida2 albicans
69	c4b4tL_	Alignment	not modelled	99.9	19	**PDB header:**hydrolase **Chain:** L: **PDB Molecule:**26s protease subunit rpt4; **PDBTitle:** near-atomic resolution structural model of the yeast 26s proteasome
70	c3m6aC_	Alignment	not modelled	99.9	23	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**atp-dependent protease la 1; **PDBTitle:** crystal structure of bacillus subtilis lon c-terminal domain
71	c4b4tK_	Alignment	not modelled	99.9	25	**PDB header:**hydrolase **Chain:** K: **PDB Molecule:**26s protease regulatory subunit 6b homolog; **PDBTitle:** near-atomic resolution structural model of the yeast 26s proteasome
72	c5kzfJ_	Alignment	not modelled	99.9	26	**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
73	c1s3sA_	Alignment	not modelled	99.9	18	**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
74	c6eesA_	Alignment	not modelled	99.9	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
75	c4xbiA_	Alignment	not modelled	99.9	24	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**clpb protein, putative,green fluorescent protein; **PDBTitle:** structure of a malarial protein involved in proteostasis
76	c3eihB_	Alignment	not modelled	99.9	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
77	c2zamA_	Alignment	not modelled	99.9	20	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**vacuolar protein sorting-associating protein 4b; **PDBTitle:** crystal structure of mouse skd1/vps4b apo-form
78	c1ny5A_	Alignment	not modelled	99.9	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** crystal structure of sigm54 activator (aaa+ atpase) in the inactive2 state
79	c5gjqL_	Alignment	not modelled	99.9	19	**PDB header:**hydrolase **Chain:** L: **PDB Molecule:**26s protease regulatory subunit 10b; **PDBTitle:** structure of the human 26s proteasome bound to usp14-ubal

80	c2r44A_	Alignment	not modelled	99.9	19	**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
81	c5nugB_	Alignment	not modelled	99.9	14	**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
82	c6hecH_	Alignment	not modelled	99.9	21	**PDB header:**hydrolase **Chain:** H: **PDB Molecule:**proteasome-activating nucleotidase; **PDBTitle:** pan-proteasome in state 4
83	c4l16A_	Alignment	not modelled	99.9	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**fidgetin-like protein 1; **PDBTitle:** crystal structure of figl-1 aaa domain in complex with adp
84	c5mpaL_	Alignment	not modelled	99.9	19	**PDB header:**hydrolase **Chain:** L: **PDB Molecule:**26s protease subunit rpt4; **PDBTitle:** 26s proteasome in presence of atp (s2)
85	c3b9pA_	Alignment	not modelled	99.9	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cg5977-pa, isoform a; **PDBTitle:** spastin
86	c3vkgA_	Alignment	not modelled	99.9	13	**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
87	c4b4tM_	Alignment	not modelled	99.9	20	**PDB header:**hydrolase **Chain:** M: **PDB Molecule:**26s protease regulatory subunit 6a; **PDBTitle:** near-atomic resolution structural model of the yeast 26s proteasome
88	c4xguB_	Alignment	not modelled	99.9	22	**PDB header:**atp-binding protein **Chain:** B: **PDB Molecule:**putative pachytene checkpoint protein 2; **PDBTitle:** structure of c. elegans pch-2
89	c3vkgB_	Alignment	not modelled	99.9	14	**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
90	c2dhrC_	Alignment	not modelled	99.9	22	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**ftsh; **PDBTitle:** whole cytosolic region of atp-dependent metalloprotease2 ftsh (g399l)
91	c5t0gA_	Alignment	not modelled	99.9	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**26s protease regulatory subunit 7; **PDBTitle:** structural basis for dynamic regulation of the human 26s proteasome
92	c5ep0A_	Alignment	not modelled	99.9	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative repressor protein luxo; **PDBTitle:** quorum-sensing signal integrator luxo - receiver+catalytic domains
93	c3d8bB_	Alignment	not modelled	99.9	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**fidgetin-like protein 1; **PDBTitle:** crystal structure of human fidgetin-like protein 1 in complex with adp
94	c3vfdA_	Alignment	not modelled	99.9	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**spastin; **PDBTitle:** human spastin aaa domain
95	c5m7nA_	Alignment	not modelled	99.9	19	**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
96	c6blbA_	Alignment	not modelled	99.9	22	**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
97	c3nbxX_	Alignment	not modelled	99.9	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
98	d1khya_	Alignment	not modelled	99.9	31	**Fold:**Double Clp-N motif **Superfamily:**Double Clp-N motif **Family:**Double Clp-N motif
99	c4lcbA_	Alignment	not modelled	99.9	19	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**cell division protein cdvc, vps4; **PDBTitle:** structure of vps4 homolog from acidianus hospitalis
100	c3dzdA_	Alignment	not modelled	99.9	17	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** crystal structure of sigma54 activator ntrc4 in the inactive2 state
101	c4akgB_	Alignment	not modelled	99.9	15	**PDB header:**motor protein **Chain:** B: **PDB Molecule:**glutathione s-transferase class-mu 26 kda isozyme, dynein **PDBTitle:** dynein motor domain - atp complex
102	c5guiA_	Alignment	not modelled	99.9	22	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**chaperone protein clpc1, chloroplastic; **PDBTitle:** crystal structure of the n-terminal domain of caseinolytic protease2 associated chaperone clpc1 from arabidopsis thaliana
103	c6nyyA_	Alignment	not modelled	99.9	20	**PDB header:**translocase **Chain:** A: **PDB Molecule:**afg3-like protein 2; **PDBTitle:** human m-aaa protease afg3l2, substrate-bound
104	c5w0tA_	Alignment	not modelled	99.9	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein msp1; **PDBTitle:** crystal structure of monomeric msp1 from s. cerevisiae
105	c6az0A_	Alignment	not modelled	99.9	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mitochondrial inner membrane i-aaa protease supercomplex

						PDBTitle: mitochondrial atpase protease yme1
106	c1in8A_	Alignment	not modelled	99.9	17	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**holliday junction dna helicase ruvb; **PDBTitle:** thermotoga maritima ruvb t158v
107	c6b5cA_	Alignment	not modelled	99.9	19	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**katanin p60 atpase-containing subunit a-like 1; **PDBTitle:** structural basis for katanin self-assembly
108	c6genX_	Alignment	not modelled	99.9	29	**PDB header:**nuclear protein **Chain:** X: **PDB Molecule:**ruvb-like protein 1; **PDBTitle:** chromatin remodeller-nucleosome complex at 4.5 a resolution.
109	c3zw6B_	Alignment	not modelled	99.9	13	**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.
110	c5oafB_	Alignment	not modelled	99.9	27	**PDB header:**gene regulation **Chain:** B: **PDB Molecule:**ruvb-like 2; **PDBTitle:** human rvb1/rvb2 heterohexamer in ino80 complex
111	c4uqwA_	Alignment	not modelled	99.9	22	**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
112	c2k77A_	Alignment	not modelled	99.9	26	**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
113	c4w8fA_	Alignment	not modelled	99.9	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
114	c3fh2A_	Alignment	not modelled	99.9	20	**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
115	c3fesB_	Alignment	not modelled	99.9	23	**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
116	d1qvra1	Alignment	not modelled	99.9	29	**Fold:**Double Clp-N motif **Superfamily:**Double Clp-N motif **Family:**Double Clp-N motif
117	d2ce7a2	Alignment	not modelled	99.9	23	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
118	c5wc0D_	Alignment	not modelled	99.9	19	**PDB header:**motor protein **Chain:** D: **PDB Molecule:**meiotic spindle formation protein mei-1; **PDBTitle:** katanin hexamer in spiral conformation
119	c2qz4A_	Alignment	not modelled	99.9	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**paraplegin; **PDBTitle:** human paraplegin, aaa domain in complex with adp
120	c2c9oA_	Alignment	not modelled	99.9	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ruvb-like 1; **PDBTitle:** 3d structure of the human ruvb-like helicase ruvbl1