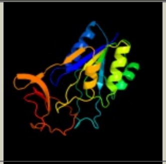
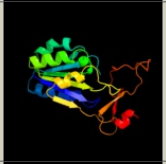
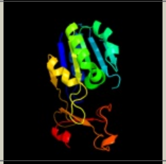
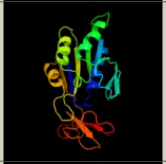
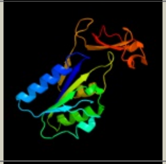
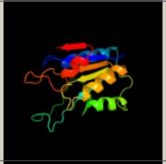
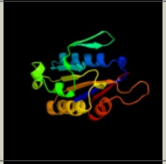
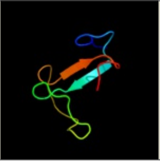
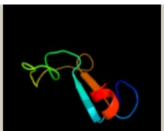
Email	l.a.kelley@imperial.ac.uk
Description	P23331
Date	Thu Jan 5 11:39:23 GMT 2012
Unique Job ID	5dc004b84284dc9c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2b8tA_	Alignment		100.0	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**thymidine kinase; **PDBTitle:** crystal structure of thymidine kinase from u.urealyticum in2 complex with thymidine
2	c3e2iA_	Alignment		100.0	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**thymidine kinase; **PDBTitle:** crystal structure of thymidine kinase from s. aureus
3	c1w4rC_	Alignment		100.0	28	**PDB header:**transferase **Chain:** C: **PDB Molecule:**thymidine kinase; **PDBTitle:** structure of a type ii thymidine kinase with bound dttp
4	c2orvB_	Alignment		100.0	28	**PDB header:**transferase **Chain:** B: **PDB Molecule:**thymidine kinase; **PDBTitle:** human thymidine kinase 1 in complex with tp4a
5	c2qq0B_	Alignment		100.0	25	**PDB header:**transferase **Chain:** B: **PDB Molecule:**thymidine kinase; **PDBTitle:** thymidine kinase from thermotoga maritima in complex with2 thymidine + appnhp
6	c2ja1A_	Alignment		100.0	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**thymidine kinase; **PDBTitle:** thymidine kinase from b. cereus with ttp bound as phosphate2 donor.
7	c1xx6B_	Alignment		100.0	23	**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.
8	d2b8ta1	Alignment		100.0	23	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Type II thymidine kinase
9	d1xx6a1	Alignment		100.0	22	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Type II thymidine kinase
10	d1xbta1	Alignment		100.0	23	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Type II thymidine kinase
11	d2b8ta2	Alignment		99.5	37	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Type II thymidine kinase zinc finger

12	d1xbta2	Alignment		99.2	45	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Type II thymidine kinase zinc finger
13	c2zroA_	Alignment		98.9	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein reca; **PDBTitle:** msreca adp form iv
14	c2j7pA_	Alignment		98.9	16	**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
15	d1xx6a2	Alignment		98.9	33	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Type II thymidine kinase zinc finger
16	c3e1sA_	Alignment		98.9	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exodeoxyribonuclease v, subunit recd; **PDBTitle:** structure of an n-terminal truncation of deinococcus radiodurans recd2
17	c3b85A_	Alignment		98.9	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphate starvation-inducible protein; **PDBTitle:** crystal structure of predicted phosphate starvation-induced atpase2 phoh2 from corynebacterium glutamicum
18	c3b9qA_	Alignment		98.9	13	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**chloroplast srp receptor homolog, alpha subunit **PDBTitle:** the crystal structure of cpftsy from arabidopsis thaliana
19	c2j37W_	Alignment		98.8	12	**PDB header:**ribosome **Chain:** W: **PDB Molecule:**signal recognition particle 54 kda protein **PDBTitle:** model of mammalian srp bound to 80s rncs
20	c2vbcA_	Alignment		98.8	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dengue 4 ns3 full-length protein; **PDBTitle:** crystal structure of the ns3 protease-helicase from dengue2 virus
21	c2cnwF_	Alignment	not modelled	98.8	16	**PDB header:**signal recognition **Chain:** F: **PDB Molecule:**cell division protein ftsy; **PDBTitle:** gdpalf4 complex of the srp gtpases ffh and ftsy
22	d1mo6a1	Alignment	not modelled	98.8	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
23	c3dm5A_	Alignment	not modelled	98.8	11	**PDB header:**rna binding protein, transport protein **Chain:** A: **PDB Molecule:**signal recognition 54 kda protein; **PDBTitle:** structures of srp54 and srp19, the two proteins assembling2 the ribonucleic core of the signal recognition particle3 from the archaeon pyrococcus furiosus.
24	c2iy3A_	Alignment	not modelled	98.8	16	**PDB header:**rna-binding **Chain:** A: **PDB Molecule:**signal recognition particle protein ffh; **PDBTitle:** structure of the e. coli signal recognition particle2 bound to a translating ribosome
25	c2recB_	Alignment	not modelled	98.7	18	**PDB header:**helicase **PDB COMPND:**
26	d1u94a1	Alignment	not modelled	98.7	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
27	c3dmdA_	Alignment	not modelled	98.7	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**signal recognition particle receptor; **PDBTitle:** structures and conformations in solution of the signal recognition2 particle receptor from the archaeon pyrococcus furiosus
28	d1w36d1	Alignment	not modelled	98.7	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases

						Family: Tandem AAA-ATPase domain
29	c1xp8A_	Alignment	not modelled	98.7	18	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**reca protein; **PDBTitle:** "deinococcus radiodurans reca in complex with atp-gamma-s"
30	d1ubea1	Alignment	not modelled	98.7	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
31	c3hr8A_	Alignment	not modelled	98.7	16	**PDB header:**recombination **Chain:** A: **PDB Molecule:**protein reca; **PDBTitle:** crystal structure of thermotoga maritima reca
32	c2og2A_	Alignment	not modelled	98.7	12	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**putative signal recognition particle receptor; **PDBTitle:** crystal structure of chloroplast ftsy from arabidopsis2 thaliana
33	d1cr2a_	Alignment	not modelled	98.7	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
34	c2wv9A_	Alignment	not modelled	98.7	13	**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
35	c2qy9A_	Alignment	not modelled	98.6	12	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**cell division protein ftsy; **PDBTitle:** structure of the ng+1 construct of the e. coli srp receptor2 ftsy
36	c2yhsA_	Alignment	not modelled	98.6	12	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**cell division protein ftsy; **PDBTitle:** structure of the e. coli srp receptor ftsy
37	d1xp8a1	Alignment	not modelled	98.6	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
38	c2v6jA_	Alignment	not modelled	98.6	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**rna helicase; **PDBTitle:** kokobera virus helicase: mutant met47thr
39	d1tf7a2	Alignment	not modelled	98.6	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
40	c1w36G_	Alignment	not modelled	98.6	12	**PDB header:**recombination **Chain:** G: **PDB Molecule:**exodeoxyribonuclease v alpha chain; **PDBTitle:** recbcd:dna complex
41	c1vmaA_	Alignment	not modelled	98.6	13	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**cell division protein ftsy; **PDBTitle:** crystal structure of cell division protein ftsy (tm0570) from2 thermotoga maritima at 1.60 a resolution
42	c1zu4A_	Alignment	not modelled	98.6	16	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**ftsy; **PDBTitle:** crystal structure of ftsy from mycoplasma mycoides-space2 group p21212
43	c2jlrA_	Alignment	not modelled	98.6	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**serine protease subunit ns3; **PDBTitle:** dengue virus 4 ns3 helicase in complex with amppnp
44	c3bh0A_	Alignment	not modelled	98.5	18	**PDB header:**replication **Chain:** A: **PDB Molecule:**dnab-like replicative helicase; **PDBTitle:** atpase domain of g40p
45	d1yksa1	Alignment	not modelled	98.5	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RNA helicase
46	c2vyeA_	Alignment	not modelled	98.5	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**replicative dna helicase; **PDBTitle:** crystal structure of the dnac-ssdna complex
47	c2v3cC_	Alignment	not modelled	98.5	9	**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
48	c2j289_	Alignment	not modelled	98.5	11	**PDB header:**ribosome **Chain:** 9: **PDB Molecule:**signal recognition particle 54; **PDBTitle:** model of e. coli srp bound to 70s rncs
49	c2q6tB_	Alignment	not modelled	98.4	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dnab replication fork helicase; **PDBTitle:** crystal structure of the thermus aquaticus dnab monomer
50	c3te6A_	Alignment	not modelled	98.4	9	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**regulatory protein sir3; **PDBTitle:** crystal structure of the s. cerevisiae sir3 aaa+ domain
51	c2ztsB_	Alignment	not modelled	98.4	14	**PDB header:**atp-binding protein **Chain:** B: **PDB Molecule:**putative uncharacterized protein ph0186; **PDBTitle:** crystal structure of kaic-like protein ph0186 from2 hyperthermophilic archaea pyrococcus horikoshii ot3
52	c2w0mA_	Alignment	not modelled	98.4	15	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**sso2452; **PDBTitle:** crystal structure of sso2452 from sulfolobus solfataricus2 p2
53	d1qzxa3	Alignment	not modelled	98.4	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
54	c2z83A_	Alignment	not modelled	98.4	12	**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
55	c2qeqA_	Alignment	not modelled	98.4	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**flavivirin protease ns3 catalytic subunit; **PDBTitle:** crystal structure of kunjin virus ns3 helicase
56	c3cmvG_	Alignment	not modelled	98.4	17	**PDB header:**recombination **Chain:** G: **PDB Molecule:**protein reca; **PDBTitle:** mechanism of homologous recombination from the reca-2 ssdna/dsdna structures
57	c1qzwC_	Alignment	not modelled	98.4	12	**PDB header:**signaling protein/rna **Chain:** C: **PDB Molecule:**signal recognition 54 kda protein; **PDBTitle:** crystal structure of the complete core of archaeal srp and2 implications for inter-domain communication
58	d1fnna2	Alignment	not modelled	98.4	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
59	c3bgwD_	Alignment	not modelled	98.4	16	**PDB header:**replication **Chain:** D: **PDB Molecule:**dnab-like replicative helicase; **PDBTitle:** the structure of a dnab-like replicative helicase and its interactions2 with primase
60	d1pjra1	Alignment	not modelled	98.4	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
61	d1g5ta_	Alignment	not modelled	98.3	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
62	c1ymfA_	Alignment	not modelled	98.3	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**genome polyprotein [contains: flavivirin **PDBTitle:** crystal structure of yellow fever virus ns3 helicase2 complexed with adp
63	d1g64b_	Alignment	not modelled	98.3	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
64	c1q57G_	Alignment	not modelled	98.3	13	**PDB header:**transferase **Chain:** G: **PDB Molecule:**dna primase/helicase; **PDBTitle:** the crystal structure of the bifunctional primase-helicase of2 bacteriophage t7
65	c2wjyA_	Alignment	not modelled	98.3	16	**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
66	c1u9iA_	Alignment	not modelled	98.3	14	**PDB header:**circadian clock protein **Chain:** A: **PDB Molecule:**kaic; **PDBTitle:** crystal structure of circadian clock protein kaic with phosphorylation2 sites
67	d1tf7a1	Alignment	not modelled	98.3	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
68	c3pfiB_	Alignment	not modelled	98.3	16	**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
69	c2kjqA_	Alignment	not modelled	98.3	18	**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.
70	c2hcbC_	Alignment	not modelled	98.2	17	**PDB header:**replication **Chain:** C: **PDB Molecule:**chromosomal replication initiator protein dnaa; **PDBTitle:** structure of amppcp-bound dnaa from aquifex aeolicus
71	c2xzlA_	Alignment	not modelled	98.2	19	**PDB header:**hydrolase/rna **Chain:** A: **PDB Molecule:**atp-dependent helicase nam7; **PDBTitle:** upf1-rna complex
72	d1n0wa_	Alignment	not modelled	98.2	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
73	c1fnnB_	Alignment	not modelled	98.2	13	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**cell division control protein 6; **PDBTitle:** crystal structure of cdc6p from pyrobaculum aerophilum
74	d1uaaa1	Alignment	not modelled	98.2	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
75	d1a1va1	Alignment	not modelled	98.2	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RNA helicase
76	c2eyqA_	Alignment	not modelled	98.2	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**transcription-repair coupling factor; **PDBTitle:** crystal structure of escherichia coli transcription-repair2 coupling factor
77	c3pvsA_	Alignment	not modelled	98.2	11	**PDB header:**recombination **Chain:** A: **PDB Molecule:**replication-associated recombination protein a; **PDBTitle:** structure and biochemical activities of escherichia coli mgsa
78	c3ec2A_	Alignment	not modelled	98.2	10	**PDB header:**replication **Chain:** A: **PDB Molecule:**dna replication protein dnac; **PDBTitle:** crystal structure of the dnac helicase loader

79	d1ls1a2	Alignment	not modelled	98.2	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
80	c2is6B_	Alignment	not modelled	98.1	20	**PDB header:**hydrolase/dna **Chain:** B: **PDB Molecule:**dna helicase ii; **PDBTitle:** crystal structure of uvrd-dna-adpmgf3 ternary complex
81	c2dr3A_	Alignment	not modelled	98.1	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0273 protein ph0284; **PDBTitle:** crystal structure of reca superfamily atpase ph0284 from pyrococcus2 horikoshii ot3
82	c2px0D_	Alignment	not modelled	98.1	17	**PDB header:**biosynthetic protein **Chain:** D: **PDB Molecule:**flagellar biosynthesis protein flhf; **PDBTitle:** crystal structure of flhf complexed with gmppnp/mg(2+)
83	d2eyqa3	Alignment	not modelled	98.1	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
84	c2ia5C_	Alignment	not modelled	98.1	9	**PDB header:**transferase **Chain:** C: **PDB Molecule:**polynucleotide kinase; **PDBTitle:** t4 polynucleotide kinase/phosphatase with bound sulfate and2 magnesium.
85	c3ldaA_	Alignment	not modelled	98.1	18	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna repair protein rad51; **PDBTitle:** yeast rad51 h352y filament interface mutant
86	c3jvvA_	Alignment	not modelled	98.1	12	**PDB header:**atp binding protein **Chain:** A: **PDB Molecule:**twitching mobility protein; **PDBTitle:** crystal structure of p. aeruginosa pilt with bound amp-pcp
87	c2w58B_	Alignment	not modelled	98.1	7	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**primosome component (helicase loader); **PDBTitle:** crystal structure of the dnai
88	c1cu1B_	Alignment	not modelled	98.1	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protein (protease/helicase ns3); **PDBTitle:** crystal structure of an enzyme complex from hepatitis c2 virus
89	d1p9ra_	Alignment	not modelled	98.1	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
90	d2bmfa2	Alignment	not modelled	98.0	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RNA helicase
91	c1szpC_	Alignment	not modelled	98.0	16	**PDB header:**dna binding protein **Chain:** C: **PDB Molecule:**dna repair protein rad51; **PDBTitle:** a crystal structure of the rad51 filament
92	c1ly1A_	Alignment	not modelled	98.0	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**polynucleotide kinase; **PDBTitle:** structure and mechanism of t4 polynucleotide kinase
93	d1ly1a_	Alignment	not modelled	98.0	9	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
94	c1sxjC_	Alignment	not modelled	98.0	14	**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)
95	c2gk7A_	Alignment	not modelled	98.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**regulator of nonsense transcripts 1; **PDBTitle:** structural and functional insights into the human upf1 helicase core
96	c2yvuA_	Alignment	not modelled	98.0	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable adenylyl-sulfate kinase; **PDBTitle:** crystal structure of ape1195
97	d1ny5a2	Alignment	not modelled	98.0	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
98	c2pjrF_	Alignment	not modelled	98.0	20	**PDB header:**hydrolase/dna **Chain:** F: **PDB Molecule:**protein (helicase pcra); **PDBTitle:** helicase product complex
99	c3io5B_	Alignment	not modelled	98.0	13	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**recombination and repair protein; **PDBTitle:** crystal structure of a dimeric form of the uvsx recombinase core2 domain from enterobacteria phage t4
100	d1szpa2	Alignment	not modelled	98.0	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
101	d1nlfa_	Alignment	not modelled	98.0	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
102	c2r2aB_	Alignment	not modelled	98.0	14	**PDB header:**toxin **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of n-terminal domain of zonular occludens toxin from2 neisseria meningitidis
103	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
104	c2eyuA_	Alignment	not modelled	98.0	11	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**twitching motility protein pilt; **PDBTitle:** the crystal structure of the c-terminal domain of aquifex2 aeolicus pilt

105	d2i1qa2	Alignment	not modelled	97.9	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
106	c1in8A_	Alignment	not modelled	97.9	11	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**holliday junction dna helicase ruvb; **PDBTitle:** thermotoga maritima ruvb t158v
107	c2qgzA_	Alignment	not modelled	97.9	16	**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
108	c1sxjD_	Alignment	not modelled	97.9	8	**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)
109	d1v5wa_	Alignment	not modelled	97.9	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
110	c3pxiB_	Alignment	not modelled	97.9	15	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**negative regulator of genetic competence clpc/mecb; **PDBTitle:** structure of meca108:clpc
111	c3d8bB_	Alignment	not modelled	97.9	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
112	d2qy9a2	Alignment	not modelled	97.9	9	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
113	c1sxjA_	Alignment	not modelled	97.9	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)
114	c3b9pA_	Alignment	not modelled	97.9	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cg5977-pa, isoform a; **PDBTitle:** spastin
115	c2v1uA_	Alignment	not modelled	97.8	13	**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
116	d1l8qa2	Alignment	not modelled	97.8	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
117	c1uaaB_	Alignment	not modelled	97.8	18	**PDB header:**hydrolase/dna **Chain:** B: **PDB Molecule:**protein (atp-dependent dna helicase rep.); **PDBTitle:** e. coli rep helicase/dna complex
118	d2gnoa2	Alignment	not modelled	97.8	9	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
119	c2gszE_	Alignment	not modelled	97.8	12	**PDB header:**protein transport **Chain:** E: **PDB Molecule:**twitching motility protein pilt; **PDBTitle:** structure of a. aeolicus pilt with 6 monomers per2 asymmetric unit
120	c1jr3E_	Alignment	not modelled	97.8	9	**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