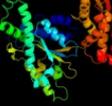
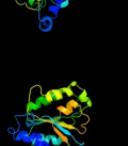
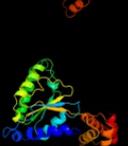
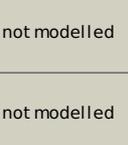


# Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P0A6H5
Date	Thu Jan 5 11:03:09 GMT 2012
Unique Job ID	67695dd1ace55010

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1e94e_</a>	 Alignment		100.0	100	<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
2	<a href="#">d1g41a_</a>	 Alignment		100.0	83	<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
3	<a href="#">d1um8a_</a>	 Alignment		100.0	30	<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="#">d1ofha_</a>	 Alignment		100.0	86	<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
5	<a href="#">c1qvrB_</a>	 Alignment		100.0	29	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> clpb protein; <b>PDBTitle:</b> crystal structure analysis of clpb
6	<a href="#">c3hteC_</a>	 Alignment		100.0	32	<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
7	<a href="#">c1r6bX_</a>	 Alignment		100.0	26	<b>PDB header:</b> hydrolase <b>Chain:</b> X: <b>PDB Molecule:</b> clpa protein; <b>PDBTitle:</b> high resolution crystal structure of clpa
8	<a href="#">c3pxiB_</a>	 Alignment		100.0	27	<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
9	<a href="#">c3cf1C_</a>	 Alignment		100.0	17	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> transitional endoplasmic reticulum atpase; <b>PDBTitle:</b> structure of p97/vcp in complex with adp/adp.alfx
10	<a href="#">d1qvra3</a>	 Alignment		100.0	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
11	<a href="#">d1r6bx3</a>	 Alignment		100.0	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

12	<a href="#">c2dhrC_</a>	Alignment		100.0	18	<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)
13	<a href="#">c3hu2C_</a>	Alignment		99.9	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
14	<a href="#">c1s3sA_</a>	Alignment		99.9	20	<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
15	<a href="#">c2ce7B_</a>	Alignment		99.9	18	<b>PDB header:</b> cell division protein <b>Chain:</b> B: <b>PDB Molecule:</b> cell division protein ftsh; <b>PDBTitle:</b> edta treated
16	<a href="#">c1xwiA_</a>	Alignment		99.9	14	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> skd1 protein; <b>PDBTitle:</b> crystal structure of vps4b
17	<a href="#">c3h4mC_</a>	Alignment		99.9	19	<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
18	<a href="#">c2zamA_</a>	Alignment		99.9	15	<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
19	<a href="#">d2ce7a2</a>	Alignment		99.9	20	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
20	<a href="#">c3eihB_</a>	Alignment		99.8	14	<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
21	<a href="#">c3d8bB_</a>	Alignment	not modelled	99.8	20	<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
22	<a href="#">d1ixza_</a>	Alignment	not modelled	99.8	22	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
23	<a href="#">c1iy2A_</a>	Alignment	not modelled	99.8	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent metalloprotease ftsh; <b>PDBTitle:</b> crystal structure of the ftsh atpase domain from thermus2 thermophilus
24	<a href="#">d1e32a2</a>	Alignment	not modelled	99.8	20	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
25	<a href="#">c3b9pA_</a>	Alignment	not modelled	99.8	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cg5977-pa, isoform a; <b>PDBTitle:</b> spastin
26	<a href="#">c2x8aA_</a>	Alignment	not modelled	99.8	16	<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
27	<a href="#">c2qz4A_</a>	Alignment	not modelled	99.8	22	<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
28	<a href="#">d1lv7a_</a>	Alignment	not modelled	99.8	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
						<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases

29	<a href="#">d1r7ra3</a>	Alignment	not modelled	99.8	19	<b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
30	<a href="#">c2r65A</a>	Alignment	not modelled	99.8	21	<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
31	<a href="#">c1nsfA</a>	Alignment	not modelled	99.8	17	<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="#">d1d2na</a>	Alignment	not modelled	99.8	17	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
33	<a href="#">c3pfiB</a>	Alignment	not modelled	99.7	14	<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
34	<a href="#">d1gvnb</a>	Alignment	not modelled	99.7	11	<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
35	<a href="#">c3m6aC</a>	Alignment	not modelled	99.7	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
36	<a href="#">c2r44A</a>	Alignment	not modelled	99.7	13	<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
37	<a href="#">c2c9oC</a>	Alignment	not modelled	99.7	20	<b>PDB header:</b> hydrolase <b>Chain:</b> C; <b>PDB Molecule:</b> ruvb-like 1; <b>PDBTitle:</b> 3d structure of the human ruvb-like helicase ruvb1
38	<a href="#">c3pvsA</a>	Alignment	not modelled	99.7	29	<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
39	<a href="#">d1oz4a3</a>	Alignment	not modelled	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
40	<a href="#">d1g8pa</a>	Alignment	not modelled	99.6	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
41	<a href="#">c1in8A</a>	Alignment	not modelled	99.6	18	<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
42	<a href="#">d1in4a2</a>	Alignment	not modelled	99.5	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
43	<a href="#">c1hqcB</a>	Alignment	not modelled	99.5	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
44	<a href="#">d1w5sa2</a>	Alignment	not modelled	99.5	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
45	<a href="#">c2p5tD</a>	Alignment	not modelled	99.5	24	<b>PDB header:</b> transcription regulator <b>Chain:</b> D; <b>PDB Molecule:</b> pez2; <b>PDBTitle:</b> molecular and structural characterization of the pezat chromosomal2 toxin-antitoxin system of the human pathogen streptococcus pneumoniae
46	<a href="#">d1ixsb2</a>	Alignment	not modelled	99.5	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
47	<a href="#">c1ojlF</a>	Alignment	not modelled	99.4	16	<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
48	<a href="#">d1jbka</a>	Alignment	not modelled	99.4	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
49	<a href="#">d1qvra2</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
50	<a href="#">d1r6bx2</a>	Alignment	not modelled	99.4	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="#">c2c99A</a>	Alignment	not modelled	99.4	19	<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
52	<a href="#">c3u5zM</a>	Alignment	not modelled	99.4	16	<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
						<b>PDB header:</b> replication <b>Chain:</b> C; <b>PDB Molecule:</b> activator 1 40 kda subunit;

53	<a href="#">c1sxC</a>	Alignment	not modelled	99.4	17	<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)
54	<a href="#">d1ny5a2</a>	Alignment	not modelled	99.4	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
55	<a href="#">c2chvE</a>	Alignment	not modelled	99.4	16	<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
56	<a href="#">c2p65A</a>	Alignment	not modelled	99.3	19	<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 of 2 chaperone clpb1, putative, (pv089580) from plasmodium vivax
57	<a href="#">c2hcbC</a>	Alignment	not modelled	99.3	20	<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
58	<a href="#">c1iqpF</a>	Alignment	not modelled	99.3	18	<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
59	<a href="#">d1sxa2</a>	Alignment	not modelled	99.3	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
60	<a href="#">c1sxE</a>	Alignment	not modelled	99.3	12	<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)
61	<a href="#">c1sxD</a>	Alignment	not modelled	99.3	18	<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)
62	<a href="#">d1sxc2</a>	Alignment	not modelled	99.2	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
63	<a href="#">c1sxB</a>	Alignment	not modelled	99.2	13	<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)
64	<a href="#">c3k1jA</a>	Alignment	not modelled	99.2	29	<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
65	<a href="#">c1sxA</a>	Alignment	not modelled	99.2	17	<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)
66	<a href="#">c3nbxX</a>	Alignment	not modelled	99.2	28	<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
67	<a href="#">d1l8qa2</a>	Alignment	not modelled	99.2	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
68	<a href="#">c3bosA</a>	Alignment	not modelled	99.2	15	<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
69	<a href="#">d1fnna2</a>	Alignment	not modelled	99.2	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
70	<a href="#">c1xxhB</a>	Alignment	not modelled	99.2	25	<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
71	<a href="#">c3pxgA</a>	Alignment	not modelled	99.1	19	<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
72	<a href="#">d1njfa</a>	Alignment	not modelled	99.1	30	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
73	<a href="#">c2chgB</a>	Alignment	not modelled	99.1	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
74	<a href="#">d1iqpa2</a>	Alignment	not modelled	99.1	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
75	<a href="#">d1sxe2</a>	Alignment	not modelled	99.1	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
76	<a href="#">c2z4rB</a>	Alignment	not modelled	99.1	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
77	<a href="#">d1sxb2</a>	Alignment	not modelled	99.1	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 <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases
78	<a href="#">d1a5ta2</a>	Alignment	not modelled	99.0	9	<b>Family:</b> Extended AAA-ATPase domain <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases
79	<a href="#">d1sxjd2</a>	Alignment	not modelled	98.9	34	<b>Family:</b> Extended AAA-ATPase domain <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases
80	<a href="#">c3ec2A_</a>	Alignment	not modelled	98.9	24	<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="#">c1fnnB_</a>	Alignment	not modelled	98.8	16	<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
82	<a href="#">c2kjqA_</a>	Alignment	not modelled	98.7	17	<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.
83	<a href="#">c3te6A_</a>	Alignment	not modelled	98.7	13	<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
84	<a href="#">c3dzdA_</a>	Alignment	not modelled	98.7	15	<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
85	<a href="#">c2w58B_</a>	Alignment	not modelled	98.7	15	<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
86	<a href="#">c3tlxA_</a>	Alignment	not modelled	98.6	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
87	<a href="#">c3f8tA_</a>	Alignment	not modelled	98.6	18	<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
88	<a href="#">c1ny5A_</a>	Alignment	not modelled	98.6	17	<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
89	<a href="#">c3be4A_</a>	Alignment	not modelled	98.6	21	<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
90	<a href="#">c2qgzA_</a>	Alignment	not modelled	98.6	14	<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
91	<a href="#">d1kaga_</a>	Alignment	not modelled	98.6	38	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Shikimate kinase (AroK)
92	<a href="#">c2v1uA_</a>	Alignment	not modelled	98.6	32	<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
93	<a href="#">d1ye8a1</a>	Alignment	not modelled	98.6	23	<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)
94	<a href="#">c1w5sB_</a>	Alignment	not modelled	98.5	20	<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)
95	<a href="#">c1zuiA_</a>	Alignment	not modelled	98.5	18	<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
96	<a href="#">c2qbyA_</a>	Alignment	not modelled	98.5	21	<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)
97	<a href="#">d1svma_</a>	Alignment	not modelled	98.5	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
98	<a href="#">c2qbyB_</a>	Alignment	not modelled	98.5	23	<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)
99	<a href="#">d1lw7a2</a>	Alignment	not modelled	98.5	23	<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
100	<a href="#">d2iyva1</a>	Alignment	not modelled	98.5	38	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Shikimate kinase (AroK)
101	<a href="#">c3trfB_</a>	Alignment	not modelled	98.5	38	<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
102	<a href="#">d2ak3a1</a>	Alignment	not modelled	98.5	17	<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

103	<a href="#">c2ak3B_</a>	Alignment	not modelled	98.5	17	<b>PDB header:</b> transferase (phosphotransferase) <b>Chain:</b> B: <b>PDB Molecule:</b> adenylate kinase isoenzyme-3; <b>PDBTitle:</b> the three-dimensional structure of the complex between2 mitochondrial matrix adenylate kinase and its substrate3 amp at 1.85 angstroms resolution
104	<a href="#">d1e6ca_</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> Shikimate kinase (AroK)
105	<a href="#">d1viaa_</a>	Alignment	not modelled	98.4	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)
106	<a href="#">d1ak2a1</a>	Alignment	not modelled	98.4	33	<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
107	<a href="#">c2ar7A_</a>	Alignment	not modelled	98.4	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> adenylate kinase 4; <b>PDBTitle:</b> crystal structure of human adenylate kinase 4, ak4
108	<a href="#">d2i3ba1</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> RecA protein-like (ATPase-domain)
109	<a href="#">d1qha_</a>	Alignment	not modelled	98.3	21	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Chloramphenicol phosphotransferase
110	<a href="#">c2rhmD_</a>	Alignment	not modelled	98.3	29	<b>PDB header:</b> unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> putative kinase; <b>PDBTitle:</b> crystal structure of a putative kinase (caur_3907) from chloroflexus2 aurantiacus j-10-fl at 1.70 a resolution
111	<a href="#">c2bwjC_</a>	Alignment	not modelled	98.3	24	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> adenylate kinase 5; <b>PDBTitle:</b> structure of adenylate kinase 5
112	<a href="#">d1zp6a1</a>	Alignment	not modelled	98.3	35	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Atu3015-like
113	<a href="#">d1rkba_</a>	Alignment	not modelled	98.3	44	<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
114	<a href="#">d3adka_</a>	Alignment	not modelled	98.3	18	<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
115	<a href="#">d1y63a_</a>	Alignment	not modelled	98.3	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
116	<a href="#">c1jr3E_</a>	Alignment	not modelled	98.3	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 gamma2 complex of e. coli dna polymerase iii
117	<a href="#">d1qf9a_</a>	Alignment	not modelled	98.3	14	<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
118	<a href="#">d1x6va3</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> Adenosine-5' phosphosulfate kinase (APS kinase)
119	<a href="#">c3t61A_</a>	Alignment	not modelled	98.3	29	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> gluconokinase; <b>PDBTitle:</b> crystal structure of a gluconokinase from sinorhizobium meliloti 1021
120	<a href="#">c3cm0A_</a>	Alignment	not modelled	98.2	28	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> adenylate kinase; <b>PDBTitle:</b> crystal structure of adenylate kinase from thermophilus hb8