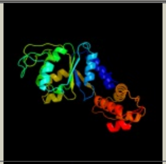
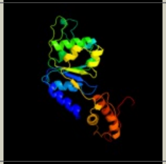
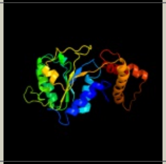
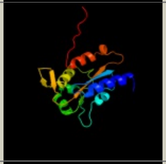
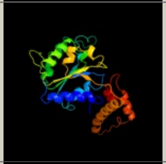
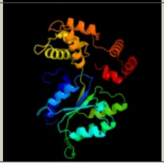
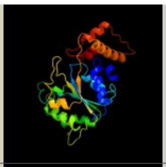
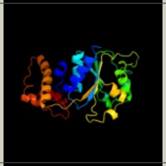
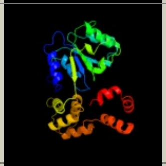
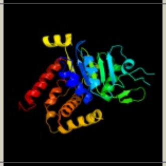
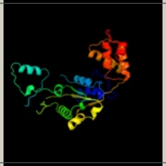
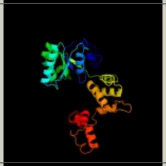
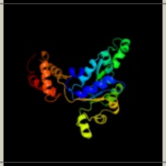
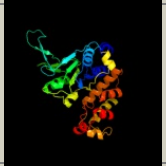
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P37344
Date	Thu Jan 5 11:55:23 GMT 2012
Unique Job ID	f45b95884bb774e9

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1ny5A_	Alignment		100.0	43	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** crystal structure of sigm54 activator (aaa+ atpase) in the inactive2 state
2	c3dzdA_	Alignment		100.0	45	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** crystal structure of sigma54 activator ntrc4 in the inactive2 state
3	c2c99A_	Alignment		100.0	100	**PDB header:**transcription regulation **Chain:** A: **PDB Molecule:**psp operon transcriptional activator; **PDBTitle:** structural basis of the nucleotide driven conformational2 changes in the aaa domain of transcription activator pspf
4	d1ny5a2	Alignment		100.0	43	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
5	c1ojlF_	Alignment		100.0	45	**PDB header:**response regulator **Chain:** F: **PDB Molecule:**transcriptional regulatory protein zrar; **PDBTitle:** crystal structure of a sigma54-activator suggests the2 mechanism for the conformational switch necessary for3 sigma54 binding
6	c1qvrB_	Alignment		99.9	23	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**clpb protein; **PDBTitle:** crystal structure analysis of clpb
7	c3co5B_	Alignment		99.9	26	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**putative two-component system transcriptional response **PDBTitle:** crystal structure of sigma-54 interaction domain of putative2 transcriptional response regulator from neisseria gonorrhoeae
8	d1r6bx3	Alignment		99.9	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
9	d1um8a_	Alignment		99.9	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
10	c3pxiB_	Alignment		99.9	19	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**negative regulator of genetic competence clpc/mecb; **PDBTitle:** structure of meca108:clpc
11	c3pfiB_	Alignment		99.9	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**holliday junction atp-dependent dna helicase ruvb; **PDBTitle:** 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

12	c1r6bX_	Alignment		99.9	21	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**clpa protein; **PDBTitle:** high resolution crystal structure of clpa
13	d1qvra3	Alignment		99.9	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
14	c1in8A_	Alignment		99.8	14	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**holliday junction dna helicase ruvb; **PDBTitle:** thermotoga maritima ruvb t158v
15	c3nbxX_	Alignment		99.8	17	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**atpase rava; **PDBTitle:** crystal structure of e. coli rava (regulatory atpase variant a) in2 complex with adp
16	c3k1jA_	Alignment		99.8	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent protease lon; **PDBTitle:** crystal structure of lon protease from thermococcus onnurineus na1
17	c3pvsA_	Alignment		99.8	13	**PDB header:**recombination **Chain:** A: **PDB Molecule:**replication-associated recombination protein a; **PDBTitle:** structure and biochemical activities of escherichia coli mgsa
18	c3hteC_	Alignment		99.7	18	**PDB header:**motor protein **Chain:** C: **PDB Molecule:**atp-dependent clp protease atp-binding subunit clpx; **PDBTitle:** crystal structure of nucleotide-free hexameric clpx
19	c2r44A_	Alignment		99.7	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a putative atpase (chu_0153) from cytophaga2 hutchinsonii atcc 33406 at 2.00 a resolution
20	d1l8qa2	Alignment		99.7	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
21	d1g8pa_	Alignment	not modelled	99.7	23	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
22	d1g41a_	Alignment	not modelled	99.7	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
23	c1hqcB_	Alignment	not modelled	99.7	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**ruvb; **PDBTitle:** structure of ruvb from thermus thermophilus hb8
24	d1ofha_	Alignment	not modelled	99.7	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
25	c1nsfA_	Alignment	not modelled	99.7	15	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**n-ethylmaleimide sensitive factor; **PDBTitle:** d2 hexamerization domain of n-ethylmaleimide sensitive factor (nsf)
26	c2hcbC_	Alignment	not modelled	99.7	16	**PDB header:**replication **Chain:** C: **PDB Molecule:**chromosomal replication initiator protein dnaa; **PDBTitle:** structure of amppcp-bound dnaa from aquifex aeolicus
27	c3bosA_	Alignment	not modelled	99.7	11	**PDB header:**hydrolase regulator,dna binding protein **Chain:** A: **PDB Molecule:**putative dna replication factor; **PDBTitle:** crystal structure of a putative dna replication regulator hda2 (sama_1916) from shewanella amazonensis sb2b at 1.75 a resolution
28	c2c9oC_	Alignment	not modelled	99.6	18	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**ruvb-like 1; **PDBTitle:** 3d structure of the human ruvb-like helicase ruvbl1

29	d1in4a2	Alignment	not modelled	99.6	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
30	c3cf1C_	Alignment	not modelled	99.6	24	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**transitional endoplasmic reticulum atpase; **PDBTitle:** structure of p97/vcp in complex with adp/adp.alfx
31	d1ixsb2	Alignment	not modelled	99.6	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
32	c3f8tA_	Alignment	not modelled	99.6	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**predicted atpase involved in replication control, **PDBTitle:** crystal structure analysis of a full-length mcm homolog2 from methanopyrus kandleri
33	c2z4rB_	Alignment	not modelled	99.6	14	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**chromosomal replication initiator protein dnaa; **PDBTitle:** crystal structure of domain iii from the thermotoga2 maritima replication initiation protein dnaa
34	d1sxjd2	Alignment	not modelled	99.6	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
35	d1d2na_	Alignment	not modelled	99.6	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
36	c3eihB_	Alignment	not modelled	99.6	19	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**vacuolar protein sorting-associated protein 4; **PDBTitle:** crystal structure of s.cerevisiae vps4 in the presence of atpgammas
37	c2dhrC_	Alignment	not modelled	99.6	21	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**ftsh; **PDBTitle:** whole cytosolic region of atp-dependent metalloprotease2 ftsh (g399l)
38	d1fnna2	Alignment	not modelled	99.5	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
39	c1xwiA_	Alignment	not modelled	99.5	18	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**skd1 protein; **PDBTitle:** crystal structure of vps4b
40	c3b9pA_	Alignment	not modelled	99.5	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cg5977-pa, isoform a; **PDBTitle:** spastin
41	c2chgB_	Alignment	not modelled	99.5	20	**PDB header:**dna-binding protein **Chain:** B: **PDB Molecule:**replication factor c small subunit; **PDBTitle:** replication factor c domains 1 and 2
42	c3hu2C_	Alignment	not modelled	99.5	22	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**transitional endoplasmic reticulum atpase; **PDBTitle:** structure of p97 n-d1 r86a mutant in complex with atpgs
43	d1iqpa2	Alignment	not modelled	99.5	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
44	c3u5zM_	Alignment	not modelled	99.5	15	**PDB header:**dna binding protein/dna **Chain:** M: **PDB Molecule:**dna polymerase accessory protein 44; **PDBTitle:** structure of t4 bacteriophage clamp loader bound to the t4 clamp,2 primer-template dna, and atp analog
45	c1xxhB_	Alignment	not modelled	99.5	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**dna polymerase iii subunit gamma; **PDBTitle:** atpgs bound e. coli clamp loader complex
46	c2zamA_	Alignment	not modelled	99.5	19	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**vacuolar protein sorting-associating protein 4b; **PDBTitle:** crystal structure of mouse skd1/vps4b apo-form
47	c2p65A_	Alignment	not modelled	99.5	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein pf08_0063; **PDBTitle:** crystal structure of the first nucleotide binding domain of2 chaperone clpb1, putative, (pv089580) from plasmodium vivax
48	d1ntca_	Alignment	not modelled	99.5	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
49	c3d8bB_	Alignment	not modelled	99.5	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**fidgetin-like protein 1; **PDBTitle:** crystal structure of human fidgetin-like protein 1 in complex with adp
50	d2ce7a2	Alignment	not modelled	99.5	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
51	d1njfa_	Alignment	not modelled	99.4	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
52	c2ce7B_	Alignment	not modelled	99.4	18	**PDB header:**cell division protein **Chain:** B: **PDB Molecule:**cell division protein ftsh; **PDBTitle:** edta treated
53	c2r65A_	Alignment	not modelled	99.4	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cell division protease ftsh homolog; **PDBTitle:** crystal structure of helicobacter pylori atp dependent protease, ftsh2 adp complex
54	c3h4mC	Alignment	not modelled	99.4	23	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**proteasome-activating nucleotidase;

		Alignment				**PDBTitle:** aaa atpase domain of the proteasome- activating nucleotidase
55	c1sxjD_	Alignment	not modelled	99.4	14	**PDB header:**replication **Chain:** D: **PDB Molecule:**activator 1 41 kda subunit; **PDBTitle:** crystal structure of the eukaryotic clamp loader2 (replication factor c, rfc) bound to the dna sliding clamp3 (proliferating cell nuclear antigen, pcna)
56	d1sxjb2	Alignment	not modelled	99.4	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
57	d1sxjc2	Alignment	not modelled	99.4	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
58	c3f9vA_	Alignment	not modelled	99.4	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**minichromosome maintenance protein mcm; **PDBTitle:** crystal structure of a near full-length archaeal mcm: functional2 insights for an aaa+ hexameric helicase
59	d1qvra2	Alignment	not modelled	99.4	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
60	c1sxjC_	Alignment	not modelled	99.4	20	**PDB header:**replication **Chain:** C: **PDB Molecule:**activator 1 40 kda subunit; **PDBTitle:** crystal structure of the eukaryotic clamp loader2 (replication factor c, rfc) bound to the dna sliding clamp3 (proliferating cell nuclear antigen, pcna)
61	d1r6bx2	Alignment	not modelled	99.4	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
62	c1iy2A_	Alignment	not modelled	99.4	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent metalloprotease ftsh; **PDBTitle:** crystal structure of the ftsh atpase domain from thermus2 thermophilus
63	c1s3sA_	Alignment	not modelled	99.4	25	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**transitional endoplasmic reticulum atpase (ter **PDBTitle:** crystal structure of aaa atpase p97/vcp nd1 in complex with2 p47 c
64	c1sxjB_	Alignment	not modelled	99.4	17	**PDB header:**replication **Chain:** B: **PDB Molecule:**activator 1 37 kda subunit; **PDBTitle:** crystal structure of the eukaryotic clamp loader2 (replication factor c, rfc) bound to the dna sliding clamp3 (proliferating cell nuclear antigen, pcna)
65	d1e32a2	Alignment	not modelled	99.3	23	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
66	c1sxjA_	Alignment	not modelled	99.3	12	**PDB header:**replication **Chain:** A: **PDB Molecule:**activator 1 95 kda subunit; **PDBTitle:** crystal structure of the eukaryotic clamp loader2 (replication factor c, rfc) bound to the dna sliding clamp3 (proliferating cell nuclear antigen, pcna)
67	c2qz4A_	Alignment	not modelled	99.3	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**paraplegin; **PDBTitle:** human paraplegin, aaa domain in complex with adp
68	c2chvE_	Alignment	not modelled	99.3	20	**PDB header:**dna-binding protein **Chain:** E: **PDB Molecule:**replication factor c small subunit; **PDBTitle:** replication factor c adpnp complex
69	d1sxja2	Alignment	not modelled	99.3	11	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
70	d1fipa_	Alignment	not modelled	99.3	30	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
71	c1iqpF_	Alignment	not modelled	99.3	19	**PDB header:**replication **Chain:** F: **PDB Molecule:**rfcs; **PDBTitle:** crystal structure of the clamp loader small subunit from2 pyrococcus furiosus
72	d1jbka_	Alignment	not modelled	99.3	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
73	d1ixza_	Alignment	not modelled	99.3	24	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
74	c3e7lD_	Alignment	not modelled	99.3	24	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** crystal structure of sigma54 activator ntrc4's dna binding2 domain
75	c2kjqA_	Alignment	not modelled	99.3	22	**PDB header:**replication **Chain:** A: **PDB Molecule:**dnaa-related protein; **PDBTitle:** solution structure of protein nmb1076 from neisseria meningitidis.2 northeast structural genomics consortium target mr101b.
76	d1e94e_	Alignment	not modelled	99.3	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
77	d1etob_	Alignment	not modelled	99.3	30	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
78	c3pxgA_	Alignment	not modelled	99.3	21	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**negative regulator of genetic competence clpc/mecb;

						PDBTitle: structure of meca121 and clpc1-485 complex
79	c2x8aA_	Alignment	not modelled	99.3	21	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**nuclear valosin-containing protein-like; **PDBTitle:** human nuclear valosin containing protein like (nvl), c-2 terminal aaa-atpase domain
80	d1etxa_	Alignment	not modelled	99.3	28	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
81	d1sxje2	Alignment	not modelled	99.2	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
82	d1w5sa2	Alignment	not modelled	99.2	10	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
83	d1lv7a_	Alignment	not modelled	99.2	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
84	c1umqA_	Alignment	not modelled	99.2	16	**PDB header:**dna-binding protein **Chain:** A: **PDB Molecule:**photosynthetic apparatus regulatory protein; **PDBTitle:** solution structure and dna binding of the effector domain2 from the global regulator prra(rega) from r. sphaeroides:3 insights into dna binding specificity
85	d1umqa_	Alignment	not modelled	99.2	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
86	c1sxjE_	Alignment	not modelled	99.2	14	**PDB header:**replication **Chain:** E: **PDB Molecule:**activator 1 40 kda subunit; **PDBTitle:** crystal structure of the eukaryotic clamp loader2 (replication factor c, rfc) bound to the dna sliding clamp3 (proliferating cell nuclear antigen, pcna)
87	d1g2ha_	Alignment	not modelled	99.2	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
88	c1fnnB_	Alignment	not modelled	99.1	11	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**cell division control protein 6; **PDBTitle:** crystal structure of cdc6p from pyrobaculum aerophilum
89	c2qbyA_	Alignment	not modelled	99.1	12	**PDB header:**replication/dna **Chain:** A: **PDB Molecule:**cell division control protein 6 homolog 1; **PDBTitle:** crystal structure of a heterodimer of cdc6/orc1 initiators2 bound to origin dna (from s. solfataricus)
90	c2v1uA_	Alignment	not modelled	99.0	18	**PDB header:**replication **Chain:** A: **PDB Molecule:**cell division control protein 6 homolog; **PDBTitle:** structure of the aeropyrum pernix orc1 protein in complex2 with dna
91	c2qbyB_	Alignment	not modelled	99.0	15	**PDB header:**replication/dna **Chain:** B: **PDB Molecule:**cell division control protein 6 homolog 3; **PDBTitle:** crystal structure of a heterodimer of cdc6/orc1 initiators2 bound to origin dna (from s. solfataricus)
92	d1r7ra3	Alignment	not modelled	99.0	26	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
93	c3ec2A_	Alignment	not modelled	99.0	15	**PDB header:**replication **Chain:** A: **PDB Molecule:**dna replication protein dnac; **PDBTitle:** crystal structure of the dnac helicase loader
94	c3te6A_	Alignment	not modelled	98.9	9	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**regulatory protein sir3; **PDBTitle:** crystal structure of the s. cerevisiae sir3 aaa+ domain
95	d1oz4a3	Alignment	not modelled	98.9	30	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
96	d1a5ta2	Alignment	not modelled	98.9	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
97	c2w58B_	Alignment	not modelled	98.8	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**primosome component (helicase loader); **PDBTitle:** crystal structure of the dnai
98	c1jr3E_	Alignment	not modelled	98.7	19	**PDB header:**transferase **Chain:** E: **PDB Molecule:**dna polymerase iii, delta' subunit; **PDBTitle:** crystal structure of the processivity clamp loader gamma2 complex of e. coli dna polymerase iii
99	c1w5sB_	Alignment	not modelled	98.7	12	**PDB header:**replication **Chain:** B: **PDB Molecule:**origin recognition complex subunit 2 orc2; **PDBTitle:** structure of the aeropyrum pernix orc2 protein (adp form)
100	c2qgzA_	Alignment	not modelled	98.7	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative primosome component; **PDBTitle:** crystal structure of a putative primosome component from2 streptococcus pyogenes serotype m3. northeast structural3 genomics target dr58
101	d2gnoa2	Alignment	not modelled	98.7	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
102	d1gvnb_	Alignment	not modelled	98.7	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Plasmid maintenance system epsilon/zeta, toxin zeta subunit
103	c3qmzA_	Alignment	not modelled	98.5	15	**PDB header:**motor protein **Chain:** A: **PDB Molecule:**cytoplasmic dynein heavy chain; **PDBTitle:** crystal structure of the cytoplasmic dynein heavy chain

						motor domain
104	c3m6aC_	Alignment	not modelled	98.5	15	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**atp-dependent protease la 1; **PDBTitle:** crystal structure of bacillus subtilis lon c-terminal domain
105	c2p5tD_	Alignment	not modelled	98.2	24	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**pezt; **PDBTitle:** molecular and structural characterization of the pezat chromosomal2 toxin-antitoxin system of the human pathogen streptococcus pneumoniae
106	d1svma_	Alignment	not modelled	97.9	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
107	d2i3ba1	Alignment	not modelled	97.8	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
108	c2qenA_	Alignment	not modelled	97.8	13	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**walker-type atpase; **PDBTitle:** the walker-type atpase paby2304 of pyrococcus abyssi
109	d1ye8a1	Alignment	not modelled	97.8	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
110	c2fnaA_	Alignment	not modelled	97.8	21	**PDB header:**atp-binding protein **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** crystal structure of an archaeal aaa+ atpase (sso1545) from sulfolobus2 solfataricus p2 at 2.00 a resolution
111	d2fnaa2	Alignment	not modelled	97.8	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
112	c3e1sA_	Alignment	not modelled	97.8	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exodeoxyribonuclease v, subunit recd; **PDBTitle:** structure of an n-terminal truncation of deinococcus radiodurans recd2
113	c3tlxA_	Alignment	not modelled	97.7	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**adenylate kinase 2; **PDBTitle:** crystal structure of pf10_0086, adenylate kinase from plasmodium2 falciparum
114	c3n70F_	Alignment	not modelled	97.7	24	**PDB header:**transport protein **Chain:** F: **PDB Molecule:**transport activator; **PDBTitle:** the crystal structure of the p-loop ntpase domain of the sigma-542 transport activator from e. coli to 2.8a
115	c2ja1A_	Alignment	not modelled	97.6	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**thymidine kinase; **PDBTitle:** thymidine kinase from b. cereus with ttp bound as phosphate2 donor.
116	c3trfB_	Alignment	not modelled	97.5	25	**PDB header:**transferase **Chain:** B: **PDB Molecule:**shikimate kinase; **PDBTitle:** structure of a shikimate kinase (arok) from coxiella burnetii
117	d1kaga_	Alignment	not modelled	97.5	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Shikimate kinase (AroK)
118	c1z6tC_	Alignment	not modelled	97.4	20	**PDB header:**apoptosis **Chain:** C: **PDB Molecule:**apoptotic protease activating factor 1; **PDBTitle:** structure of the apoptotic protease-activating factor 12 bound to adp
119	d1w36d1	Alignment	not modelled	97.4	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
120	d1khta_	Alignment	not modelled	97.4	11	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases