







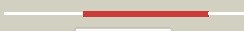
























# Phyre2

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Description	RVBD2897c_(-)_3206441_3207952
Date	Thu Aug 8 16:20:05 BST 2019
Unique Job ID	ad755d1634de6410

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4r7zB_</a>	 Alignment		100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> cell division control protein 21; <b>PDBTitle:</b> pfmcm-aaa double-octamer
2	<a href="#">c5udb7_</a>	 Alignment		100.0	21	<b>PDB header:</b> replication <b>Chain:</b> 7; <b>PDB Molecule:</b> dna replication licensing factor mcm7; <b>PDBTitle:</b> structural basis of mcm2-7 replicative helicase loading by orc-cdc62 and cdt1
3	<a href="#">c3ja87_</a>	 Alignment		100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> 7; <b>PDB Molecule:</b> minichromosome maintenance 7; <b>PDBTitle:</b> cryo-em structure of the mcm2-7 double hexamer
4	<a href="#">c3ja82_</a>	 Alignment		100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> 2; <b>PDB Molecule:</b> minichromosome maintenance 2; <b>PDBTitle:</b> cryo-em structure of the mcm2-7 double hexamer
5	<a href="#">c3ja85_</a>	 Alignment		100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> 5; <b>PDB Molecule:</b> minichromosome maintenance 5; <b>PDBTitle:</b> cryo-em structure of the mcm2-7 double hexamer
6	<a href="#">c3ja83_</a>	 Alignment		100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> 3; <b>PDB Molecule:</b> minichromosome maintenance 3; <b>PDBTitle:</b> cryo-em structure of the mcm2-7 double hexamer
7	<a href="#">c3jc76_</a>	 Alignment		100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> 6; <b>PDB Molecule:</b> dna replication licensing factor mcm6; <b>PDBTitle:</b> structure of the eukaryotic replicative cmg helicase and pumpjack2 motion
8	<a href="#">c3ja84_</a>	 Alignment		100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> 4; <b>PDB Molecule:</b> minichromosome maintenance 4; <b>PDBTitle:</b> cryo-em structure of the mcm2-7 double hexamer
9	<a href="#">c3ja86_</a>	 Alignment		100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> 6; <b>PDB Molecule:</b> minichromosome maintenance 6; <b>PDBTitle:</b> cryo-em structure of the mcm2-7 double hexamer
10	<a href="#">c3f8tA_</a>	 Alignment		100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> predicted atpase involved in replication control, cdc46/mcm <b>PDBTitle:</b> crystal structure analysis of a full-length mcm homolog from2 methanopyrus kandleri
11	<a href="#">c3jc57_</a>	 Alignment		100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> 7; <b>PDB Molecule:</b> dna replication licensing factor mcm7; <b>PDBTitle:</b> structure of the eukaryotic replicative cmg helicase and pumpjack2 motion

12	<a href="#">c5h7i7_</a>	Alignment		100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> 7: <b>PDB Molecule:</b> dna replication licensing factor mcm7; <b>PDBTitle:</b> cryo-em structure of the cdt1-mcm2-7 complex in amppnp state
13	<a href="#">c5v8f3_</a>	Alignment		100.0	21	<b>PDB header:</b> replication <b>Chain:</b> 3: <b>PDB Molecule:</b> dna replication licensing factor mcm3; <b>PDBTitle:</b> structural basis of mcm2-7 replicative helicase loading by orc-cdc62 and cdt1
14	<a href="#">c6hv93_</a>	Alignment		100.0	22	<b>PDB header:</b> dna binding protein <b>Chain:</b> 3: <b>PDB Molecule:</b> dna replication licensing factor mcm3; <b>PDBTitle:</b> s. cerevisiae cmg-pol epsilon-dna
15	<a href="#">c5udb5_</a>	Alignment		100.0	21	<b>PDB header:</b> replication <b>Chain:</b> 5: <b>PDB Molecule:</b> minichromosome maintenance protein 5; <b>PDBTitle:</b> structural basis of mcm2-7 replicative helicase loading by orc-cdc62 and cdt1
16	<a href="#">c3jc72_</a>	Alignment		100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> 2: <b>PDB Molecule:</b> dna replication licensing factor mcm2; <b>PDBTitle:</b> structure of the eukaryotic replicative cmg helicase and pumpjack2 motion
17	<a href="#">c5udb3_</a>	Alignment		100.0	22	<b>PDB header:</b> replication <b>Chain:</b> 3: <b>PDB Molecule:</b> dna replication licensing factor mcm3; <b>PDBTitle:</b> structural basis of mcm2-7 replicative helicase loading by orc-cdc62 and cdt1
18	<a href="#">c5u8s4_</a>	Alignment		100.0	19	<b>PDB header:</b> replication <b>Chain:</b> 4: <b>PDB Molecule:</b> dna replication licensing factor mcm4; <b>PDBTitle:</b> structure of eukaryotic cmg helicase at a replication fork
19	<a href="#">c3jc55_</a>	Alignment		100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> 5: <b>PDB Molecule:</b> minichromosome maintenance protein 5; <b>PDBTitle:</b> structure of the eukaryotic replicative cmg helicase and pumpjack2 motion
20	<a href="#">c3f9vA_</a>	Alignment		100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> minichromosome maintenance protein mcm; <b>PDBTitle:</b> crystal structure of a near full-length archaeal mcm: functional2 insights for an aaa+ hexameric helicase
21	<a href="#">c6hv92_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> dna binding protein <b>Chain:</b> 2: <b>PDB Molecule:</b> dna replication licensing factor mcm2; <b>PDBTitle:</b> s. cerevisiae cmg-pol epsilon-dna
22	<a href="#">c3jc73_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> 3: <b>PDB Molecule:</b> dna replication licensing factor mcm3; <b>PDBTitle:</b> structure of the eukaryotic replicative cmg helicase and pumpjack2 motion
23	<a href="#">d1g8pa_</a>	Alignment	not modelled	100.0	24	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
24	<a href="#">c6hv96_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> dna binding protein <b>Chain:</b> 6: <b>PDB Molecule:</b> dna replication licensing factor mcm6; <b>PDBTitle:</b> s. cerevisiae cmg-pol epsilon-dna
25	<a href="#">c6hv97_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> dna binding protein <b>Chain:</b> 7: <b>PDB Molecule:</b> dna replication licensing factor mcm7; <b>PDBTitle:</b> s. cerevisiae cmg-pol epsilon-dna
26	<a href="#">d1rrea_</a>	Alignment	not modelled	100.0	23	<b>Fold:</b> Ribosomal protein S5 domain 2-like <b>Superfamily:</b> Ribosomal protein S5 domain 2-like <b>Family:</b> ATP-dependent protease Lon (La), catalytic domain
27	<a href="#">c5e7sG_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> hydrolase <b>Chain:</b> G: <b>PDB Molecule:</b> lon protease; <b>PDBTitle:</b> hexameric structure of a lon protease domain in active state
28	<a href="#">c6on2A_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent protease la; <b>PDBTitle:</b> lon protease from yersinia pestis with y2853 substrate
29	<a href="#">c5lkmB_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> dna repair protein rada;

						<b>PDBTitle:</b> rada bound to dtdp
30	<a href="#">c3k1jA_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent protease lon; <b>PDBTitle:</b> crystal structure of lon protease from thermococcus onnurineus na1
31	<a href="#">c2x36F_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> lon protease homolog, mitochondrial; <b>PDBTitle:</b> structure of the proteolytic domain of the human2 mitochondrial lon protease
32	<a href="#">d1xhka_</a>	Alignment	not modelled	100.0	24	<b>Fold:</b> Ribosomal protein S5 domain 2-like <b>Superfamily:</b> Ribosomal protein S5 domain 2-like <b>Family:</b> ATP-dependent protease Lon (La), catalytic domain
33	<a href="#">c4ww4A_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ruvb-like 1; <b>PDBTitle:</b> double-heterohexameric rings of full-length rvb1(adp)/rvb2(adp)
34	<a href="#">c3nbxX_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> X: <b>PDB Molecule:</b> atpase rava; <b>PDBTitle:</b> crystal structure of e. coli rava (regulatory atpase variant a) in2 complex with adp
35	<a href="#">c3jc54_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> hydrolase <b>Chain:</b> 4: <b>PDB Molecule:</b> dna replication licensing factor mcm4; <b>PDBTitle:</b> structure of the eukaryotic replicative cmg helicase and pumpjack2 motion
36	<a href="#">c5h45A_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna repair protein rada; <b>PDBTitle:</b> crystal structure of the c-terminal lon protease-like domain of2 thermus thermophilus rada/sms
37	<a href="#">c1z0eF_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> putative protease la homolog type; <b>PDBTitle:</b> crystal structure of a. fulgidus lon proteolytic domain
38	<a href="#">c3m6aC_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> atp-dependent protease la 1; <b>PDBTitle:</b> crystal structure of bacillus subtilis lon c-terminal domain
39	<a href="#">c2r44A_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a putative atpase (chu_0153) from cytophaga2 hutchinsonii atcc 33406 at 2.00 a resolution
40	<a href="#">c4fw9A_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ttc1975 peptidase; <b>PDBTitle:</b> crystal structure of the lon-like protease mtalonc
41	<a href="#">c4yp1E_</a>	Alignment	not modelled	99.9	25	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> lon protease; <b>PDBTitle:</b> crystal structure of a hexameric lona protease bound to three adps
42	<a href="#">c2c9oA_</a>	Alignment	not modelled	99.9	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ruvb-like 1; <b>PDBTitle:</b> 3d structure of the human ruvb-like helicase ruvb1
43	<a href="#">c5oafB_</a>	Alignment	not modelled	99.9	22	<b>PDB header:</b> gene regulation <b>Chain:</b> B: <b>PDB Molecule:</b> ruvb-like 2; <b>PDBTitle:</b> human rvb1/rvb2 heterohexamer in ino80 complex
44	<a href="#">d1um8a_</a>	Alignment	not modelled	99.9	20	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
45	<a href="#">c6blbA_</a>	Alignment	not modelled	99.8	30	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> holliday junction atp-dependent dna helicase ruvb; <b>PDBTitle:</b> 1.88 angstrom resolution crystal structure holliday junction atp-2 dependent dna helicase (ruvb) from pseudomonas aeruginosa in complex3 with adp
46	<a href="#">c3uk6H_</a>	Alignment	not modelled	99.8	19	<b>PDB header:</b> hydrolase <b>Chain:</b> H: <b>PDB Molecule:</b> ruvb-like 2; <b>PDBTitle:</b> crystal structure of the tip48 (tip49b) hexamer
47	<a href="#">d1g41a_</a>	Alignment	not modelled	99.8	20	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
48	<a href="#">c2c9oC_</a>	Alignment	not modelled	99.8	20	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> ruvb-like 1; <b>PDBTitle:</b> 3d structure of the human ruvb-like helicase ruvb1
49	<a href="#">c6genX_</a>	Alignment	not modelled	99.8	30	<b>PDB header:</b> nuclear protein <b>Chain:</b> X: <b>PDB Molecule:</b> ruvb-like protein 1; <b>PDBTitle:</b> chromatin remodeller-nucleosome complex at 4.5 a resolution.
50	<a href="#">c4ww4B_</a>	Alignment	not modelled	99.8	23	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> ruvb-like 2; <b>PDBTitle:</b> double-heterohexameric rings of full-length rvb1(adp)/rvb2(adp)
51	<a href="#">c6azyA_</a>	Alignment	not modelled	99.8	21	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> heat shock protein hsp104; <b>PDBTitle:</b> crystal structure of hsp104 r328m/r757m mutant from calcarisporiella2 thermophila
52	<a href="#">c1qvrB_</a>	Alignment	not modelled	99.8	26	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> clpb protein; <b>PDBTitle:</b> crystal structure analysis of clpb
53	<a href="#">c5kneD_</a>	Alignment	not modelled	99.8	17	<b>PDB header:</b> chaperone <b>Chain:</b> D: <b>PDB Molecule:</b> heat shock protein 104; <b>PDBTitle:</b> cryoem reconstruction of hsp104 hexamer
54	<a href="#">c6qi8E_</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> chaperone <b>Chain:</b> E: <b>PDB Molecule:</b> ruvb-like 2; <b>PDBTitle:</b> truncated human r2tp complex, structure 3 (adp-filled)
55	<a href="#">c3pfiB_</a>	Alignment	not modelled	99.8	26	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> holliday junction atp-dependent dna helicase ruvb; <b>PDBTitle:</b> 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
56	<a href="#">c4d2qC_</a>	Alignment	not modelled	99.8	19	<b>PDB header:</b> chaperone <b>Chain:</b> C: <b>PDB Molecule:</b> clpb; <b>PDBTitle:</b> negative-stain electron microscopy of e. coli clpb mutant e432a (bap2 form bound to clpb)
57	<a href="#">c1ojjD_</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> response regulator <b>Chain:</b> D: <b>PDB Molecule:</b> transcriptional regulatory protein zrar; <b>PDBTitle:</b> crystal structure of a sigma54-activator suggests the mechanism for2 the conformational switch necessary for sigma54 binding
58	<a href="#">d1ny5a2</a>	Alignment	not modelled	99.8	17	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
59	<a href="#">c5exsA_</a>	Alignment	not modelled	99.8	17	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator fleq; <b>PDBTitle:</b> aaa+ atpase fleq from pseudomonas aeruginosa bound to atp-gamma-s
60	<a href="#">c1ojfF_</a>	Alignment	not modelled	99.8	18	<b>PDB header:</b> response regulator <b>Chain:</b> F: <b>PDB Molecule:</b> transcriptional regulatory protein zrar; <b>PDBTitle:</b> crystal structure of a sigma54-activator suggests the mechanism for2 the conformational switch necessary for sigma54 binding
61	<a href="#">d1r6bx3</a>	Alignment	not modelled	99.8	22	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
62	<a href="#">c5vy9C_</a>	Alignment	not modelled	99.8	21	<b>PDB header:</b> chaperone <b>Chain:</b> C: <b>PDB Molecule:</b> heat shock protein 104; <b>PDBTitle:</b> s. cerevisiae hsp104:casein complex, middle domain conformation
63	<a href="#">c1r6bX_</a>	Alignment	not modelled	99.8	26	<b>PDB header:</b> hydrolase <b>Chain:</b> X: <b>PDB Molecule:</b> clpa protein; <b>PDBTitle:</b> high resolution crystal structure of clpa
64	<a href="#">c6nyyC_</a>	Alignment	not modelled	99.8	22	<b>PDB header:</b> translocase <b>Chain:</b> C: <b>PDB Molecule:</b> afg3-like protein 2; <b>PDBTitle:</b> human m-aaa protease afg3l2, substrate-bound
65	<a href="#">c6em8F_</a>	Alignment	not modelled	99.8	19	<b>PDB header:</b> chaperone <b>Chain:</b> F: <b>PDB Molecule:</b> atp-dependent clp protease atp-binding subunit clpc; <b>PDBTitle:</b> s.aureus clpc resting state, c2 symmetrised
66	<a href="#">c3pxiB_</a>	Alignment	not modelled	99.8	21	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> negative regulator of genetic competence clpc/mecb; <b>PDBTitle:</b> structure of meca108:clpc
67	<a href="#">c5ep4A_</a>	Alignment	not modelled	99.7	20	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative repressor protein luxo; <b>PDBTitle:</b> structure, regulation, and inhibition of the quorum-sensing signal2 integrator luxo
68	<a href="#">c5d4wB_</a>	Alignment	not modelled	99.7	22	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> putative heat shock protein; <b>PDBTitle:</b> crystal structure of hsp104
69	<a href="#">d1ofha_</a>	Alignment	not modelled	99.7	23	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
70	<a href="#">c4ciuA_</a>	Alignment	not modelled	99.7	19	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> chaperone protein clpb; <b>PDBTitle:</b> crystal structure of e. coli clpb
71	<a href="#">c3hteC_</a>	Alignment	not modelled	99.7	19	<b>PDB header:</b> motor protein <b>Chain:</b> C: <b>PDB Molecule:</b> atp-dependent clp protease atp-binding subunit clpx; <b>PDBTitle:</b> crystal structure of nucleotide-free hexameric clpx
72	<a href="#">d1qvra3</a>	Alignment	not modelled	99.7	24	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
73	<a href="#">c1in8A_</a>	Alignment	not modelled	99.7	24	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> holliday junction dna helicase ruvb; <b>PDBTitle:</b> thermotoga maritima ruvb t158v
74	<a href="#">c5kneF_</a>	Alignment	not modelled	99.7	17	<b>PDB header:</b> chaperone <b>Chain:</b> F: <b>PDB Molecule:</b> heat shock protein 104; <b>PDBTitle:</b> cryoem reconstruction of hsp104 hexamer
75	<a href="#">c2c99A_</a>	Alignment	not modelled	99.7	22	<b>PDB header:</b> transcription regulation <b>Chain:</b> A: <b>PDB Molecule:</b> psp operon transcriptional activator; <b>PDBTitle:</b> structural basis of the nucleotide driven conformational2 changes in the aaa domain of transcription activator pspf
76	<a href="#">c6em8H_</a>	Alignment	not modelled	99.7	18	<b>PDB header:</b> chaperone <b>Chain:</b> H: <b>PDB Molecule:</b> atp-dependent clp protease atp-binding subunit clpc; <b>PDBTitle:</b> s.aureus clpc resting state, c2 symmetrised
77	<a href="#">c6em8E_</a>	Alignment	not modelled	99.7	19	<b>PDB header:</b> chaperone <b>Chain:</b> E: <b>PDB Molecule:</b> atp-dependent clp protease atp-binding subunit clpc; <b>PDBTitle:</b> s.aureus clpc resting state, c2 symmetrised
78	<a href="#">c6e111_</a>	Alignment	not modelled	99.7	20	<b>PDB header:</b> protein transport <b>Chain:</b> 1: <b>PDB Molecule:</b> heat shock protein 101; <b>PDBTitle:</b> ptex core complex in the resetting (compact) state
79	<a href="#">d1ixsb2</a>	Alignment	not modelled	99.7	26	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
80	<a href="#">c2dhrC_</a>	Alignment	not modelled	99.6	25	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> ftsh; <b>PDBTitle:</b> whole cytosolic region of atp-dependent metalloprotease2 ftsh (g399l)
81	<a href="#">d1in4a2</a>	Alignment	not modelled	99.6	23	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases

				Family:Extended AAA-ATPase domain		
82	<a href="#">c1hqcb_</a>	Alignment	not modelled	99.6	25	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> ruvb; <b>PDBTitle:</b> structure of ruvb from thermus thermophilus hb8
83	<a href="#">c6hz4B_</a>	Alignment	not modelled	99.6	14	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> 5-methylcytosine-specific restriction enzyme b; <b>PDBTitle:</b> structure of mcrcb without dna binding domains (one half of the full2 complex)
84	<a href="#">c5g4gF_</a>	Alignment	not modelled	99.6	18	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> vcp-like atpase; <b>PDBTitle:</b> structure of the atpgs-bound vat complex
85	<a href="#">c6djuA_</a>	Alignment	not modelled	99.6	24	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> chaperone protein clpb; <b>PDBTitle:</b> mtb clpb in complex with atpgammas and casein, conformer 1
86	<a href="#">c5kzfj_</a>	Alignment	not modelled	99.6	21	<b>PDB header:</b> hydrolase <b>Chain:</b> J: <b>PDB Molecule:</b> proteasome-associated atpase; <b>PDBTitle:</b> crystal structure of near full-length hexameric mycobacterium2 tuberculosis proteasomal atpase mpa in apo form
87	<a href="#">c3cf1C_</a>	Alignment	not modelled	99.6	17	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> transitional endoplasmic reticulum atpase; <b>PDBTitle:</b> structure of p97/vcp in complex with adp/adp.alfx
88	<a href="#">c5e7pA_</a>	Alignment	not modelled	99.6	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cell division control protein cdc48; <b>PDBTitle:</b> crystal structure of msmeq_0858 (uniprot a0qqs4), a aaa atpase.
89	<a href="#">c4b4tl_</a>	Alignment	not modelled	99.6	23	<b>PDB header:</b> hydrolase <b>Chain:</b> I: <b>PDB Molecule:</b> 26s protease regulatory subunit 4 homolog; <b>PDBTitle:</b> near-atomic resolution structural model of the yeast 26s proteasome
90	<a href="#">c6i26A_</a>	Alignment	not modelled	99.6	21	<b>PDB header:</b> motor protein <b>Chain:</b> A: <b>PDB Molecule:</b> midasin,midasin,midasin,midasin; <b>PDBTitle:</b> rea1 wild type amppnp state
91	<a href="#">c3b9pA_</a>	Alignment	not modelled	99.6	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cg5977-pa, isoform a; <b>PDBTitle:</b> spastin
92	<a href="#">c6djvE_</a>	Alignment	not modelled	99.6	24	<b>PDB header:</b> chaperone <b>Chain:</b> E: <b>PDB Molecule:</b> chaperone protein clpb; <b>PDBTitle:</b> mtb clpb in complex with atpgammas and casein, conformer 2
93	<a href="#">c5c3cB_</a>	Alignment	not modelled	99.6	21	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> cbbq/nirq/norq domain protein; <b>PDBTitle:</b> structural characterization of a newly identified component of alpha-2 carboxisomes: the aaa+ domain protein cso-cbbq
94	<a href="#">c4b4tl_</a>	Alignment	not modelled	99.6	23	<b>PDB header:</b> hydrolase <b>Chain:</b> L: <b>PDB Molecule:</b> 26s protease subunit rpt4; <b>PDBTitle:</b> near-atomic resolution structural model of the yeast 26s proteasome
95	<a href="#">c6epdM_</a>	Alignment	not modelled	99.6	21	<b>PDB header:</b> hydrolase <b>Chain:</b> M: <b>PDB Molecule:</b> 26s proteasome regulatory subunit 6a; <b>PDBTitle:</b> substrate processing state 26s proteasome (sps1)
96	<a href="#">c5ep0A_</a>	Alignment	not modelled	99.6	19	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative repressor protein luxo; <b>PDBTitle:</b> quorum-sensing signal integrator luxo - receiver+catalytic domains
97	<a href="#">c5j1sA_</a>	Alignment	not modelled	99.6	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> torsin-1a; <b>PDBTitle:</b> torsina-lull1 complex, h. sapiens, bound to vhh-bs2
98	<a href="#">c3dzdA_</a>	Alignment	not modelled	99.6	16	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator (ntrc family); <b>PDBTitle:</b> crystal structure of sigma54 activator ntrc4 in the inactive2 state
99	<a href="#">c5kneA_</a>	Alignment	not modelled	99.6	21	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> heat shock protein 104; <b>PDBTitle:</b> cryoem reconstruction of hsp104 hexamer
100	<a href="#">c6matE_</a>	Alignment	not modelled	99.6	19	<b>PDB header:</b> ribosomal protein <b>Chain:</b> E: <b>PDB Molecule:</b> rix7 mutant; <b>PDBTitle:</b> cryo-em structure of the essential ribosome assembly aaa-atpase rix7
101	<a href="#">c3sylB_</a>	Alignment	not modelled	99.6	23	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> protein cbbx; <b>PDBTitle:</b> crystal structure of the aaa+ protein cbbx, native structure
102	<a href="#">c1xwiA_</a>	Alignment	not modelled	99.6	19	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> skd1 protein; <b>PDBTitle:</b> crystal structure of vps4b
103	<a href="#">c4b4tl_</a>	Alignment	not modelled	99.6	22	<b>PDB header:</b> hydrolase <b>Chain:</b> J: <b>PDB Molecule:</b> 26s protease regulatory subunit 8 homolog; <b>PDBTitle:</b> near-atomic resolution structural model of the yeast 26s proteasome
104	<a href="#">c6az0A_</a>	Alignment	not modelled	99.5	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> mitochondrial inner membrane i-aaa protease supercomplex <b>PDBTitle:</b> mitochondrial atpase protease yme1
105	<a href="#">c4b4th_</a>	Alignment	not modelled	99.5	23	<b>PDB header:</b> hydrolase <b>Chain:</b> H: <b>PDB Molecule:</b> 26s protease regulatory subunit 7 homolog; <b>PDBTitle:</b> near-atomic resolution structural model of the yeast 26s proteasome
106	<a href="#">c6nyyA_</a>	Alignment	not modelled	99.5	21	<b>PDB header:</b> translocase <b>Chain:</b> A: <b>PDB Molecule:</b> afg3-like protein 2; <b>PDBTitle:</b> human m-aaa protease afg3l2, substrate-bound

107	<a href="#">c4lcbA_</a>	Alignment	not modelled	99.5	20	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> cell division protein cdvc, vps4; <b>PDBTitle:</b> structure of vps4 homolog from acidianus hospitalis
108	<a href="#">c5vq9D_</a>	Alignment	not modelled	99.5	17	<b>PDB header:</b> protein binding <b>Chain:</b> D: <b>PDB Molecule:</b> pachytene checkpoint protein 2 homolog; <b>PDBTitle:</b> structure of human trip13, apo form
109	<a href="#">c6epcJ_</a>	Alignment	not modelled	99.5	23	<b>PDB header:</b> hydrolase <b>Chain:</b> J: <b>PDB Molecule:</b> 26s proteasome regulatory subunit 8; <b>PDBTitle:</b> ground state 26s proteasome (gs2)
110	<a href="#">c6edoA_</a>	Alignment	not modelled	99.5	23	<b>PDB header:</b> motor protein <b>Chain:</b> A: <b>PDB Molecule:</b> midasin; <b>PDBTitle:</b> full-length s. pombe mdn1 in the presence of amppnp (ring region)
111	<a href="#">c3eihB_</a>	Alignment	not modelled	99.5	20	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> vacuolar protein sorting-associated protein 4; <b>PDBTitle:</b> crystal structure of s.cerevisiae vps4 in the presence of atpgammas
112	<a href="#">c5ifwB_</a>	Alignment	not modelled	99.5	17	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> transitional endoplasmic reticulum atpase; <b>PDBTitle:</b> quantitative interaction mapping reveals an extended ubiquitin2 regulatory domain in aspl that disrupts functional p97 hexamers and3 induces cell death
113	<a href="#">c4z8xC_</a>	Alignment	not modelled	99.5	24	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> atp-dependent zinc metalloprotease ftsh; <b>PDBTitle:</b> truncated ftsh from a. aeolicus
114	<a href="#">c3h4mC_</a>	Alignment	not modelled	99.5	18	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> proteasome-activating nucleotidase; <b>PDBTitle:</b> aaa atpase domain of the proteasome- activating nucleotidase
115	<a href="#">d1r6bx2</a>	Alignment	not modelled	99.5	14	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
116	<a href="#">c3vfdA_</a>	Alignment	not modelled	99.5	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> spastin; <b>PDBTitle:</b> human spastin aaa domain
117	<a href="#">c4ypnA_</a>	Alignment	not modelled	99.5	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lon protease; <b>PDBTitle:</b> crystal structure of a lon fragment containing the 3-helix bundle and2 the aaa-alpha/beta domain
118	<a href="#">c2ce7B_</a>	Alignment	not modelled	99.5	21	<b>PDB header:</b> cell division protein <b>Chain:</b> B: <b>PDB Molecule:</b> cell division protein ftsh; <b>PDBTitle:</b> edta treated
119	<a href="#">d1w5sa2</a>	Alignment	not modelled	99.5	17	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
120	<a href="#">c6hecH_</a>	Alignment	not modelled	99.5	22	<b>PDB header:</b> hydrolase <b>Chain:</b> H: <b>PDB Molecule:</b> proteasome-activating nucleotidase; <b>PDBTitle:</b> pan-proteasome in state 4