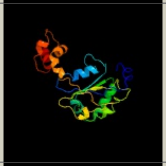
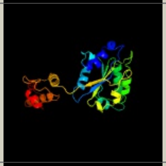
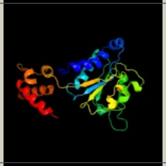
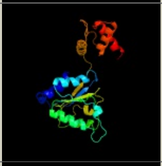
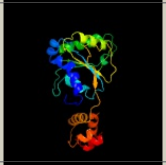
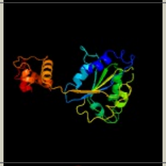
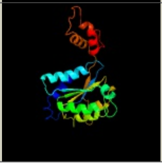
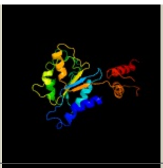
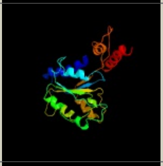
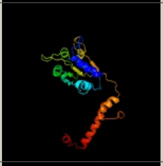
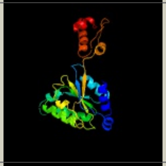
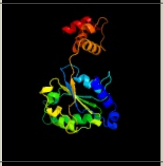
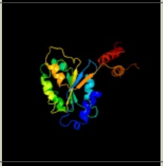
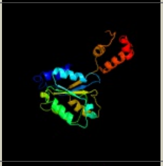
Phyre²

Email	l.a.kelley@imperial.ac.uk
Description	Good_intensive
Date	Sun Sep 7 16:58:53 BST 2014
Unique Job ID	d4a1f7b1ec99b495

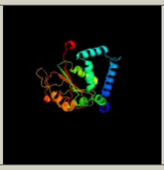
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3cf1C_	Alignment		100.0	15	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**transitional endoplasmic reticulum atpase; **PDBTitle:** structure of p97/vcp in complex with adp/adp.alfx
2	c3cf2B_	Alignment		99.9	20	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**transitional endoplasmic reticulum atpase; **PDBTitle:** structure of p97/vcp in complex with adp/amp-pnp
3	c3hu2C_	Alignment		99.9	17	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**transitional endoplasmic reticulum atpase; **PDBTitle:** structure of p97 n-d1 r86a mutant in complex with atpgs
4	c4b4tH_	Alignment		99.9	14	**PDB header:**hydrolase **Chain:** H: **PDB Molecule:**26s protease regulatory subunit 7 homolog; **PDBTitle:** near-atomic resolution structural model of the yeast 26s proteasome
5	c4b4tK_	Alignment		99.9	13	**PDB header:**hydrolase **Chain:** K: **PDB Molecule:**26s protease regulatory subunit 6b homolog; **PDBTitle:** near-atomic resolution structural model of the yeast 26s proteasome
6	c4b4tJ_	Alignment		99.9	14	**PDB header:**hydrolase **Chain:** J: **PDB Molecule:**26s protease regulatory subunit 8 homolog; **PDBTitle:** near-atomic resolution structural model of the yeast 26s proteasome
7	c4b4tI_	Alignment		99.9	12	**PDB header:**hydrolase **Chain:** I: **PDB Molecule:**26s protease regulatory subunit 4 homolog; **PDBTitle:** near-atomic resolution structural model of the yeast 26s proteasome
8	c4b4tL_	Alignment		99.9	13	**PDB header:**hydrolase **Chain:** L: **PDB Molecule:**26s protease subunit rpt4; **PDBTitle:** near-atomic resolution structural model of the yeast 26s proteasome
9	c4b4tM_	Alignment		99.9	17	**PDB header:**hydrolase **Chain:** M: **PDB Molecule:**26s protease regulatory subunit 6a; **PDBTitle:** near-atomic resolution structural model of the yeast 26s proteasome
10	c2dhrC_	Alignment		99.9	16	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**ftsh; **PDBTitle:** whole cytosolic region of atp-dependent metalloprotease2 ftsh (g399l)
11	c1s3sA_	Alignment		99.9	18	**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

12	c2zamA_	Alignment		99.9	15	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**vacuolar protein sorting-associating protein 4b; **PDBTitle:** crystal structure of mouse skd1/vps4b apo-form
13	c1xwiA_	Alignment		99.9	15	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**skd1 protein; **PDBTitle:** crystal structure of vps4b
14	c3zw6B_	Alignment		99.8	13	**PDB header:**photosynthesis **Chain:** B: **PDB Molecule:**ribulose bisphosphate carboxylase/oxygenase activase 1, **PDBTitle:** model of hexameric aaa domain arrangement of green-type2 rubisco activase from tobacco.
15	c1iy2A_	Alignment		99.8	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent metalloprotease ftsh; **PDBTitle:** crystal structure of the ftsh atpase domain from thermus2 thermophilus
16	d2ce7a2	Alignment		99.8	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
17	c3eihB_	Alignment		99.8	18	**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
18	c4l16A_	Alignment		99.8	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**fidgetin-like protein 1; **PDBTitle:** crystal structure of figl-1 aaa domain in complex with adp
19	d1ixza_	Alignment		99.8	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
20	c3b9pA_	Alignment		99.8	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cg5977-pa, isoform a; **PDBTitle:** spastin
21	c2r65A_	Alignment	not modelled	99.8	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cell division protease ftsh homolog; **PDBTitle:** crystal structure of helicobacter pylori atp dependent protease, ftsh2 adp complex
22	c2ce7B_	Alignment	not modelled	99.8	16	**PDB header:**cell division protein **Chain:** B: **PDB Molecule:**cell division protein ftsh; **PDBTitle:** edta treated
23	c3d8bB_	Alignment	not modelled	99.8	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
24	c2x8aA_	Alignment	not modelled	99.8	13	**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
25	c3vfdA_	Alignment	not modelled	99.8	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**spastin; **PDBTitle:** human spastin aaa domain
26	c2qz4A_	Alignment	not modelled	99.8	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**paraplegin; **PDBTitle:** human paraplegin, aaa domain in complex with adp
27	c3h4mC_	Alignment	not modelled	99.8	15	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**proteasome-activating nucleotidase; **PDBTitle:** aaa atpase domain of the proteasome- activating nucleotidase
28	c4lcbA_	Alignment	not modelled	99.8	14	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**cell division protein cdvc, vps4; **PDBTitle:** structure of vps4 homolog from acidianus hospitalis
						Fold:P-loop containing nucleoside triphosphate hydrolases

29	d1e32a2	Alignment	not modelled	99.7	17	**Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
30	d1r7ra3	Alignment	not modelled	99.7	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
31	d1lv7a_	Alignment	not modelled	99.7	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
32	c1qvrB_	Alignment	not modelled	99.7	9	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**clpb protein; **PDBTitle:** crystal structure analysis of clpb
33	c3pxiB_	Alignment	not modelled	99.6	6	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**negative regulator of genetic competence clpc/mecb; **PDBTitle:** structure of meca108:clpc
34	c4ciuA_	Alignment	not modelled	99.6	12	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**chaperone protein clpb; **PDBTitle:** crystal structure of e. coli clpb
35	c1nsfA_	Alignment	not modelled	99.6	9	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**n-ethylmaleimide sensitive factor; **PDBTitle:** d2 hexamerization domain of n-ethylmaleimide sensitive factor (nsf)
36	c1r6bX_	Alignment	not modelled	99.6	10	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**clpa protein; **PDBTitle:** high resolution crystal structure of clpa
37	d1d2na_	Alignment	not modelled	99.6	9	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
38	c4d2qC_	Alignment	not modelled	99.5	11	**PDB header:**chaperone **Chain:** C: **PDB Molecule:**clpb; **PDBTitle:** negative-stain electron microscopy of e. coli clpb2 mutant e432a (bap form bound to clpp)
39	c3sylB_	Alignment	not modelled	99.5	11	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**protein cbbx; **PDBTitle:** crystal structure of the aaa+ protein cbbx, native structure
40	d1r6bx3	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
41	d1oz4a3	Alignment	not modelled	99.5	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
42	d1in4a2	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
43	c1sxjA_	Alignment	not modelled	99.4	12	**PDB header:**replication **Chain:** A: **PDB Molecule:**activator 1 95 kda subunit; **PDBTitle:** crystal structure of the eukaryotic clamp loader (replication factor2 c, rfc) bound to the dna sliding clamp (proliferating cell nuclear3 antigen, pcna)
44	c3pfiB_	Alignment	not modelled	99.4	13	**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
45	d1ofha_	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
46	d1qvra3	Alignment	not modelled	99.4	9	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
47	d1iqpa2	Alignment	not modelled	99.4	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
48	c2c9oA_	Alignment	not modelled	99.4	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ruvb-like 1; **PDBTitle:** 3d structure of the human ruvb-like helicase ruvbl1
49	d1gvnb_	Alignment	not modelled	99.4	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Plasmid maintenance system epsilon/zeta, toxin zeta subunit
50	c1in8A_	Alignment	not modelled	99.4	14	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**holliday junction dna helicase ruvb; **PDBTitle:** thermotoga maritima ruvb t158v
51	c2z4rB_	Alignment	not modelled	99.4	9	**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
52	c2chvE_	Alignment	not modelled	99.4	14	**PDB header:**dna-binding protein **Chain:** E: **PDB Molecule:**replication factor c small subunit; **PDBTitle:** replication factor c adpnp complex
53	c3pxgA_	Alignment	not modelled	99.4	17	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**negative regulator of genetic competence clpc/mecb; **PDBTitle:** structure of meca121 and clpc1-485 complex
54	d1jbka_	Alignment	not modelled	99.3	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
						Fold:P-loop containing nucleoside triphosphate hydrolases

55	d1ixsb2	Alignment	not modelled	99.3	11	**Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
56	d1sxjb2	Alignment	not modelled	99.3	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
57	c2chgB_	Alignment	not modelled	99.3	14	**PDB header:**dna-binding protein **Chain:** B: **PDB Molecule:**replication factor c small subunit; **PDBTitle:** replication factor c domains 1 and 2
58	d1sxja2	Alignment	not modelled	99.3	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
59	d1g41a_	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
60	d1w5sa2	Alignment	not modelled	99.3	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
61	c2hcbC_	Alignment	not modelled	99.3	13	**PDB header:**replication **Chain:** C: **PDB Molecule:**chromosomal replication initiator protein dnaa; **PDBTitle:** structure of amppcp-bound dnaa from aquifex aeolicus
62	c3uk6L_	Alignment	not modelled	99.3	16	**PDB header:**hydrolase **Chain:** L: **PDB Molecule:**ruvb-like 2; **PDBTitle:** crystal structure of the tip48 (tip49b) hexamer
63	d1l8qa2	Alignment	not modelled	99.3	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
64	c2r44A_	Alignment	not modelled	99.3	11	**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
65	c2p65A_	Alignment	not modelled	99.3	22	**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
66	c3u5zM_	Alignment	not modelled	99.3	12	**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
67	d1r6bx2	Alignment	not modelled	99.3	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
68	c1sxjE_	Alignment	not modelled	99.3	10	**PDB header:**replication **Chain:** E: **PDB Molecule:**activator 1 40 kda subunit; **PDBTitle:** crystal structure of the eukaryotic clamp loader (replication factor2 c, rfc) bound to the dna sliding clamp (proliferating cell nuclear3 antigen, pcna)
69	d1a5ta2	Alignment	not modelled	99.3	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
70	c3m6aC_	Alignment	not modelled	99.3	13	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**atp-dependent protease la 1; **PDBTitle:** crystal structure of bacillus subtilis lon c-terminal domain
71	d1sxje2	Alignment	not modelled	99.3	9	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
72	c3pvsA_	Alignment	not modelled	99.2	17	**PDB header:**recombination **Chain:** A: **PDB Molecule:**replication-associated recombination protein a; **PDBTitle:** structure and biochemical activities of escherichia coli mgsa
73	c3nbxX_	Alignment	not modelled	99.2	13	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**atpase rava; **PDBTitle:** crystal structure of e. coli rava (regulatory atpase variant a) in2 complex with adp
74	d1qvra2	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
75	d1sxjc2	Alignment	not modelled	99.2	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
76	c2p5tD_	Alignment	not modelled	99.2	14	**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
77	d1um8a_	Alignment	not modelled	99.2	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
78	d1fnna2	Alignment	not modelled	99.2	9	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
79	d1njfa_	Alignment	not modelled	99.2	11	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
80	c2c9oC_	Alignment	not modelled	99.2	14	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**ruvb-like 1; **PDBTitle:** 3d structure of the human ruvb-like helicase ruvbl1
81	c1sxjC_	Alignment	not modelled	99.2	11	**PDB header:**replication **Chain:** C: **PDB Molecule:**activator 1 40 kda subunit; **PDBTitle:** crystal structure of the eukaryotic clamp loader

						(replication factor2 c, rfc) bound to the dna sliding clamp (proliferating cell nuclear3 antigen, pcna)
82	d1svma_	Alignment		99.1	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
83	c3te6A_	Alignment	not modelled	99.1	5	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**regulatory protein sir3; **PDBTitle:** crystal structure of the s. cerevisiae sir3 aaa+ domain
84	c1sxjB_	Alignment	not modelled	99.1	13	**PDB header:**replication **Chain:** B: **PDB Molecule:**activator 1 37 kda subunit; **PDBTitle:** crystal structure of the eukaryotic clamp loader (replication factor2 c, rfc) bound to the dna sliding clamp (proliferating cell nuclear3 antigen, pcna)
85	c3bosA_	Alignment	not modelled	99.1	10	**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
86	c1iqpF_	Alignment	not modelled	99.1	12	**PDB header:**replication **Chain:** F: **PDB Molecule:**rfcs; **PDBTitle:** crystal structure of the clamp loader small subunit from2 pyrococcus furiosus
87	d1sxjd2	Alignment	not modelled	99.1	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
88	c4gdfF_	Alignment	not modelled	99.1	10	**PDB header:**hydrolase/dna **Chain:** F: **PDB Molecule:**large t antigen; **PDBTitle:** a crystal structure of sv40 large t antigen
89	c1hqcB_	Alignment	not modelled	99.0	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**ruvb; **PDBTitle:** structure of ruvb from thermus thermophilus hb8
90	c3uk6H_	Alignment	not modelled	99.0	13	**PDB header:**hydrolase **Chain:** H: **PDB Molecule:**ruvb-like 2; **PDBTitle:** crystal structure of the tip48 (tip49b) hexamer
91	c3hteC_	Alignment	not modelled	99.0	10	**PDB header:**motor protein **Chain:** C: **PDB Molecule:**atp-dependent clp protease atp-binding subunit clpx; **PDBTitle:** crystal structure of nucleotide-free hexameric clpx
92	c1sxjD_	Alignment	not modelled	99.0	12	**PDB header:**replication **Chain:** D: **PDB Molecule:**activator 1 41 kda subunit; **PDBTitle:** crystal structure of the eukaryotic clamp loader (replication factor2 c, rfc) bound to the dna sliding clamp (proliferating cell nuclear3 antigen, pcna)
93	c1jr3E_	Alignment	not modelled	98.9	12	**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
94	d1g8pa_	Alignment	not modelled	98.9	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
95	c1xxhB_	Alignment	not modelled	98.8	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**dna polymerase iii subunit gamma; **PDBTitle:** atpgs bound e. coli clamp loader complex
96	c3ec2A_	Alignment	not modelled	98.8	16	**PDB header:**replication **Chain:** A: **PDB Molecule:**dna replication protein dnac; **PDBTitle:** crystal structure of the dnac helicase loader
97	c2kjqA_	Alignment	not modelled	98.8	14	**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.
98	c1ojlD_	Alignment	not modelled	98.8	15	**PDB header:**response regulator **Chain:** D: **PDB Molecule:**transcriptional regulatory protein zrar; **PDBTitle:** crystal structure of a sigma54-activator suggests the2 mechanism for the conformational switch necessary for3 sigma54 binding
99	c1fnnB_	Alignment	not modelled	98.8	8	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**cell division control protein 6; **PDBTitle:** crystal structure of cdc6p from pyrobaculum aerophilum
100	c1w5sB_	Alignment	not modelled	98.7	11	**PDB header:**replication **Chain:** B: **PDB Molecule:**origin recognition complex subunit 2 orc2; **PDBTitle:** structure of the aeropyrum pernix orc2 protein (adp form)
101	c2v1uA_	Alignment	not modelled	98.7	12	**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
102	c2w58B_	Alignment	not modelled	98.7	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**primosome component (helicase loader); **PDBTitle:** crystal structure of the dnai
103	d1ny5a2	Alignment	not modelled	98.7	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
104	d1e94e_	Alignment	not modelled	98.7	8	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
105	c2gxaA_	Alignment	not modelled	98.6	13	**PDB header:**replication/dna **Chain:** A: **PDB Molecule:**replication protein e1; **PDBTitle:** crystal structure of papillomavirus e1 hexameric helicase2 with ssdna and mgadp

106	c2qbyA_	Alignment	not modelled	98.6	9	**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)
107	c2qgzA_	Alignment	not modelled	98.6	20	**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	c2qbyB_	Alignment	not modelled	98.5	11	**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)
109	d1tuea_	Alignment	not modelled	98.5	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
110	d1ye8a1	Alignment	not modelled	98.5	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
111	c1ojlF_	Alignment	not modelled	98.4	13	**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
112	c2c99A_	Alignment	not modelled	98.4	13	**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
113	c4m4wO_	Alignment	not modelled	98.4	16	**PDB header:**replication **Chain:** O: **PDB Molecule:**primosomal protein dnai; **PDBTitle:** mechanistic implications for the bacterial primosome assembly of the2 structure of a helicase-helicase loader complex
114	c3tlxA_	Alignment	not modelled	98.1	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**adenylate kinase 2; **PDBTitle:** crystal structure of pf10_0086, adenylate kinase from plasmodium2 falciparum
115	d1sq5a_	Alignment	not modelled	98.1	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Phosphoribulokinase/pantothenate kinase
116	d2gnoa2	Alignment	not modelled	98.1	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
117	c4akgB_	Alignment	not modelled	98.1	19	**PDB header:**motor protein **Chain:** B: **PDB Molecule:**glutathione s-transferase class-mu 26 kda isozyme, dynein **PDBTitle:** dynein motor domain - atp complex
118	c1zuiA_	Alignment	not modelled	98.1	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**shikimate kinase; **PDBTitle:** structural basis for shikimate-binding specificity of helicobacter2 pylori shikimate kinase
119	c3vkhB_	Alignment	not modelled	98.1	14	**PDB header:**motor protein **Chain:** B: **PDB Molecule:**dynein heavy chain, cytoplasmic; **PDBTitle:** x-ray structure of a functional full-length dynein motor domain
120	c3umfA_	Alignment	not modelled	98.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**adenylate kinase; **PDBTitle:** schistosoma mansoni adenylate kinase