
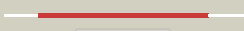






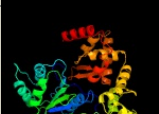













# Phyre2

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Description	RVBD0894 (-) _996527_997708
Date	Fri Jul 26 01:50:48 BST 2019
Unique Job ID	8eec8bf3099cc466

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1z6tC_</a>	 Alignment		100.0	17	<b>PDB header:</b> apoptosis <b>Chain:</b> C; <b>PDB Molecule:</b> apoptotic protease activating factor 1; <b>PDBTitle:</b> structure of the apoptotic protease-activating factor 12 bound to adp
2	<a href="#">c3iytG_</a>	 Alignment		100.0	16	<b>PDB header:</b> apoptosis <b>Chain:</b> G; <b>PDB Molecule:</b> apoptotic protease-activating factor 1; <b>PDBTitle:</b> structure of an apoptosome-procaspase-9 card complex
3	<a href="#">c2a5yB_</a>	 Alignment		100.0	14	<b>PDB header:</b> apoptosis <b>Chain:</b> B; <b>PDB Molecule:</b> ced-4; <b>PDBTitle:</b> structure of a ced-4/ced-9 complex
4	<a href="#">c5juyB_</a>	 Alignment		100.0	17	<b>PDB header:</b> apoptosis <b>Chain:</b> B; <b>PDB Molecule:</b> apoptotic protease-activating factor 1; <b>PDBTitle:</b> active human apoptosome with procaspase-9
5	<a href="#">c6mfvC_</a>	 Alignment		100.0	19	<b>PDB header:</b> signaling protein <b>Chain:</b> C; <b>PDB Molecule:</b> tetratricopeptide repeat sensor ph0952; <b>PDBTitle:</b> crystal structure of the signal transduction atpase with numerous2 domains (stand) protein with a tetratricopeptide repeat sensor ph09523 from pyrococcus horikoshii
6	<a href="#">c3iz8F_</a>	 Alignment		100.0	17	<b>PDB header:</b> apoptosis <b>Chain:</b> F; <b>PDB Molecule:</b> apaf-1 related killer dark; <b>PDBTitle:</b> structure of the drosophila apoptosome
7	<a href="#">c3iz8C_</a>	 Alignment		100.0	17	<b>PDB header:</b> apoptosis <b>Chain:</b> C; <b>PDB Molecule:</b> apaf-1 related killer dark; <b>PDBTitle:</b> structure of the drosophila apoptosome
8	<a href="#">c3iz8H_</a>	 Alignment		100.0	17	<b>PDB header:</b> apoptosis <b>Chain:</b> H; <b>PDB Molecule:</b> apaf-1 related killer dark; <b>PDBTitle:</b> structure of the drosophila apoptosome
9	<a href="#">c3iz8G_</a>	 Alignment		100.0	17	<b>PDB header:</b> apoptosis <b>Chain:</b> G; <b>PDB Molecule:</b> apaf-1 related killer dark; <b>PDBTitle:</b> structure of the drosophila apoptosome
10	<a href="#">c1vt4I_</a>	 Alignment		100.0	17	<b>PDB header:</b> apoptosis <b>Chain:</b> I; <b>PDB Molecule:</b> apaf-1 related killer dark; <b>PDBTitle:</b> structure of the drosophila apoptosome
11	<a href="#">c1vt4O_</a>	 Alignment		100.0	17	<b>PDB header:</b> apoptosis <b>Chain:</b> O; <b>PDB Molecule:</b> apaf-1 related killer dark; <b>PDBTitle:</b> structure of the drosophila apoptosome

12	<a href="#">c1vt4L_</a>	Alignment		100.0	17	<b>PDB header:</b> apoptosis <b>Chain:</b> L: <b>PDB Molecule:</b> apaf-1 related killer dark; <b>PDBTitle:</b> structure of the drosophila apoptosome
13	<a href="#">c3iz8D_</a>	Alignment		100.0	17	<b>PDB header:</b> apoptosis <b>Chain:</b> D: <b>PDB Molecule:</b> apaf-1 related killer dark; <b>PDBTitle:</b> structure of the drosophila apoptosome
14	<a href="#">c1vt4J_</a>	Alignment		100.0	17	<b>PDB header:</b> apoptosis <b>Chain:</b> J: <b>PDB Molecule:</b> apaf-1 related killer dark; <b>PDBTitle:</b> structure of the drosophila apoptosome
15	<a href="#">c1vt4M_</a>	Alignment		100.0	17	<b>PDB header:</b> apoptosis <b>Chain:</b> M: <b>PDB Molecule:</b> apaf-1 related killer dark; <b>PDBTitle:</b> structure of the drosophila apoptosome
16	<a href="#">c3iz8A_</a>	Alignment		100.0	17	<b>PDB header:</b> apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> apaf-1 related killer dark; <b>PDBTitle:</b> structure of the drosophila apoptosome
17	<a href="#">c1vt4P_</a>	Alignment		100.0	17	<b>PDB header:</b> apoptosis <b>Chain:</b> P: <b>PDB Molecule:</b> apaf-1 related killer dark; <b>PDBTitle:</b> structure of the drosophila apoptosome
18	<a href="#">c3iz8E_</a>	Alignment		100.0	17	<b>PDB header:</b> apoptosis <b>Chain:</b> E: <b>PDB Molecule:</b> apaf-1 related killer dark; <b>PDBTitle:</b> structure of the drosophila apoptosome
19	<a href="#">c3iz8B_</a>	Alignment		100.0	17	<b>PDB header:</b> apoptosis <b>Chain:</b> B: <b>PDB Molecule:</b> apaf-1 related killer dark; <b>PDBTitle:</b> structure of the drosophila apoptosome
20	<a href="#">c1vt4N_</a>	Alignment		100.0	17	<b>PDB header:</b> apoptosis <b>Chain:</b> N: <b>PDB Molecule:</b> apaf-1 related killer dark; <b>PDBTitle:</b> structure of the drosophila apoptosome
21	<a href="#">c1vt4K_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> apoptosis <b>Chain:</b> K: <b>PDB Molecule:</b> apaf-1 related killer dark; <b>PDBTitle:</b> structure of the drosophila apoptosome
22	<a href="#">c2qenA_</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> walker-type atpase; <b>PDBTitle:</b> the walker-type atpase paby2304 of pyrococcus abyssi
23	<a href="#">c6j5tC_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> plant protein <b>Chain:</b> C: <b>PDB Molecule:</b> disease resistance rpp13-like protein 4; <b>PDBTitle:</b> reconstitution and structure of a plant nlr resistosome conferring2 immunity
24	<a href="#">c2fnaA_</a>	Alignment	not modelled	99.9	11	<b>PDB header:</b> atp-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> conserved hypothetical protein; <b>PDBTitle:</b> crystal structure of an archaeal aaa+ atpase (sso1545) from sulfolobus2 solfataricus p2 at 2.00 a resolution
25	<a href="#">c4xgcE_</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> dna binding protein <b>Chain:</b> E: <b>PDB Molecule:</b> origin recognition complex subunit 5; <b>PDBTitle:</b> crystal structure of the eukaryotic origin recognition complex
26	<a href="#">c2qbyB_</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> replication/dna <b>Chain:</b> B: <b>PDB Molecule:</b> cell division control protein 6 homolog 3; <b>PDBTitle:</b> crystal structure of a heterodimer of cdc6/orc1 initiators2 bound to origin dna (from s. solfataricus)
27	<a href="#">c1fnnB_</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> cell cycle <b>Chain:</b> B: <b>PDB Molecule:</b> cell division control protein 6; <b>PDBTitle:</b> crystal structure of cdc6p from pyrobaculum aerophilum
28	<a href="#">c6s2pN_</a>	Alignment	not modelled	99.8	20	<b>PDB header:</b> plant protein <b>Chain:</b> N: <b>PDB Molecule:</b> nrc1; <b>PDBTitle:</b> structure of the nb-arc domain from the tomato immune receptor nrc1
						<b>PDB header:</b> replication/dna

29	<a href="#">c2qbyA</a>	Alignment	not modelled	99.8	12	<b>Chain:</b> A: <b>PDB Molecule:</b> cell division control protein 6 homolog 1; <b>PDBTitle:</b> crystal structure of a heterodimer of cdc6/orc1 initiators2 bound to origin dna (from s. solfataricus)
30	<a href="#">c5ujmE</a>	Alignment	not modelled	99.7	12	<b>PDB header:</b> replication <b>Chain:</b> E: <b>PDB Molecule:</b> origin recognition complex subunit 5; <b>PDBTitle:</b> structure of the active form of human origin recognition complex and2 its atpase motor module
31	<a href="#">c2v1uA</a>	Alignment	not modelled	99.7	13	<b>PDB header:</b> replication <b>Chain:</b> A: <b>PDB Molecule:</b> cell division control protein 6 homolog; <b>PDBTitle:</b> structure of the aeropyrum pernix orc1 protein in complex2 with dna
32	<a href="#">c1w5sB</a>	Alignment	not modelled	99.6	15	<b>PDB header:</b> replication <b>Chain:</b> B: <b>PDB Molecule:</b> origin recognition complex subunit 2 orc2; <b>PDBTitle:</b> structure of the aeropyrum pernix orc2 protein (adp form)
33	<a href="#">c5udb9</a>	Alignment	not modelled	99.6	13	<b>PDB header:</b> replication <b>Chain:</b> 9: <b>PDB Molecule:</b> cell division control protein 6; <b>PDBTitle:</b> structural basis of mcm2-7 replicative helicase loading by orc-cdc62 and cdt1
34	<a href="#">c5uj7C</a>	Alignment	not modelled	99.6	10	<b>PDB header:</b> dna binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> origin recognition complex subunit 4; <b>PDBTitle:</b> structure of the active form of human origin recognition complex2 atpase motor module, complex subunits 1, 4, 5
35	<a href="#">c5udbA</a>	Alignment	not modelled	99.6	8	<b>PDB header:</b> replication <b>Chain:</b> A: <b>PDB Molecule:</b> origin recognition complex subunit 1; <b>PDBTitle:</b> structural basis of mcm2-7 replicative helicase loading by orc-cdc62 and cdt1
36	<a href="#">d2fnaa2</a>	Alignment	not modelled	99.5	13	<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
37	<a href="#">c5uj7B</a>	Alignment	not modelled	99.5	15	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> origin recognition complex subunit 1; <b>PDBTitle:</b> structure of the active form of human origin recognition complex2 atpase motor module, complex subunits 1, 4, 5
38	<a href="#">c4xgcD</a>	Alignment	not modelled	99.5	23	<b>PDB header:</b> dna binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> origin recognition complex subunit 4; <b>PDBTitle:</b> crystal structure of the eukaryotic origin recognition complex
39	<a href="#">c4kxfP</a>	Alignment	not modelled	99.4	17	<b>PDB header:</b> immune system <b>Chain:</b> P: <b>PDB Molecule:</b> nlr family card domain-containing protein 4; <b>PDBTitle:</b> crystal structure of nlr4 reveals its autoinhibition mechanism
40	<a href="#">c4kxfF</a>	Alignment	not modelled	99.4	17	<b>PDB header:</b> immune system <b>Chain:</b> F: <b>PDB Molecule:</b> nlr family card domain-containing protein 4; <b>PDBTitle:</b> crystal structure of nlr4 reveals its autoinhibition mechanism
41	<a href="#">d1fnna2</a>	Alignment	not modelled	99.4	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
42	<a href="#">c4xgcA</a>	Alignment	not modelled	99.4	15	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> origin recognition complex subunit 1; <b>PDBTitle:</b> crystal structure of the eukaryotic origin recognition complex
43	<a href="#">c6npyA</a>	Alignment	not modelled	99.2	19	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> nacht, Irr and pyd domains-containing protein 3; <b>PDBTitle:</b> cryo-em structure of nlrp3 bound to nek7
44	<a href="#">d1w5sa2</a>	Alignment	not modelled	99.2	13	<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="#">c5yudA</a>	Alignment	not modelled	99.2	13	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> baculoviral iap repeat-containing protein 1e; <b>PDBTitle:</b> flagellin derivative in complex with the nlr protein naip5
46	<a href="#">c6b5bA</a>	Alignment	not modelled	99.2	15	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> baculoviral iap repeat-containing protein 1e; <b>PDBTitle:</b> cryo-em structure of the naip5-nlr4-flagellin inflammasome
47	<a href="#">c6blbA</a>	Alignment	not modelled	99.1	18	<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
48	<a href="#">c2chgB</a>	Alignment	not modelled	99.1	14	<b>PDB header:</b> dna-binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> replication factor c small subunit; <b>PDBTitle:</b> replication factor c domains 1 and 2
49	<a href="#">c1sxC</a>	Alignment	not modelled	99.1	16	<b>PDB header:</b> replication <b>Chain:</b> C: <b>PDB Molecule:</b> activator 1 40 kda subunit; <b>PDBTitle:</b> crystal structure of the eukaryotic clamp loader (replication factor2 c, rfc) bound to the dna sliding clamp (proliferating cell nuclear3 antigen, pcna)
50	<a href="#">d1sxb2</a>	Alignment	not modelled	99.1	12	<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
51	<a href="#">c5zr1A</a>	Alignment	not modelled	99.0	10	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> origin recognition complex subunit 1; <b>PDBTitle:</b> saccharomyces cerevisiae origin recognition complex bound to a 72-bp2 origin dna containing acs and b1 element
52	<a href="#">c3pfiB</a>	Alignment	not modelled	99.0	16	<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
						<b>PDB header:</b> hydrolase

53	<a href="#">c1hqcB</a>	Alignment	not modelled	99.0	16	<b>Chain:</b> B; <b>PDB Molecule:</b> ruvb; <b>PDBTitle:</b> structure of ruvb from thermus thermophilus hb8
54	<a href="#">c2chvE</a>	Alignment	not modelled	99.0	13	<b>PDB header:</b> dna-binding protein <b>Chain:</b> E; <b>PDB Molecule:</b> replication factor c small subunit; <b>PDBTitle:</b> replication factor c adnpn complex
55	<a href="#">c5kneA</a>	Alignment	not modelled	99.0	22	<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
56	<a href="#">c1sxD</a>	Alignment	not modelled	99.0	11	<b>PDB header:</b> replication <b>Chain:</b> D; <b>PDB Molecule:</b> activator 1 41 kda subunit; <b>PDBTitle:</b> crystal structure of the eukaryotic clamp loader (replication factor2 c, rfc) bound to the dna sliding clamp (proliferating cell nuclear3 antigen, pcna)
57	<a href="#">c1iqpF</a>	Alignment	not modelled	99.0	12	<b>PDB header:</b> replication <b>Chain:</b> F; <b>PDB Molecule:</b> rfcs; <b>PDBTitle:</b> crystal structure of the clamp loader small subunit from2 pyrococcus furiosus
58	<a href="#">c1sxB</a>	Alignment	not modelled	98.9	11	<b>PDB header:</b> replication <b>Chain:</b> B; <b>PDB Molecule:</b> activator 1 37 kda subunit; <b>PDBTitle:</b> crystal structure of the eukaryotic clamp loader (replication factor2 c, rfc) bound to the dna sliding clamp (proliferating cell nuclear3 antigen, pcna)
59	<a href="#">d1sxD2</a>	Alignment	not modelled	98.9	11	<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
60	<a href="#">d1sxD2</a>	Alignment	not modelled	98.9	13	<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
61	<a href="#">c5udbE</a>	Alignment	not modelled	98.9	17	<b>PDB header:</b> replication <b>Chain:</b> E; <b>PDB Molecule:</b> origin recognition complex subunit 5; <b>PDBTitle:</b> structural basis of mcm2-7 replicative helicase loading by orc-cdc62 and cdt1
62	<a href="#">c3te6A</a>	Alignment	not modelled	98.9	11	<b>PDB header:</b> gene regulation <b>Chain:</b> A; <b>PDB Molecule:</b> regulatory protein sir3; <b>PDBTitle:</b> crystal structure of the s. cerevisiae sir3 aaa+ domain
63	<a href="#">c5d4wB</a>	Alignment	not modelled	98.9	21	<b>PDB header:</b> chaperone <b>Chain:</b> B; <b>PDB Molecule:</b> putative heat shock protein; <b>PDBTitle:</b> crystal structure of hsp104
64	<a href="#">d1jbka</a>	Alignment	not modelled	98.9	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
65	<a href="#">c5kneF</a>	Alignment	not modelled	98.9	25	<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
66	<a href="#">d1r6bx2</a>	Alignment	not modelled	98.9	25	<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
67	<a href="#">d1iqa2</a>	Alignment	not modelled	98.9	15	<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
68	<a href="#">c3pvsA</a>	Alignment	not modelled	98.9	16	<b>PDB header:</b> recombination <b>Chain:</b> A; <b>PDB Molecule:</b> replication-associated recombination protein a; <b>PDBTitle:</b> structure and biochemical activities of escherichia coli mgsa
69	<a href="#">c6e111</a>	Alignment	not modelled	98.9	18	<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
70	<a href="#">d1qvr2</a>	Alignment	not modelled	98.9	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
71	<a href="#">c5kneD</a>	Alignment	not modelled	98.8	20	<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
72	<a href="#">c6djuA</a>	Alignment	not modelled	98.8	27	<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
73	<a href="#">c6em8H</a>	Alignment	not modelled	98.8	29	<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
74	<a href="#">c4ciuA</a>	Alignment	not modelled	98.8	26	<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
75	<a href="#">c1in8A</a>	Alignment	not modelled	98.8	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
76	<a href="#">c6djvE</a>	Alignment	not modelled	98.8	27	<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
77	<a href="#">c2p65A</a>	Alignment	not modelled	98.7	24	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> hypothetical protein pf08_0063; <b>PDBTitle:</b> crystal structure of the first nucleotide binding domain of2 chaperone clpb1, putative, (pv089580) from plasmodium vivax
78	<a href="#">c1sxA</a>	Alignment	not modelled	98.7	15	<b>PDB header:</b> replication <b>Chain:</b> A; <b>PDB Molecule:</b> activator 1 95 kda subunit; <b>PDBTitle:</b> crystal structure of the eukaryotic clamp loader (replication factor2 c, rfc) bound to the dna sliding clamp (proliferating cell nuclear3 antigen, pcna)
						<b>PDB header:</b> hydrolase regulator.dna binding protein

79	<a href="#">c3bosA_</a>	Alignment	not modelled	98.7	17	<b>Chain:</b> A: <b>PDB Molecule:</b> putative dna replication factor; <b>PDBTitle:</b> crystal structure of a putative dna replication regulator hda2 (sama_1916) from shewanella amazonensis sb2b at 1.75 a resolution
80	<a href="#">d1njfa_</a>	Alignment	not modelled	98.7	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
81	<a href="#">c5udbD_</a>	Alignment	not modelled	98.7	11	<b>PDB header:</b> replication <b>Chain:</b> D: <b>PDB Molecule:</b> origin recognition complex subunit 4; <b>PDBTitle:</b> structural basis of mcm2-7 replicative helicase loading by orc-cdc62 and cdt1
82	<a href="#">c6em8F_</a>	Alignment	not modelled	98.6	25	<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
83	<a href="#">c1xxhB_</a>	Alignment	not modelled	98.6	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> dna polymerase iii subunit gamma; <b>PDBTitle:</b> atpgs bound e. coli clamp loader complex
84	<a href="#">c1r6bX_</a>	Alignment	not modelled	98.6	18	<b>PDB header:</b> hydrolase <b>Chain:</b> X: <b>PDB Molecule:</b> clpa protein; <b>PDBTitle:</b> high resolution crystal structure of clpa
85	<a href="#">c3pxgA_</a>	Alignment	not modelled	98.6	32	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> negative regulator of genetic competence clpc/mecb; <b>PDBTitle:</b> structure of meca121 and clpc1-485 complex
86	<a href="#">c1qvrB_</a>	Alignment	not modelled	98.6	27	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> clpb protein; <b>PDBTitle:</b> crystal structure analysis of clpb
87	<a href="#">c3pxiB_</a>	Alignment	not modelled	98.6	33	<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
88	<a href="#">d1sxja2</a>	Alignment	not modelled	98.5	12	<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
89	<a href="#">c5kzfj_</a>	Alignment	not modelled	98.5	13	<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
90	<a href="#">c6em8E_</a>	Alignment	not modelled	98.5	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
91	<a href="#">c5vy9C_</a>	Alignment	not modelled	98.5	25	<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
92	<a href="#">d1ny5a2</a>	Alignment	not modelled	98.5	15	<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
93	<a href="#">c6matE_</a>	Alignment	not modelled	98.5	23	<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
94	<a href="#">d1ixsb2</a>	Alignment	not modelled	98.5	27	<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
95	<a href="#">c1ojlf_</a>	Alignment	not modelled	98.5	14	<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
96	<a href="#">d1sxje2</a>	Alignment	not modelled	98.4	21	<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
97	<a href="#">c5x06G_</a>	Alignment	not modelled	98.4	18	<b>PDB header:</b> replication <b>Chain:</b> G: <b>PDB Molecule:</b> dnaa regulatory inactivator hda; <b>PDBTitle:</b> dna replication regulation protein
98	<a href="#">c6azyA_</a>	Alignment	not modelled	98.4	30	<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
99	<a href="#">c3uk6H_</a>	Alignment	not modelled	98.4	25	<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
100	<a href="#">c3hteC_</a>	Alignment	not modelled	98.4	22	<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
101	<a href="#">c1sxeE_</a>	Alignment	not modelled	98.4	25	<b>PDB header:</b> replication <b>Chain:</b> E: <b>PDB Molecule:</b> activator 1 40 kda subunit; <b>PDBTitle:</b> crystal structure of the eukaryotic clamp loader (replication factor2 c, rfc) bound to the dna sliding clamp (proliferating cell nuclear3 antigen, pcna)
102	<a href="#">d1in4a2</a>	Alignment	not modelled	98.4	29	<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
103	<a href="#">c2c9oC_</a>	Alignment	not modelled	98.4	28	<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
104	<a href="#">c5ep4A_</a>	Alignment	not modelled	98.3	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 <b>PDB header:</b> hydrolase



105	<a href="#">c2r44A_</a>	Alignment	not modelled	98.3	13	<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
106	<a href="#">c4z8xC_</a>	Alignment	not modelled	98.3	15	<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
107	<a href="#">c2ce7B_</a>	Alignment	not modelled	98.3	16	<b>PDB header:</b> cell division protein <b>Chain:</b> B: <b>PDB Molecule:</b> cell division protein ftsh; <b>PDBTitle:</b> edta treated
108	<a href="#">c4d2qC_</a>	Alignment	not modelled	98.3	25	<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 clpp)
109	<a href="#">c2z4rB_</a>	Alignment	not modelled	98.3	15	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> chromosomal replication initiator protein dnaa; <b>PDBTitle:</b> crystal structure of domain iii from the thermotoga2 maritima replication initiation protein dnaa
110	<a href="#">c4lcbA_</a>	Alignment	not modelled	98.3	15	<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
111	<a href="#">c3d8bB_</a>	Alignment	not modelled	98.3	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> fidgetin-like protein 1; <b>PDBTitle:</b> crystal structure of human fidgetin-like protein 1 in complex with adp
112	<a href="#">c5exsA_</a>	Alignment	not modelled	98.3	16	<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
113	<a href="#">c1xwiA_</a>	Alignment	not modelled	98.3	15	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> skd1 protein; <b>PDBTitle:</b> crystal structure of vps4b
114	<a href="#">c3u5zM_</a>	Alignment	not modelled	98.3	13	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> M: <b>PDB Molecule:</b> dna polymerase accessory protein 44; <b>PDBTitle:</b> structure of t4 bacteriophage clamp loader bound to the t4 clamp,2 primer-template dna, and atp analog
115	<a href="#">c2dhrC_</a>	Alignment	not modelled	98.3	14	<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)
116	<a href="#">c2kjqA_</a>	Alignment	not modelled	98.3	21	<b>PDB header:</b> replication <b>Chain:</b> A: <b>PDB Molecule:</b> dnaa-related protein; <b>PDBTitle:</b> solution structure of protein nmb1076 from neisseria meningitidis.2 northeast structural genomics consortium target mr101b.
117	<a href="#">c6az0A_</a>	Alignment	not modelled	98.3	41	<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
118	<a href="#">c2qz4A_</a>	Alignment	not modelled	98.2	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> paraplegin; <b>PDBTitle:</b> human paraplegin, aaa domain in complex with adp
119	<a href="#">c3nbxX_</a>	Alignment	not modelled	98.2	16	<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
120	<a href="#">c3eihB_</a>	Alignment	not modelled	98.2	18	<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