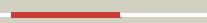


# Phyre<sup>2</sup>

Email	i.a.kelley@imperial.ac.uk
Description	P64612
Date	Thu Jan 5 12:09:55 GMT 2012
Unique Job ID	4e3c15d7821830a8

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2w58B_</a>			99.8	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
2	<a href="#">c2hcbC_</a>			99.8	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
3	<a href="#">c2qgzA_</a>			99.8	17	<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 from streptococcus pyogenes serotype m3. northeast structural genomics target dr58
4	<a href="#">c3ec2A_</a>			99.7	15	<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
5	<a href="#">c3cf1C_</a>			99.6	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/vcp in complex with adp/adp.alfx
6	<a href="#">c3hu2C_</a>			99.5	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 n-d1 r86a mutant in complex with atpgs
7	<a href="#">d1l8qa2</a>			99.3	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
8	<a href="#">c1s3sA_</a>			99.3	18	<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
9	<a href="#">c2kjgA_</a>			99.2	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.
10	<a href="#">c1qvrB_</a>			99.2	14	<b>PDB header:</b> chaperone <b>Chain:</b> B; <b>PDB Molecule:</b> clpb protein; <b>PDBTitle:</b> crystal structure analysis of clpb
11	<a href="#">c2zamA_</a>			99.1	17	<b>PDB header:</b> protein transport <b>Chain:</b> A; <b>PDB Molecule:</b> vacuolar protein sorting-associating protein 4b; <b>PDBTitle:</b> crystal structure of mouse skd1/vps4b apo-form

12	<a href="#">c3pxiB_</a>			99.1	16	<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
13	<a href="#">c2dhrC_</a>			99.1	20	<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)
14	<a href="#">c3eiB_</a>			99.1	15	<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
15	<a href="#">c1xwiA_</a>			99.1	17	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> skd1 protein; <b>PDBTitle:</b> crystal structure of vps4
16	<a href="#">d1g4la_</a>			99.0	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
17	<a href="#">c1iy2A_</a>			99.0	17	<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
18	<a href="#">c3b9pA_</a>			99.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cg5977-pa, isoform a; <b>PDBTitle:</b> spastin
19	<a href="#">d2ce7a2</a>			99.0	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="#">c2z4rB_</a>			99.0	19	<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
21	<a href="#">d1r7ra3</a>		not modelled	99.0	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
22	<a href="#">c1r6bX_</a>		not modelled	99.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> X: <b>PDB Molecule:</b> clpa protein; <b>PDBTitle:</b> high resolution crystal structure of clpa
23	<a href="#">c3d8bB_</a>		not modelled	99.0	18	<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
24	<a href="#">d1d2na_</a>		not modelled	98.9	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
25	<a href="#">c3bosA_</a>		not modelled	98.9	17	<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
26	<a href="#">c3pf1B_</a>		not modelled	98.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> holliday junction atp-dependent dna helicase ruvb; <b>PDBTitle:</b> 2.7 angstrom resolution crystal structure of a probable holliday2 junction dna helicase (ruvb) from campylobacter jejuni subsp. jejuni3 nctc 11168 in complex with adenosine-5'-diphosphate
27	<a href="#">c3u5zM_</a>		not modelled	98.9	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

28	<a href="#">c2ce7B</a>	Alignment	not modelled	98.9	20	<b>PDB header:</b> cell division protein <b>Chain:</b> B: <b>PDB Molecule:</b> cell division protein ftsh; <b>PDBTitle:</b> edta treated
29	<a href="#">d1ofha</a>	Alignment	not modelled	98.9	15	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
30	<a href="#">c1nsfA</a>	Alignment	not modelled	98.9	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)
31	<a href="#">d1ixza</a>	Alignment	not modelled	98.9	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
32	<a href="#">d1sxja2</a>	Alignment	not modelled	98.8	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
33	<a href="#">c2x8aA</a>	Alignment	not modelled	98.8	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
34	<a href="#">c2r65A</a>	Alignment	not modelled	98.8	16	<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
35	<a href="#">c2qz4A</a>	Alignment	not modelled	98.8	18	<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
36	<a href="#">d1gvr43</a>	Alignment	not modelled	98.8	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
37	<a href="#">d1e32a2</a>	Alignment	not modelled	98.7	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
38	<a href="#">c3pvsA</a>	Alignment	not modelled	98.7	16	<b>PDB header:</b> recombination <b>Chain:</b> A: <b>PDB Molecule:</b> replication-associated recombination protein a; <b>PDBTitle:</b> structure and biochemical activities of escherichia coli mgsa
39	<a href="#">d1r6bx3</a>	Alignment	not modelled	98.7	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
40	<a href="#">c3h4mC</a>	Alignment	not modelled	98.7	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
41	<a href="#">d1um8a</a>	Alignment	not modelled	98.7	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
42	<a href="#">c1in8A</a>	Alignment	not modelled	98.6	19	<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
43	<a href="#">c3te6A</a>	Alignment	not modelled	98.6	9	<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
44	<a href="#">d1jbka</a>	Alignment	not modelled	98.6	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="#">c1sxja</a>	Alignment	not modelled	98.6	18	<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)
46	<a href="#">c3nbX</a>	Alignment	not modelled	98.5	24	<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
47	<a href="#">d1in4a2</a>	Alignment	not modelled	98.5	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
48	<a href="#">d1fnna2</a>	Alignment	not modelled	98.5	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
49	<a href="#">d1e94e</a>	Alignment		98.5	17	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
50	<a href="#">c2p65A</a>	Alignment	not modelled	98.4	16	<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 chaperone clpb1, putative, (pv089580) from plasmodium vivax
51	<a href="#">c3hteC</a>	Alignment	not modelled	98.4	17	<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
52	<a href="#">c2chgb</a>	Alignment	not modelled	98.4	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
53	<a href="#">c1xxhB_</a>	Alignment	not modelled	98.4	<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
54	<a href="#">d1ny5a2</a>	Alignment	not modelled	98.3	<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="#">c1sxje_</a>	Alignment	not modelled	98.3	<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)
56	<a href="#">d1lv7a_</a>	Alignment	not modelled	98.3	<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="#">c2v1uA_</a>	Alignment	not modelled	98.2	<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
58	<a href="#">d1oz4a3</a>	Alignment	not modelled	98.2	<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="#">c1fnnB_</a>	Alignment	not modelled	98.2	<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
60	<a href="#">c2c99A_</a>	Alignment	not modelled	98.2	<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
61	<a href="#">d1sxjc2</a>	Alignment	not modelled	98.2	<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="#">c2p5tD_</a>	Alignment	not modelled	98.2	<b>PDB header:</b> transcription regulator <b>Chain:</b> D: <b>PDB Molecule:</b> pezt; <b>PDBTitle:</b> molecular and structural characterization of the pezt chromosomal2 toxin-antitoxin system of the human pathogen streptococcus pneumoniae
63	<a href="#">c2c9oC_</a>	Alignment	not modelled	98.2	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> rvub-like 1; <b>PDBTitle:</b> 3d structure of the human rvub-like helicase rvbl1
64	<a href="#">c1ojIF_</a>	Alignment	not modelled	98.1	<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
65	<a href="#">d1lqpa2</a>	Alignment	not modelled	98.1	<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="#">d1sxjb2</a>	Alignment	not modelled	98.1	<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="#">d1gvnb_</a>	Alignment	not modelled	98.1	<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
68	<a href="#">c1sxjd_</a>	Alignment	not modelled	98.1	<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)
69	<a href="#">d1sxje2</a>	Alignment	not modelled	98.1	<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="#">c2r44A_</a>	Alignment	not modelled	98.1	<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
71	<a href="#">c1ny5A_</a>	Alignment	not modelled	98.1	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator (ntrc family); <b>PDBTitle:</b> crystal structure of sigma54 activator (aaa+ atpase) in the inactive2 state
72	<a href="#">c3co5B_</a>	Alignment	not modelled	98.0	<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
73	<a href="#">c3pxgA_</a>	Alignment	not modelled	98.0	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> negative regulator of genetic competence clpc/meccb; <b>PDBTitle:</b> structure of meca121 and clpc1-485 complex
74	<a href="#">d1a5ta2</a>	Alignment	not modelled	98.0	<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="#">c1sxjb_</a>	Alignment	not modelled	98.0	<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)
					<b>PDB header:</b> replication <b>Chain:</b> C: <b>PDB Molecule:</b> activator 1 40 kda subunit;

76	<a href="#">c1sxjC_</a>	Alignment	not modelled	98.0	11	<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)
77	<a href="#">c1hqcB_</a>	Alignment	not modelled	97.9	22	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> ruvb; <b>PDBTitle:</b> structure of ruvb from thermus thermophilus hb8
78	<a href="#">d1qvra2</a>	Alignment	not modelled	97.9	23	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
79	<a href="#">d1njfa_</a>	Alignment	not modelled	97.8	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
80	<a href="#">d1ixsb2</a>	Alignment	not modelled	97.8	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
81	<a href="#">d1ye8a1</a>	Alignment	not modelled	97.7	22	<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)
82	<a href="#">c2chvE_</a>	Alignment	not modelled	97.7	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 adnpn complex
83	<a href="#">cliqpF_</a>	Alignment	not modelled	97.7	20	<b>PDB header:</b> replication <b>Chain:</b> F: <b>PDB Molecule:</b> rfcfs; <b>PDBTitle:</b> crystal structure of the clamp loader small subunit from2 pyrococcus furiosus
84	<a href="#">c1jr3E_</a>	Alignment	not modelled	97.7	18	<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
85	<a href="#">c2qbyB_</a>	Alignment	not modelled	97.6	19	<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)
86	<a href="#">c3dzdA_</a>	Alignment	not modelled	97.6	17	<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
87	<a href="#">d1sxjd2</a>	Alignment	not modelled	97.6	12	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
88	<a href="#">d1vpla_</a>	Alignment	not modelled	97.5	18	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> ABC transporter ATPase domain-like
89	<a href="#">d1b0ua_</a>	Alignment	not modelled	97.5	23	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> ABC transporter ATPase domain-like
90	<a href="#">d1r6bx2</a>	Alignment	not modelled	97.5	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
91	<a href="#">c1vcia_</a>	Alignment	not modelled	97.5	24	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> sugar-binding transport atp-binding protein; <b>PDBTitle:</b> crystal structure of the atp-binding cassette of multisugar2 transporter from pyrococcus horikoshii ot3 complexed with3 atp
92	<a href="#">d1g6ha_</a>	Alignment	not modelled	97.5	20	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> ABC transporter ATPase domain-like
93	<a href="#">c2qbyA_</a>	Alignment	not modelled	97.4	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)
94	<a href="#">c2d3wb_</a>	Alignment	not modelled	97.4	19	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> probable atp-dependent transporter sufC; <b>PDBTitle:</b> crystal structure of escherichia coli sufC, an atpase2 compenent of the suf iron-sulfur cluster assembly machinery
95	<a href="#">d2eyqa3</a>	Alignment	not modelled	97.4	17	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Tandem AAA-ATPase domain
96	<a href="#">c2it1B_</a>	Alignment	not modelled	97.4	24	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> 362aa long hypothetical maltose/maltodextrin <b>PDBTitle:</b> structure of ph0203 protein from pyrococcus horikoshii
97	<a href="#">c3fvqB_</a>	Alignment	not modelled	97.4	24	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> fe(3+) ions import atp-binding protein fbpc; <b>PDBTitle:</b> crystal structure of the nucleotide binding domain fbpc2 complexed with atp
98	<a href="#">d1l7vc_</a>	Alignment	not modelled	97.4	22	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> ABC transporter ATPase domain-like
99	<a href="#">c2yz2B_</a>	Alignment	not modelled	97.3	26	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative abc transporter atp-binding protein tm_0222; <b>PDBTitle:</b> crystal structure of the abc transporter in the cobalt transport2 system
100	<a href="#">cloxtB_</a>	Alignment	not modelled	97.3	27	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> abc transporter, atp binding protein; <b>PDBTitle:</b> crystal structure of glcv, the abc-atpase of the glucose abc2 transporter from sulfolobus solfataricus

101	<a href="#">c2olkD_</a>		Alignment	not modelled	97.3	21	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> amino acid abc transporter; <b>PDBTitle:</b> abc protein artp in complex with adp-beta-s
102	<a href="#">d1alval</a>		Alignment	not modelled	97.3	14	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RNA helicase
103	<a href="#">c2ihyB_</a>		Alignment	not modelled	97.3	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> abc transporter, atp-binding protein; <b>PDBTitle:</b> structure of the staphylococcus aureus putative atpase subunit of an2 atp-binding cassette (abc) transporter
104	<a href="#">c2d2fA_</a>		Alignment	not modelled	97.3	19	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> sufc protein; <b>PDBTitle:</b> crystal structure of atypical cytoplasmic abc-atpase sufC from thermus2 thermophilus hb8
105	<a href="#">c3d31B_</a>		Alignment	not modelled	97.2	23	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> sulfate/molybdate abc transporter, atp-binding <b>PDBTitle:</b> modbc from methanosaerica acetivorans
106	<a href="#">d2awna2</a>		Alignment	not modelled	97.2	21	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> ABC transporter ATPase domain-like
107	<a href="#">c2ng2C_</a>		Alignment	not modelled	97.2	23	<b>PDB header:</b> metal transport <b>Chain:</b> C: <b>PDB Molecule:</b> hypothetical abc transporter atp-binding protein <b>PDBTitle:</b> an inward-facing conformation of a putative metal-chelate2 type abc transporter.
108	<a href="#">d1ji0a_</a>		Alignment	not modelled	97.2	17	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> ABC transporter ATPase domain-like
109	<a href="#">d2fnaa2</a>		Alignment	not modelled	97.2	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
110	<a href="#">d1sgwa_</a>		Alignment	not modelled	97.2	16	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> ABC transporter ATPase domain-like
111	<a href="#">c1z47B_</a>		Alignment	not modelled	97.2	27	<b>PDB header:</b> ligand binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> putative abc-transporter atp-binding protein; <b>PDBTitle:</b> structure of the atpase subunit cysA of the putative2 sulfate atp-binding cassette (abc) transporter from3 alicyclobacillus acidocaldarius
112	<a href="#">c2w0mA_</a>		Alignment	not modelled	97.2	17	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> sso2452; <b>PDBTitle:</b> crystal structure of sso2452 from sulfolobus solfatataricus2 p2
113	<a href="#">d1g8pa_</a>		Alignment	not modelled	97.1	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
114	<a href="#">c2yyzA_</a>		Alignment	not modelled	97.1	26	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> sugar abc transporter, atp-binding protein; <b>PDBTitle:</b> crystal structure of sugar abc transporter, atp-binding protein
115	<a href="#">c1yqtA_</a>		Alignment	not modelled	97.1	17	<b>PDB header:</b> hydrolase/translation <b>Chain:</b> A: <b>PDB Molecule:</b> rnase I inhibitor; <b>PDBTitle:</b> rnase-I inhibitor
116	<a href="#">c2fnaA_</a>		Alignment	not modelled	97.1	18	<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 solfatataricus p2 at 2.00 a resolution
117	<a href="#">c2pcjB_</a>		Alignment	not modelled	97.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> lipoprotein-releasing system atp-binding protein lolo; <b>PDBTitle:</b> crystal structure of abc transporter (aq_297) from aquifex aeolicus2 vf5
118	<a href="#">c3nhaA_</a>		Alignment	not modelled	97.0	20	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> atp-binding cassette sub-family b member 6, mitochondrial; <b>PDBTitle:</b> nucleotide binding domain of human abcb6 (adp mg bound structure)
119	<a href="#">c2px0D_</a>		Alignment	not modelled	97.0	16	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> D: <b>PDB Molecule:</b> flagellar biosynthesis protein flhf; <b>PDBTitle:</b> crystal structure of flhf complexed with gmppnp/mg(2+)
120	<a href="#">c2d62A_</a>		Alignment	not modelled	97.0	21	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> multiple sugar-binding transport atp-binding <b>PDBTitle:</b> crystal structure of multiple sugar binding transport atp-2 binding protein