























# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2008c (- )_2256625_2257950
Date	Mon Aug 5 13:25:11 BST 2019
Unique Job ID	59af98a18b32d80f

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2fnaA_</a>	 Alignment		99.6	20	<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 <i>sulfolobus2 solfataricus</i> p2 at 2.00 a resolution
2	<a href="#">c2qenA_</a>	 Alignment		99.4	18	<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 <i>pyrococcus abyssi</i>
3	<a href="#">d2fnaa2</a>	 Alignment		99.2	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
4	<a href="#">c3pfiB_</a>	 Alignment		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 <i>campylobacter jejuni</i> subsp. <i>jejuni3 nctc 11168</i> in complex with adenosine-5'-diphosphate
5	<a href="#">c1in8A_</a>	 Alignment		98.9	19	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> holliday junction dna helicase ruvb; <b>PDBTitle:</b> <i>thermotoga maritima</i> ruvb t158v
6	<a href="#">c2v1uA_</a>	 Alignment		98.8	19	<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 <i>aeropyrum pernix</i> orc1 protein in complex2 with dna
7	<a href="#">c4xgcA_</a>	 Alignment		98.8	10	<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
8	<a href="#">c4uxjB_</a>	 Alignment		98.7	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> thymidine kinase; <b>PDBTitle:</b> <i>leishmania major</i> thymidine kinase in complex with dttp
9	<a href="#">c6blbA_</a>	 Alignment		98.7	17	<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 <i>pseudomonas aeruginosa</i> in complex3 with adp
10	<a href="#">c5ujmE_</a>	 Alignment		98.7	17	<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
11	<a href="#">d1xbta1</a>	 Alignment		98.7	17	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Type II thymidine kinase

12	<a href="#">c3pvsA_</a>	Alignment		98.7	18	<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
13	<a href="#">c2qbyA_</a>	Alignment		98.7	12	<b>PDB header:</b> replication/dna <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)
14	<a href="#">c3iz8B_</a>	Alignment		98.6	18	<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
15	<a href="#">c3iz8E_</a>	Alignment		98.6	18	<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
16	<a href="#">c1vt4N_</a>	Alignment		98.6	18	<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
17	<a href="#">c3iz8H_</a>	Alignment		98.6	18	<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
18	<a href="#">c1vt4J_</a>	Alignment		98.6	18	<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
19	<a href="#">c1vt4M_</a>	Alignment		98.6	18	<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
20	<a href="#">c1vt4O_</a>	Alignment		98.6	18	<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
21	<a href="#">c3iz8D_</a>	Alignment	not modelled	98.6	18	<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
22	<a href="#">c1vt4K_</a>	Alignment	not modelled	98.6	18	<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
23	<a href="#">c3iz8G_</a>	Alignment	not modelled	98.6	18	<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
24	<a href="#">c3iz8F_</a>	Alignment	not modelled	98.6	18	<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
25	<a href="#">c3iz8C_</a>	Alignment	not modelled	98.6	18	<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
26	<a href="#">c1vt4P_</a>	Alignment	not modelled	98.6	18	<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
27	<a href="#">c1vt4I_</a>	Alignment	not modelled	98.6	18	<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
28	<a href="#">c3iz8A_</a>	Alignment	not modelled	98.6	18	<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
29	<a href="#">c1vt4L_</a>	Alignment	not modelled	98.6	18	<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

30	<a href="#">c2qbyB</a>	Alignment	not modelled	98.6	13	<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)
31	<a href="#">c1ojlD</a>	Alignment	not modelled	98.6	16	<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
32	<a href="#">c4xgcE</a>	Alignment	not modelled	98.5	21	<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
33	<a href="#">c5udb9</a>	Alignment	not modelled	98.5	10	<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="#">c6mfvc</a>	Alignment	not modelled	98.5	20	<b>PDB header:</b> signaling protein <b>Chain:</b> C: <b>PDB Molecule:</b> tetratrico peptide repeat sensor ph0952; <b>PDBTitle:</b> crystal structure of the signal transduction atpase with numerous2 domains (stand) protein with a tetratrico peptide repeat sensor ph09523 from pyrococcus horikoshii
35	<a href="#">c1sxjC</a>	Alignment	not modelled	98.5	19	<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)
36	<a href="#">d1jbka</a>	Alignment	not modelled	98.4	18	<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="#">c1xxhB</a>	Alignment	not modelled	98.4	22	<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
38	<a href="#">c1sxjE</a>	Alignment	not modelled	98.4	15	<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)
39	<a href="#">c1sxjA</a>	Alignment	not modelled	98.4	16	<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)
40	<a href="#">c4xgcD</a>	Alignment	not modelled	98.4	25	<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
41	<a href="#">c2chgB</a>	Alignment	not modelled	98.3	16	<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
42	<a href="#">c5kneA</a>	Alignment	not modelled	98.3	18	<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
43	<a href="#">d1qvra2</a>	Alignment	not modelled	98.3	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
44	<a href="#">c1sxjB</a>	Alignment	not modelled	98.3	19	<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)
45	<a href="#">c5e7pA</a>	Alignment	not modelled	98.3	17	<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 a0qq54), a aaa atpase.
46	<a href="#">c6djuA</a>	Alignment	not modelled	98.3	16	<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
47	<a href="#">c4b4tl</a>	Alignment	not modelled	98.3	16	<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
48	<a href="#">c5uj7B</a>	Alignment	not modelled	98.3	14	<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
49	<a href="#">c1fnnB</a>	Alignment	not modelled	98.3	21	<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
50	<a href="#">c5m7nA</a>	Alignment	not modelled	98.3	20	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> nitrogen assimilation regulatory protein; <b>PDBTitle:</b> crystal structure of ntrx from brucella abortus in complex with atp2 processed with the crystaldirect automated mounting and cryo-cooling3 technology
51	<a href="#">c1jr3E</a>	Alignment	not modelled	98.2	15	<b>PDB header:</b> transferase <b>Chain:</b> E: <b>PDB Molecule:</b> dna polymerase iii, delta' subunit; <b>PDBTitle:</b> crystal structure of the processivity clamp loader gamma complex of e.2 coli dna polymerase iii
52	<a href="#">c3nbxX</a>	Alignment	not modelled	98.2	17	<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
53	<a href="#">d1qvra3</a>	Alignment	not modelled	98.2	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
						<b>PDB header:</b> hydrolase

54	<a href="#">c1hqcb</a>	Alignment	not modelled	98.2	20	<b>Chain:</b> B: <b>PDB Molecule:</b> ruvb; <b>PDBTitle:</b> structure of ruvb from thermus thermophilus hb8
55	<a href="#">c5w0tA</a>	Alignment	not modelled	98.2	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protein msp1; <b>PDBTitle:</b> crystal structure of monomeric msp1 from s. cerevisiae
56	<a href="#">c4z8xC</a>	Alignment	not modelled	98.2	21	<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
57	<a href="#">d1r6bx2</a>	Alignment	not modelled	98.2	19	<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
58	<a href="#">c2x8aA</a>	Alignment	not modelled	98.2	17	<b>PDB header:</b> nuclear protein <b>Chain:</b> A: <b>PDB Molecule:</b> nuclear valosin-containing protein-like; <b>PDBTitle:</b> human nuclear valosin containing protein like (nvl), c-2 terminal aaa-atpase domain
59	<a href="#">c4ciuA</a>	Alignment	not modelled	98.2	22	<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
60	<a href="#">c5uj7C</a>	Alignment	not modelled	98.2	18	<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
61	<a href="#">c3hu2C</a>	Alignment	not modelled	98.2	21	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> translational endoplasmic reticulum atpase; <b>PDBTitle:</b> structure of p97 n-d1 r86a mutant in complex with atpgs
62	<a href="#">c2chvE</a>	Alignment	not modelled	98.2	17	<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 adpnp complex
63	<a href="#">c1qvrB</a>	Alignment	not modelled	98.2	21	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> clpb protein; <b>PDBTitle:</b> crystal structure analysis of clpb
64	<a href="#">c1s3sA</a>	Alignment	not modelled	98.1	23	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> translational endoplasmic reticulum atpase (ter <b>PDBTitle:</b> crystal structure of aaa atpase p97/vcp nd1 in complex with2 p47 c
65	<a href="#">d1sxic2</a>	Alignment	not modelled	98.1	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
66	<a href="#">c2dhrC</a>	Alignment	not modelled	98.1	24	<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)
67	<a href="#">c6azyA</a>	Alignment	not modelled	98.1	16	<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
68	<a href="#">d1sxje2</a>	Alignment	not modelled	98.1	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
69	<a href="#">c2hcbC</a>	Alignment	not modelled	98.1	18	<b>PDB header:</b> replication <b>Chain:</b> C: <b>PDB Molecule:</b> chromosomal replication initiator protein dnaa; <b>PDBTitle:</b> structure of amppcp-bound dnaa from aquifex aeolicus
70	<a href="#">d1ny5a2</a>	Alignment	not modelled	98.1	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
71	<a href="#">c5vy9C</a>	Alignment	not modelled	98.1	18	<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
72	<a href="#">c3zw6B</a>	Alignment	not modelled	98.1	17	<b>PDB header:</b> photosynthesis <b>Chain:</b> B: <b>PDB Molecule:</b> ribulose bisphosphate carboxylase/oxygenase activase 1, <b>PDBTitle:</b> model of hexameric aaa domain arrangement of green-type rubisco2 activase from tobacco.
73	<a href="#">c4ypnA</a>	Alignment	not modelled	98.1	24	<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
74	<a href="#">c4d2qC</a>	Alignment	not modelled	98.1	22	<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)
75	<a href="#">c6b5cA</a>	Alignment	not modelled	98.1	14	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> katanin p60 atpase-containing subunit a-like 1; <b>PDBTitle:</b> structural basis for katanin self-assembly
76	<a href="#">c5x06G</a>	Alignment	not modelled	98.1	20	<b>PDB header:</b> replication <b>Chain:</b> G: <b>PDB Molecule:</b> dnaa regulatory inactivator hda; <b>PDBTitle:</b> dna replication regulation protein
77	<a href="#">c2p65A</a>	Alignment	not modelled	98.1	18	<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="#">c3b9pA</a>	Alignment	not modelled	98.1	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cg5977-pa, isoform a; <b>PDBTitle:</b> spastin
79	<a href="#">c2qz4A</a>	Alignment	not modelled	98.1	21	<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
80	<a href="#">c6az0A</a>	Alignment	not modelled	98.1	22	<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
81	<a href="#">c3cf2B_</a>	Alignment	not modelled	98.1	21	<b>PDB header:</b> transport protein <b>Chain:</b> B; <b>PDB Molecule:</b> transitional endoplasmic reticulum atpase; <b>PDBTitle:</b> structure of p97/vcp in complex with adp/amp-pnp
82	<a href="#">c5d4wB_</a>	Alignment	not modelled	98.1	20	<b>PDB header:</b> chaperone <b>Chain:</b> B; <b>PDB Molecule:</b> putative heat shock protein; <b>PDBTitle:</b> crystal structure of hsp104
83	<a href="#">c3u5zM_</a>	Alignment	not modelled	98.1	15	<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
84	<a href="#">c5udbA_</a>	Alignment	not modelled	98.1	13	<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
85	<a href="#">d1iqa2</a>	Alignment	not modelled	98.1	19	<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
86	<a href="#">c5ifwB_</a>	Alignment	not modelled	98.1	23	<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
87	<a href="#">d1l8qa2</a>	Alignment	not modelled	98.1	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
88	<a href="#">c5oafB_</a>	Alignment	not modelled	98.1	19	<b>PDB header:</b> gene regulation <b>Chain:</b> B; <b>PDB Molecule:</b> rvvb-like 2; <b>PDBTitle:</b> human rvb1/rvb2 heterohexamer in ino80 complex
89	<a href="#">c1r6bX_</a>	Alignment	not modelled	98.0	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
90	<a href="#">c5lkmB_</a>	Alignment	not modelled	98.0	19	<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
91	<a href="#">d1in4a2</a>	Alignment	not modelled	98.0	18	<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
92	<a href="#">c6nyyC_</a>	Alignment	not modelled	98.0	20	<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
93	<a href="#">d1njfa_</a>	Alignment	not modelled	98.0	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
94	<a href="#">d1g41a_</a>	Alignment	not modelled	98.0	32	<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="#">d1ixza_</a>	Alignment	not modelled	98.0	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
96	<a href="#">c1iqpF_</a>	Alignment	not modelled	98.0	20	<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
97	<a href="#">c5udbE_</a>	Alignment	not modelled	98.0	13	<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
98	<a href="#">c6djevE_</a>	Alignment	not modelled	98.0	16	<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
99	<a href="#">c5kneF_</a>	Alignment	not modelled	98.0	20	<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
100	<a href="#">d1sxja2</a>	Alignment	not modelled	98.0	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
101	<a href="#">c3cf1C_</a>	Alignment	not modelled	98.0	23	<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
102	<a href="#">c6em8F_</a>	Alignment	not modelled	98.0	23	<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
103	<a href="#">d1sxjb2</a>	Alignment	not modelled	98.0	19	<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
104	<a href="#">c5mpaL_</a>	Alignment	not modelled	98.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> L; <b>PDB Molecule:</b> 26s protease subunit rpt4; <b>PDBTitle:</b> 26s proteasome in presence of atp (s2)
105	<a href="#">c2z4rB_</a>	Alignment	not modelled	98.0	16	<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
106	<a href="#">c3pxiB_</a>	Alignment	not modelled	98.0	18	<b>PDB header:</b> protein binding <b>Chain:</b> B; <b>PDB Molecule:</b> negative regulator of genetic competence clpc/mech; <b>PDBTitle:</b> structure of meca108:clpc
						<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases

107	<a href="#">d1e32a2</a>	Alignment	not modelled	98.0	21	<b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
108	<a href="#">c1nsfA</a>	Alignment	not modelled	98.0	18	<b>PDB header:</b> protein transport <b>Chain:</b> A; <b>PDB Molecule:</b> n-ethylmaleimide sensitive factor; <b>PDBTitle:</b> d2 hexamerization domain of n-ethylmaleimide sensitive factor (nsf)
109	<a href="#">c6s2pN</a>	Alignment	not modelled	97.9	17	<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
110	<a href="#">d1fnna2</a>	Alignment	not modelled	97.9	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
111	<a href="#">c4b4tj</a>	Alignment	not modelled	97.9	17	<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
112	<a href="#">c3hteC</a>	Alignment	not modelled	97.9	24	<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
113	<a href="#">c4b4tH</a>	Alignment	not modelled	97.9	22	<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
114	<a href="#">c4l16A</a>	Alignment	not modelled	97.9	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> fidgetin-like protein 1; <b>PDBTitle:</b> crystal structure of figl-1 aaa domain in complex with adp
115	<a href="#">c5j1sA</a>	Alignment	not modelled	97.9	22	<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
116	<a href="#">c6e111</a>	Alignment	not modelled	97.9	23	<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
117	<a href="#">c4b4tL</a>	Alignment	not modelled	97.9	17	<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
118	<a href="#">c2r44A</a>	Alignment	not modelled	97.9	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
119	<a href="#">d1d2na</a>	Alignment	not modelled	97.9	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
120	<a href="#">c1w4rC</a>	Alignment	not modelled	97.9	18	<b>PDB header:</b> transferase <b>Chain:</b> C; <b>PDB Molecule:</b> thymidine kinase; <b>PDBTitle:</b> structure of a type ii thymidine kinase with bound dttp