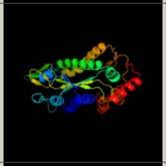
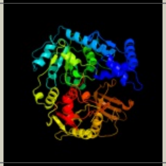
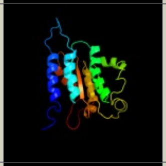
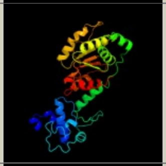
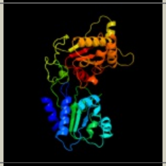
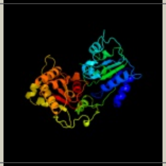
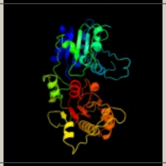
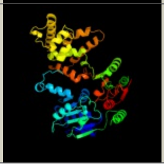
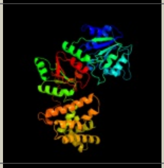
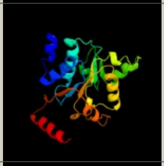
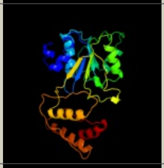
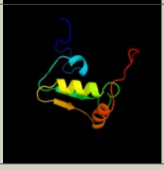
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P14565
Date	Wed Jan 25 15:20:38 GMT 2012
Unique Job ID	ec7a67129bc5f945

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1p4da_	Alignment		100.0	90	**Fold:**Origin of replication-binding domain, RBD-like **Superfamily:**Origin of replication-binding domain, RBD-like **Family:**Relaxase domain
2	d1omha_	Alignment		100.0	38	**Fold:**Origin of replication-binding domain, RBD-like **Superfamily:**Origin of replication-binding domain, RBD-like **Family:**Relaxase domain
3	c3l6tB_	Alignment		100.0	41	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**mobilization protein trai; **PDBTitle:** crystal structure of an n-terminal mutant of the plasmid pcu1 trai2 relaxase domain
4	c3e1sA_	Alignment		100.0	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exodeoxyribonuclease v, subunit recd; **PDBTitle:** structure of an n-terminal truncation of deinococcus radiodurans recd2
5	c1w36G_	Alignment		100.0	18	**PDB header:**recombination **Chain:** G: **PDB Molecule:**exodeoxyribonuclease v alpha chain; **PDBTitle:** recbcd:dna complex
6	c2l8bA_	Alignment		100.0	100	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein trai; **PDBTitle:** trai (381-569)
7	d1w36d1	Alignment		100.0	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
8	c2wjyA_	Alignment		100.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**regulator of nonsense transcripts 1; **PDBTitle:** crystal structure of the complex between human nonsense2 mediated decay factors upf1 and upf2 orthorhombic form
9	c2xzlA_	Alignment		100.0	19	**PDB header:**hydrolase/rna **Chain:** A: **PDB Molecule:**atp-dependent helicase nam7; **PDBTitle:** upf1-rna complex
10	c2gk7A_	Alignment		100.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**regulator of nonsense transcripts 1; **PDBTitle:** structural and functional insights into the human upf1 helicase core
11	c2is6B_	Alignment		99.9	20	**PDB header:**hydrolase/dna **Chain:** B: **PDB Molecule:**dna helicase ii; **PDBTitle:** crystal structure of uvrd-dna-adpmgf3 ternary complex

12	c3b85A_	Alignment		99.9	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphate starvation-inducible protein; **PDBTitle:** crystal structure of predicted phosphate starvation-induced atpase2 phoh2 from corynebacterium glutamicum
13	c1pjrA_	Alignment		99.9	19	**PDB header:**helicase **Chain:** A: **PDB Molecule:**pcra; **PDBTitle:** structure of dna helicase
14	c1uaaB_	Alignment		99.9	18	**PDB header:**hydrolase/dna **Chain:** B: **PDB Molecule:**protein (atp-dependent dna helicase rep.); **PDBTitle:** e. coli rep helicase/dna complex
15	c3lfuA_	Alignment		99.8	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dna helicase ii; **PDBTitle:** crystal structure of e. coli uvrd
16	d1pjra1	Alignment		99.7	23	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
17	c2pjrF_	Alignment		99.7	19	**PDB header:**hydrolase/dna **Chain:** F: **PDB Molecule:**protein (helicase pcra); **PDBTitle:** helicase product complex
18	c3fldA_	Alignment		99.6	100	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein trai; **PDBTitle:** crystal structure of the trai c-terminal domain
19	d1uaaa1	Alignment		99.6	24	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
20	d1w36d2	Alignment		99.5	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
21	d1w36b1	Alignment	not modelled	99.3	32	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
22	c1qhhA_	Alignment	not modelled	99.1	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein (pcra (subunit)); **PDBTitle:** structure of dna helicase with adpnp
23	c1w36E_	Alignment	not modelled	99.0	19	**PDB header:**recombination **Chain:** E: **PDB Molecule:**exodeoxyribonuclease v beta chain; **PDBTitle:** recbcd:dna complex
24	c3dmnA_	Alignment	not modelled	98.7	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative dna helicase; **PDBTitle:** the crystal structure of the c-terminal domain of a possilbe dna2 helicase from lactobacillus plantarun wcfs1
25	c2vbcA_	Alignment	not modelled	98.6	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dengue 4 ns3 full-length protein; **PDBTitle:** crystal structure of the ns3 protease-helicase from dengue2 virus
26	d1w36b2	Alignment	not modelled	98.4	35	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
27	c2wv9A_	Alignment	not modelled	98.3	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**flavivirin protease ns2b regulatory subunit, flavivirin **PDBTitle:** crystal structure of the ns3 protease-helicase from murray2 valley encephalitis virus
28	c2ja1A_	Alignment	not modelled	98.3	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**thymidine kinase; **PDBTitle:** thymidine kinase from b. cereus with ttp bound as phosphate2 donor.

29	c1qhhD_	Alignment	not modelled	98.2	20	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**protein (pcra (subunit)); **PDBTitle:** structure of dna helicase with adpnp
30	c3dkpA_	Alignment	not modelled	98.2	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable atp-dependent rna helicase ddx52; **PDBTitle:** human dead-box rna-helicase ddx52, conserved domain i in complex with2 adp
31	c2pjrB_	Alignment	not modelled	98.2	20	**PDB header:**hydrolase/dna **Chain:** B: **PDB Molecule:**protein (helicase pcra); **PDBTitle:** helicase product complex
32	c3te6A_	Alignment	not modelled	98.2	6	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**regulatory protein sir3; **PDBTitle:** crystal structure of the s. cerevisiae sir3 aaa+ domain
33	c1sxjC_	Alignment	not modelled	98.2	13	**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)
34	c1sxjD_	Alignment	not modelled	98.1	11	**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)
35	c1sxjA_	Alignment	not modelled	98.1	13	**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)
36	c1gm5A_	Alignment	not modelled	98.1	21	**PDB header:**helicase **Chain:** A: **PDB Molecule:**recg; **PDBTitle:** structure of recg bound to three-way dna junction
37	d1pjra2	Alignment	not modelled	98.0	22	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
38	c3kx2A_	Alignment	not modelled	98.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**pre-mrna-splicing factor atp-dependent rna **PDBTitle:** crystal structure of prp43p in complex with adp
39	d1rifa_	Alignment	not modelled	98.0	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**DNA helicase UvsW
40	d1a1va1	Alignment	not modelled	98.0	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RNA helicase
41	d1uaaa2	Alignment	not modelled	97.9	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
42	c2z83A_	Alignment	not modelled	97.9	22	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**helicase/nucleoside triphosphatase; **PDBTitle:** crystal structure of catalytic domain of japanese2 encephalitis virus ns3 helicase/nucleoside triphosphatase3 at a resolution 1.8
43	c1iqpF_	Alignment	not modelled	97.9	16	**PDB header:**replication **Chain:** F: **PDB Molecule:**rfcs; **PDBTitle:** crystal structure of the clamp loader small subunit from2 pyrococcus furiosus
44	c2hcbC_	Alignment	not modelled	97.9	18	**PDB header:**replication **Chain:** C: **PDB Molecule:**chromosomal replication initiator protein dnaa; **PDBTitle:** structure of amppcp-bound dnaa from aquifex aeolicus
45	c2kjqA_	Alignment	not modelled	97.9	20	**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.
46	c2zpaB_	Alignment	not modelled	97.9	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**uncharacterized protein ypfi; **PDBTitle:** crystal structure of trna(met) cytidine acetyltransferase
47	c3llmB_	Alignment	not modelled	97.9	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**atp-dependent rna helicase a; **PDBTitle:** crystal structure analysis of a rna helicase
48	d1sxja2	Alignment	not modelled	97.9	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
49	c3ec2A_	Alignment	not modelled	97.9	19	**PDB header:**replication **Chain:** A: **PDB Molecule:**dna replication protein dnac; **PDBTitle:** crystal structure of the dnac helicase loader
50	c1cu1B_	Alignment	not modelled	97.9	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protein (protease/helicase ns3); **PDBTitle:** crystal structure of an enzyme complex from hepatitis c2 virus
51	c3pvsA_	Alignment	not modelled	97.9	23	**PDB header:**recombination **Chain:** A: **PDB Molecule:**replication-associated recombination protein a; **PDBTitle:** structure and biochemical activities of escherichia coli mgsa
52	d1ny5a2	Alignment	not modelled	97.9	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
53	c2chgB_	Alignment	not modelled	97.9	13	**PDB header:**dna-binding protein **Chain:** B: **PDB Molecule:**replication factor c small subunit;

						PDBTitle: replication factor c domains 1 and 2
54	c2jlrA_	Alignment	not modelled	97.8	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**serine protease subunit ns3; **PDBTitle:** dengue virus 4 ns3 helicase in complex with amppnp
55	d1gkub1	Alignment	not modelled	97.8	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Helicase-like "domain" of reverse gyrase
56	d2eyqa3	Alignment	not modelled	97.8	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
57	d1p9ra_	Alignment	not modelled	97.8	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
58	c3i5yA_	Alignment	not modelled	97.8	19	**PDB header:**hydrolase/rna **Chain:** A: **PDB Molecule:**atp-dependent rna helicase mss116; **PDBTitle:** structure of mss116p bound to ssrna containing a single 5-bru and amp-2 pnp
59	c2qgzA_	Alignment	not modelled	97.8	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
60	d2fz4a1	Alignment	not modelled	97.8	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
61	d2fwra2	Alignment	not modelled	97.8	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
62	c2v6jA_	Alignment	not modelled	97.8	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**rna helicase; **PDBTitle:** kokobera virus helicase: mutant met47thr
63	c2p6uA_	Alignment	not modelled	97.8	13	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**afuhel308 helicase; **PDBTitle:** apo structure of the hel308 superfamily 2 helicase
64	d1iqpa2	Alignment	not modelled	97.7	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
65	c3pfiB_	Alignment	not modelled	97.7	19	**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
66	d1fnna2	Alignment	not modelled	97.7	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
67	d1njfa_	Alignment	not modelled	97.7	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
68	c1ymfA_	Alignment	not modelled	97.7	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**genome polyprotein [contains: flavivirin **PDBTitle:** crystal structure of yellow fever virus ns3 helicase2 complexed with adp
69	c1a1vA_	Alignment	not modelled	97.7	20	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**protein (ns3 protein); **PDBTitle:** hepatitis c virus ns3 helicase domain complexed with single2 stranded sdna
70	c3u5zM_	Alignment	not modelled	97.7	16	**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
71	c3iuyB_	Alignment	not modelled	97.7	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable atp-dependent rna helicase ddx53; **PDBTitle:** crystal structure of ddx53 dead-box domain
72	c3b9qA_	Alignment	not modelled	97.6	15	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**chloroplast srp receptor homolog, alpha subunit **PDBTitle:** the crystal structure of cpftsy from arabidopsis thaliana
73	c1xxhB_	Alignment	not modelled	97.6	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**dna polymerase iii subunit gamma; **PDBTitle:** atpgs bound e. coli clamp loader complex
74	c2r44A_	Alignment	not modelled	97.6	9	**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
75	d1yksa1	Alignment	not modelled	97.6	23	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RNA helicase
76	c2qeqA_	Alignment	not modelled	97.6	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**flavivirin protease ns3 catalytic subunit; **PDBTitle:** crystal structure of kunjin virus ns3 helicase
77	c2cnwF_	Alignment	not modelled	97.6	19	**PDB header:**signal recognition **Chain:** F: **PDB Molecule:**cell division protein ftsy; **PDBTitle:** gdpalf4 complex of the srp gtpases ffh and ftsy
78	c2chvE_	Alignment	not modelled	97.6	15	**PDB header:**dna-binding protein **Chain:** E: **PDB Molecule:**replication factor c small subunit; **PDBTitle:** replication factor c adpnp complex

79	c2c99A_	Alignment	not modelled	97.6	16	**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
80	c2ocaA_	Alignment	not modelled	97.6	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent dna helicase uvsw; **PDBTitle:** the crystal structure of t4 uvsw
81	c3pxiB_	Alignment	not modelled	97.6	18	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**negative regulator of genetic competence clpc/mecb; **PDBTitle:** structure of meca108:clpc
82	c2j7pA_	Alignment	not modelled	97.5	18	**PDB header:**signal recognition **Chain:** A: **PDB Molecule:**signal recognition particle protein; **PDBTitle:** gmppnp-stabilized ng domain complex of the srp gtpases ffh2 and ftsy
83	c1sxjB_	Alignment	not modelled	97.5	12	**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)
84	d1gm5a3	Alignment	not modelled	97.5	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
85	d1l8qa2	Alignment	not modelled	97.5	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
86	c3bosA_	Alignment	not modelled	97.5	15	**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
87	c2fwrA_	Alignment	not modelled	97.5	18	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna repair protein rad25; **PDBTitle:** structure of archaeoglobus fulgidis xpb
88	c2og2A_	Alignment	not modelled	97.5	14	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**putative signal recognition particle receptor; **PDBTitle:** crystal structure of chloroplast ftsy from arabidopsis2 thaliana
89	c2va8A_	Alignment	not modelled	97.5	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ski2-type helicase; **PDBTitle:** dna repair helicase hel308
90	c3jvvA_	Alignment	not modelled	97.5	13	**PDB header:**atp binding protein **Chain:** A: **PDB Molecule:**twitching mobility protein; **PDBTitle:** crystal structure of p. aeruginosa pilt with bound amp-pcp
91	d1hv8a1	Alignment	not modelled	97.5	24	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
92	d1sxjc2	Alignment	not modelled	97.5	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
93	c2xgjA_	Alignment	not modelled	97.5	19	**PDB header:**hydrolase/rna **Chain:** A: **PDB Molecule:**atp-dependent rna helicase dob1; **PDBTitle:** structure of mtr4, a dexh helicase involved in nuclear rna2 processing and surveillance
94	c3ly5A_	Alignment	not modelled	97.5	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent rna helicase ddx18; **PDBTitle:** ddx18 dead-domain
95	d1r6bx3	Alignment	not modelled	97.5	23	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
96	c1xx6B_	Alignment	not modelled	97.5	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**thymidine kinase; **PDBTitle:** x-ray structure of clostridium acetobutylicum thymidine kinase with2 adp. northeast structural genomics target car26.
97	d1um8a_	Alignment	not modelled	97.5	23	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
98	c2eyqA_	Alignment	not modelled	97.4	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**transcription-repair coupling factor; **PDBTitle:** crystal structure of escherichia coli transcription-repair2 coupling factor
99	d1qdea_	Alignment	not modelled	97.4	24	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
100	d1c4oa1	Alignment	not modelled	97.4	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
101	c2gxqA_	Alignment	not modelled	97.4	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**heat resistant rna dependent atpase; **PDBTitle:** hera n-terminal domain in complex with amp, crystal form 1
102	c2zj2A_	Alignment	not modelled	97.4	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative ski2-type helicase; **PDBTitle:** archaeal dna helicase hjm apo state in form 1
103	d1sxje2	Alignment	not modelled	97.4	11	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
						PDB header:response regulator

104	c1ojlF_	Alignment	not modelled	97.4	18	**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
105	c2z4rB_	Alignment	not modelled	97.4	15	**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
106	c3fe2B_	Alignment	not modelled	97.4	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable atp-dependent rna helicase ddx5; **PDBTitle:** human dead-box rna helicase ddx5 (p68), conserved domain i in complex2 with adp
107	d1sxjd2	Alignment	not modelled	97.4	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
108	d1jbka_	Alignment	not modelled	97.4	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
109	d1q0ua_	Alignment	not modelled	97.4	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
110	c2c9oC_	Alignment	not modelled	97.4	21	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**ruvb-like 1; **PDBTitle:** 3d structure of the human ruvb-like helicase ruvbl1
111	c2z0mA_	Alignment	not modelled	97.4	19	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**337aa long hypothetical atp-dependent rna **PDBTitle:** crystal structure of hypothetical atp-dependent rna2 helicase from sulfolobus tokodaii
112	d1a5ta2	Alignment	not modelled	97.4	10	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
113	d1sxjb2	Alignment	not modelled	97.3	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
114	c2v1xB_	Alignment	not modelled	97.3	10	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**atp-dependent dna helicase q1; **PDBTitle:** crystal structure of human recq-like dna helicase
115	c1in8A_	Alignment	not modelled	97.3	28	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**holliday junction dna helicase ruvb; **PDBTitle:** thermotoga maritima ruvb t158v
116	c2f55C_	Alignment	not modelled	97.3	21	**PDB header:**hydrolase/dna **Chain:** C: **PDB Molecule:**polyprotein; **PDBTitle:** two hepatitis c virus ns3 helicase domains complexed with2 the same strand of dna
117	c3d8bB_	Alignment	not modelled	97.3	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**fidgetin-like protein 1; **PDBTitle:** crystal structure of human fidgetin-like protein 1 in complex with adp
118	c2v3cC_	Alignment	not modelled	97.3	11	**PDB header:**signaling protein **Chain:** C: **PDB Molecule:**signal recognition 54 kda protein; **PDBTitle:** crystal structure of the srp54-srp19-7s.s srp rna complex2 of m. jannaschii
119	c3k1jA_	Alignment	not modelled	97.3	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent protease lon; **PDBTitle:** crystal structure of lon protease from thermococcus onnurineus na1
120	d1s2ma1	Alignment	not modelled	97.3	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain