

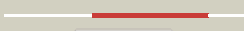
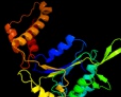























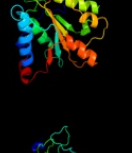


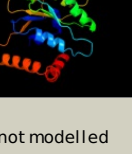

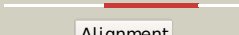
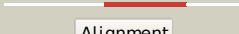
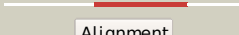
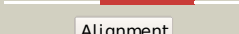




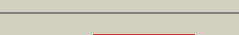
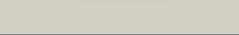
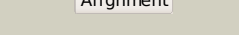
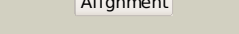
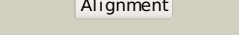


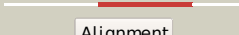
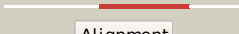



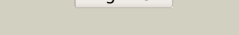
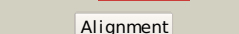



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1qvrB_</a>	 Alignment		99.9	17	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> clpb protein; <b>PDBTitle:</b> crystal structure analysis of clpb
2	<a href="#">c1r6bX_</a>	 Alignment		99.9	19	<b>PDB header:</b> hydrolase <b>Chain:</b> X: <b>PDB Molecule:</b> clpa protein; <b>PDBTitle:</b> high resolution crystal structure of clpa
3	<a href="#">c3pxiB_</a>	 Alignment		99.9	19	<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
4	<a href="#">c2r44A_</a>	 Alignment		99.8	18	<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
5	<a href="#">d1r6bx3</a>	 Alignment		99.8	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
6	<a href="#">c3cf1C_</a>	 Alignment		99.8	19	<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
7	<a href="#">c3nbxX_</a>	 Alignment		99.7	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
8	<a href="#">d1jbka_</a>	 Alignment		99.7	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
9	<a href="#">c2p65A_</a>	 Alignment		99.7	25	<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
10	<a href="#">d1qvra3</a>	 Alignment		99.7	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
11	<a href="#">c1xwiA_</a>	 Alignment		99.7	21	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> skd1 protein; <b>PDBTitle:</b> crystal structure of vps4b

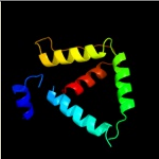
12	<a href="#">c2zamA</a>	Alignment		99.7	25	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> vacuolar protein sorting-associated protein 4b; <b>PDBTitle:</b> crystal structure of mouse skd1/vps4b apo-form
13	<a href="#">c3eihB</a>	Alignment		99.7	18	<b>PDB header:</b> protein 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
14	<a href="#">c3hteC</a>	Alignment		99.7	18	<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
15	<a href="#">c3b9pA</a>	Alignment		99.7	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cg5977-pa, isoform a; <b>PDBTitle:</b> spastin
16	<a href="#">d1g41a</a>	Alignment		99.6	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
17	<a href="#">c3d8bB</a>	Alignment		99.6	22	<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
18	<a href="#">d1um8a</a>	Alignment		99.6	16	<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
19	<a href="#">d1ofha</a>	Alignment		99.6	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
20	<a href="#">d1g8pa</a>	Alignment		99.6	16	<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
21	<a href="#">c3hu2C</a>	Alignment	not modelled	99.5	20	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> transitional endoplasmic reticulum atpase; <b>PDBTitle:</b> structure of p97 n-d1 r86a mutant in complex with atpgs
22	<a href="#">c3k1jA</a>	Alignment	not modelled	99.5	20	<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
23	<a href="#">c3qmzA</a>	Alignment	not modelled	99.5	17	<b>PDB header:</b> motor protein <b>Chain:</b> A: <b>PDB Molecule:</b> cytoplasmic dynein heavy chain; <b>PDBTitle:</b> crystal structure of the cytoplasmic dynein heavy chain motor domain
24	<a href="#">c1s3sA</a>	Alignment	not modelled	99.5	22	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> transitional endoplasmic reticulum atpase (ter <b>PDBTitle:</b> crystal structure of aaa atpase p97/vcp nd1 in complex with2 p47 c
25	<a href="#">c2chvE</a>	Alignment	not modelled	99.5	21	<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
26	<a href="#">d1qvra2</a>	Alignment	not modelled	99.5	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
27	<a href="#">d1ny5a2</a>	Alignment	not modelled	99.5	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
28	<a href="#">c3pxgA</a>	Alignment	not modelled	99.5	23	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> negative regulator of genetic competence clpc/mecc; <b>PDBTitle:</b> structure of meca121 and clpc1-485 complex

29	<a href="#">c2dhrC</a>	Alignment	not modelled	99.5	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)
30	<a href="#">c2x8aA</a>	Alignment	not modelled	99.5	19	<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
31	<a href="#">c1nsfA</a>	Alignment	not modelled	99.5	19	<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)
32	<a href="#">c3pfiB</a>	Alignment	not modelled	99.5	21	<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
33	<a href="#">c1sxiC</a>	Alignment	not modelled	99.5	20	<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 loader2 (replication factor c, rfc) bound to the dna sliding clamp3 (proliferating cell nuclear antigen, pcna)
34	<a href="#">c1iqpF</a>	Alignment	not modelled	99.5	22	<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
35	<a href="#">c2chgB</a>	Alignment	not modelled	99.4	20	<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
36	<a href="#">c2r65A</a>	Alignment	not modelled	99.4	28	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cell division protease ftsh homolog; <b>PDBTitle:</b> crystal structure of helicobacter pylori atp dependent protease, ftsh2 adp complex
37	<a href="#">c3pvsA</a>	Alignment	not modelled	99.4	22	<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
38	<a href="#">c3te6A</a>	Alignment	not modelled	99.4	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
39	<a href="#">c1sxiD</a>	Alignment	not modelled	99.4	15	<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 loader2 (replication factor c, rfc) bound to the dna sliding clamp3 (proliferating cell nuclear antigen, pcna)
40	<a href="#">c1sxiE</a>	Alignment	not modelled	99.4	17	<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 loader2 (replication factor c, rfc) bound to the dna sliding clamp3 (proliferating cell nuclear antigen, pcna)
41	<a href="#">d1d2na</a>	Alignment	not modelled	99.4	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
42	<a href="#">d2ce7a2</a>	Alignment	not modelled	99.4	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
43	<a href="#">d1iqa2</a>	Alignment	not modelled	99.4	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
44	<a href="#">d1sxiB2</a>	Alignment	not modelled	99.4	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
45	<a href="#">d1r6bx2</a>	Alignment	not modelled	99.4	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
46	<a href="#">c2c99A</a>	Alignment	not modelled	99.4	18	<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
47	<a href="#">d1sxiE2</a>	Alignment	not modelled	99.4	16	<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="#">c1sxiB</a>	Alignment	not modelled	99.3	18	<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 loader2 (replication factor c, rfc) bound to the dna sliding clamp3 (proliferating cell nuclear antigen, pcna)
49	<a href="#">c3h4mC</a>	Alignment	not modelled	99.3	29	<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
50	<a href="#">d1sxiC2</a>	Alignment	not modelled	99.3	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
51	<a href="#">c1o1fF</a>	Alignment	not modelled	99.3	11	<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 the2 mechanism for the conformational switch necessary for3 sigma54 binding
52	<a href="#">c1iv2A</a>	Alignment	not modelled	99.3	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent metalloprotease ftsh;

52	<a href="#">c1yzA_</a>	Alignment	not modelled	99.3	49	<b>PDBTitle:</b> crystal structure of the ftsH atpase domain from thermus2 thermophilus <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
53	<a href="#">d1a5ta2</a>	Alignment	not modelled	99.3	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
54	<a href="#">d1ixza_</a>	Alignment	not modelled	99.3	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
55	<a href="#">c2qz4A_</a>	Alignment	not modelled	99.3	25	<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
56	<a href="#">d1e32a2</a>	Alignment	not modelled	99.3	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
57	<a href="#">c1xxhB_</a>	Alignment	not modelled	99.3	17	<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
58	<a href="#">d1r7ra3</a>	Alignment	not modelled	99.3	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
59	<a href="#">c2ce7B_</a>	Alignment	not modelled	99.3	28	<b>PDB header:</b> cell division protein <b>Chain:</b> B: <b>PDB Molecule:</b> cell division protein ftsH; <b>PDBTitle:</b> edta treated
60	<a href="#">c2hcbC_</a>	Alignment	not modelled	99.2	15	<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
61	<a href="#">d1sxd2</a>	Alignment	not modelled	99.2	16	<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="#">c1in8A_</a>	Alignment	not modelled	99.2	23	<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
63	<a href="#">c1jr3E_</a>	Alignment	not modelled	99.2	11	<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 gamma2 complex of e. coli dna polymerase iii
64	<a href="#">d1ixsb2</a>	Alignment	not modelled	99.2	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
65	<a href="#">d1in4a2</a>	Alignment	not modelled	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
66	<a href="#">d1sxja2</a>	Alignment	not modelled	99.2	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
67	<a href="#">d1fnna2</a>	Alignment	not modelled	99.2	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
68	<a href="#">c3f8tA_</a>	Alignment	not modelled	99.2	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> predicted atpase involved in replication control, <b>PDBTitle:</b> crystal structure analysis of a full-length mcm homolog2 from methanopyrus kandleri
69	<a href="#">d1njfa_</a>	Alignment	not modelled	99.2	16	<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="#">c1sxjA_</a>	Alignment	not modelled	99.2	19	<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 loader2 (replication factor c, rfc) bound to the dna sliding clamp3 (proliferating cell nuclear antigen, pcna)
71	<a href="#">d1l8qa2</a>	Alignment	not modelled	99.1	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
72	<a href="#">c3m6aC_</a>	Alignment	not modelled	99.1	24	<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
73	<a href="#">c1hqcb_</a>	Alignment	not modelled	99.1	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> ruvb; <b>PDBTitle:</b> structure of ruvb from thermus thermophilus hb8
74	<a href="#">d1w5sa2</a>	Alignment	not modelled	99.0	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
75	<a href="#">c2v1uA_</a>	Alignment	not modelled	99.0	18	<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
76	<a href="#">c1fnbB_</a>	Alignment	not modelled	99.0	15	<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
77	<a href="#">c3f9vA_</a>	Alignment	not modelled	99.0	15	<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

78	<a href="#">c2kjqA</a>	 Alignment	not modelled	99.0	16	<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.
79	<a href="#">d1oz4a3</a>	 Alignment	not modelled	99.0	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
80	<a href="#">c3ec2A</a>	 Alignment	not modelled	99.0	20	<b>PDB header:</b> replication <b>Chain:</b> A: <b>PDB Molecule:</b> dna replication protein dnac; <b>PDBTitle:</b> crystal structure of the dnac helicase loader
81	<a href="#">d1lv7a</a>	 Alignment	not modelled	99.0	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
82	<a href="#">c2c9oC</a>	 Alignment	not modelled	99.0	15	<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
83	<a href="#">c2z4rB</a>	 Alignment	not modelled	99.0	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
84	<a href="#">c2w58B</a>	 Alignment	not modelled	99.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> primosome component (helicase loader); <b>PDBTitle:</b> crystal structure of the dnaI
85	<a href="#">c3dzdA</a>	 Alignment	not modelled	98.9	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
86	<a href="#">c2qbyA</a>	 Alignment	not modelled	98.8	18	<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)
87	<a href="#">c3bosA</a>	 Alignment	not modelled	98.8	13	<b>PDB header:</b> hydrolase regulator,dna binding protein <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
88	<a href="#">c2qbyB</a>	 Alignment	not modelled	98.8	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)
89	<a href="#">c1ny5A</a>	 Alignment	not modelled	98.8	19	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator (ntrc family); <b>PDBTitle:</b> crystal structure of sigm54 activator (aaa+ atpase) in the inactive2 state
90	<a href="#">d2gnoa2</a>	 Alignment	not modelled	98.7	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
91	<a href="#">c2qgzA</a>	 Alignment	not modelled	98.7	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative primosome component; <b>PDBTitle:</b> crystal structure of a putative primosome component from2 streptococcus pyogenes serotype m3. northeast structural3 genomics target dr58
92	<a href="#">d1e94e</a>	 Alignment	not modelled	98.6	59	<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="#">c2gxaA</a>	 Alignment	not modelled	98.6	16	<b>PDB header:</b> replication/dna <b>Chain:</b> A: <b>PDB Molecule:</b> replication protein e1; <b>PDBTitle:</b> crystal structure of papillomavirus e1 hexameric helicase2 with ssdna and mgadp
94	<a href="#">d1tuea</a>	 Alignment	not modelled	98.4	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
95	<a href="#">d1ye8a1</a>	 Alignment	not modelled	98.4	19	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
96	<a href="#">d1gvnb</a>	 Alignment	not modelled	98.4	32	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Plasmid maintenance system epsilon/zeta, toxin zeta subunit
97	<a href="#">c2p5tD</a>	 Alignment	not modelled	98.2	30	<b>PDB header:</b> transcription regulator <b>Chain:</b> D: <b>PDB Molecule:</b> pezt; <b>PDBTitle:</b> molecular and structural characterization of the pezat chromosomal2 toxin-antitoxin system of the human pathogen streptococcus pneumoniae
98	<a href="#">c3co5B</a>	 Alignment	not modelled	98.2	16	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> putative two-component system transcriptional response <b>PDBTitle:</b> crystal structure of sigma-54 interaction domain of putative2 transcriptional response regulator from neisseria gonorrhoeae
99	<a href="#">d1kaga</a>	 Alignment	not modelled	98.2	50	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Shikimate kinase (AroK)
100	<a href="#">c2v9pH</a>	 Alignment	not modelled	98.2	17	<b>PDB header:</b> hydrolase <b>Chain:</b> H: <b>PDB Molecule:</b> replication protein e1; <b>PDBTitle:</b> crystal structure of papillomavirus e1 hexameric helicase2 dna-free form
101	<a href="#">d2fnaa2</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



102	<a href="#">d2i3ba1</a>	Alignment	not modelled	98.2	40	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
103	<a href="#">d2iyva1</a>	Alignment	not modelled	98.2	44	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Shikimate kinase (AroK)
104	<a href="#">c3tlxA</a>	Alignment	not modelled	98.1	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> adenylate kinase 2; <b>PDBTitle:</b> crystal structure of pf10_0086, adenylate kinase from plasmodium2 falciparum
105	<a href="#">c1zuiA</a>	Alignment	not modelled	98.0	32	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> shikimate kinase; <b>PDBTitle:</b> structural basis for shikimate-binding specificity of helicobacter2 pylori shikimate kinase
106	<a href="#">c3be4A</a>	Alignment	not modelled	98.0	32	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> adenylate kinase; <b>PDBTitle:</b> crystal structure of cryptosporidium parvum adenylate kinase cgd5_3360
107	<a href="#">d1lw7a2</a>	Alignment	not modelled	98.0	24	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nucleotide and nucleoside kinases
108	<a href="#">c1w5sB</a>	Alignment	not modelled	98.0	17	<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)
109	<a href="#">d1e6ca</a>	Alignment	not modelled	98.0	37	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Shikimate kinase (AroK)
110	<a href="#">d1svma</a>	Alignment		98.0	16	<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="#">d3adka</a>	Alignment	not modelled	98.0	28	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nucleotide and nucleoside kinases
112	<a href="#">d1rkba</a>	Alignment	not modelled	98.0	48	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nucleotide and nucleoside kinases
113	<a href="#">c3trfB</a>	Alignment	not modelled	98.0	50	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> shikimate kinase; <b>PDBTitle:</b> structure of a shikimate kinase (arok) from coxiella burnetii
114	<a href="#">d2bdta1</a>	Alignment	not modelled	98.0	48	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Atu3015-like
115	<a href="#">c2xzlA</a>	Alignment	not modelled	98.0	28	<b>PDB header:</b> hydrolase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent helicase nam7; <b>PDBTitle:</b> upf1-rna complex
116	<a href="#">c2fnaA</a>	Alignment	not modelled	98.0	19	<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
117	<a href="#">c3b85A</a>	Alignment	not modelled	97.9	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphate starvation-inducible protein; <b>PDBTitle:</b> crystal structure of predicted phosphate starvation-induced atpase2 phoh2 from corynebacterium glutamicum
118	<a href="#">c3cm0A</a>	Alignment	not modelled	97.9	44	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> adenylate kinase; <b>PDBTitle:</b> crystal structure of adenylate kinase from thermus2 thermophilus hb8
119	<a href="#">d1viaa</a>	Alignment	not modelled	97.9	48	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Shikimate kinase (AroK)
120	<a href="#">c2wjyA</a>	Alignment	not modelled	97.9	28	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> regulator of nonsense transcripts 1; <b>PDBTitle:</b> crystal structure of the complex between human nonsense2 mediated decay factors upf1 and upf2 orthorhombic form