Phyre^2

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Description	P0A6H1
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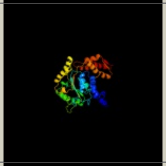
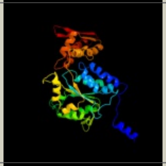
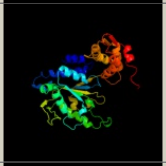
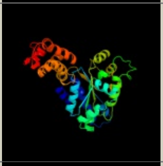
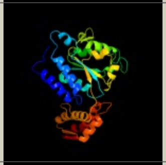
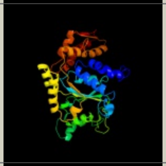
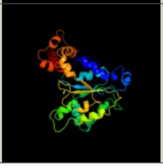
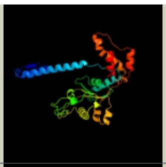
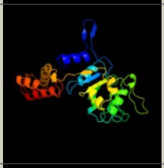
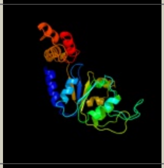
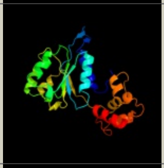
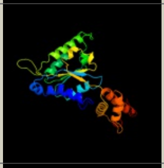
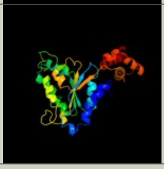
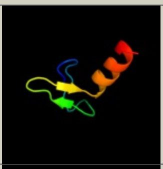
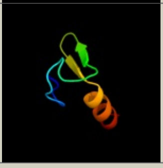
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1e94e_	Alignment		100.0	28	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
2	d1um8a_	Alignment		100.0	57	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
3	c1qvrB_	Alignment		100.0	23	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**clpb protein; **PDBTitle:** crystal structure analysis of clpb
4	d1g41a_	Alignment		100.0	41	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
5	c1r6bX_	Alignment		100.0	23	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**clpa protein; **PDBTitle:** high resolution crystal structure of clpa
6	c3pxiB_	Alignment		100.0	25	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**negative regulator of genetic competence clpc/mecb; **PDBTitle:** structure of meca108:clpc
7	d1ofha_	Alignment		100.0	40	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
8	c3hteC_	Alignment		100.0	93	**PDB header:**motor protein **Chain:** C: **PDB Molecule:**atp-dependent clp protease atp-binding subunit clpx; **PDBTitle:** crystal structure of nucleotide-free hexameric clpx
9	d1r6bx3	Alignment		100.0	23	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
10	d1qvra3	Alignment		100.0	23	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
11	c3cf1C_	Alignment		99.9	19	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**transitional endoplasmic reticulum atpase; **PDBTitle:** structure of p97/vcp in complex with adp/adp.alfx

12	c1ny5A_	Alignment		99.9	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** crystal structure of sigm54 activator (aaa+ atpase) in the inactive2 state
13	c2c99A_	Alignment		99.9	21	**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
14	c3dzdA_	Alignment		99.9	18	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** crystal structure of sigma54 activator ntrc4 in the inactive2 state
15	c2dhrC_	Alignment		99.9	24	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**ftsh; **PDBTitle:** whole cytosolic region of atp-dependent metalloprotease2 ftsh (g399l)
16	d1ny5a2	Alignment		99.9	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
17	c3pfiB_	Alignment		99.9	25	**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
18	c3hu2C_	Alignment		99.9	23	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**transitional endoplasmic reticulum atpase; **PDBTitle:** structure of p97 n-d1 r86a mutant in complex with atpgs
19	c1ojlF_	Alignment		99.9	22	**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
20	c3eihB_	Alignment		99.9	23	**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
21	c3b9pA_	Alignment	not modelled	99.8	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cg5977-pa, isoform a; **PDBTitle:** spastin
22	c2r44A_	Alignment	not modelled	99.8	23	**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
23	c1xwiA_	Alignment	not modelled	99.8	23	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**skd1 protein; **PDBTitle:** crystal structure of vps4b
24	c1s3sA_	Alignment	not modelled	99.8	23	**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
25	c3pvsA_	Alignment	not modelled	99.8	30	**PDB header:**recombination **Chain:** A: **PDB Molecule:**replication-associated recombination protein a; **PDBTitle:** structure and biochemical activities of escherichia coli mgsa
26	c3m6aC_	Alignment	not modelled	99.8	21	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**atp-dependent protease la 1; **PDBTitle:** crystal structure of bacillus subtilis lon c-terminal domain
27	c3d8bB_	Alignment	not modelled	99.8	24	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**fidgetin-like protein 1; **PDBTitle:** crystal structure of human fidgetin-like protein 1 in complex with adp
28	d1g8pa_	Alignment	not modelled	99.8	23	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases

						Family: Extended AAA-ATPase domain
29	c3h4mC_	Alignment	not modelled	99.8	25	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**proteasome-activating nucleotidase; **PDBTitle:** aaa atpase domain of the proteasome- activating nucleotidase
30	c2zamA_	Alignment	not modelled	99.8	23	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**vacuolar protein sorting-associating protein 4b; **PDBTitle:** crystal structure of mouse skd1/vps4b apo-form
31	c1nsfA_	Alignment	not modelled	99.8	24	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**n-ethylmaleimide sensitive factor; **PDBTitle:** d2 hexamerization domain of n-ethylmaleimide sensitive factor (nsf)
32	c1in8A_	Alignment	not modelled	99.8	26	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**holliday junction dna helicase ruvb; **PDBTitle:** thermotoga maritima ruvb t158v
33	d1d2na_	Alignment	not modelled	99.8	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
34	c2x8aA_	Alignment	not modelled	99.8	22	**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
35	c2ce7B_	Alignment	not modelled	99.8	26	**PDB header:**cell division protein **Chain:** B: **PDB Molecule:**cell division protein ftsh; **PDBTitle:** edta treated
36	d1ixza_	Alignment	not modelled	99.7	26	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
37	d2ce7a2	Alignment	not modelled	99.7	27	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
38	c3nbxX_	Alignment	not modelled	99.7	21	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**atpase rava; **PDBTitle:** crystal structure of e. coli rava (regulatory atpase variant a) in2 complex with adp
39	c2c9oC_	Alignment	not modelled	99.7	23	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**ruvb-like 1; **PDBTitle:** 3d structure of the human ruvb-like helicase ruvbl1
40	d1r7ra3	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
41	d1e32a2	Alignment	not modelled	99.7	22	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
42	d1in4a2	Alignment	not modelled	99.7	27	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
43	c2r65A_	Alignment	not modelled	99.7	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cell division protease ftsh homolog; **PDBTitle:** crystal structure of helicobacter pylori atp dependent protease, ftsh2 adp complex
44	c1iy2A_	Alignment	not modelled	99.7	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent metalloprotease ftsh; **PDBTitle:** crystal structure of the ftsh atpase domain from thermus2 thermophilus
45	d1ixsb2	Alignment	not modelled	99.7	22	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
46	c3k1jA_	Alignment	not modelled	99.7	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent protease lon; **PDBTitle:** crystal structure of lon protease from thermococcus onnurineus na1
47	c2qz4A_	Alignment	not modelled	99.7	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**paraplegin; **PDBTitle:** human paraplegin, aaa domain in complex with adp
48	d1l8qa2	Alignment	not modelled	99.7	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
49	c1hqcB_	Alignment	not modelled	99.7	24	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**ruvb; **PDBTitle:** structure of ruvb from thermus thermophilus hb8
50	d1lv7a_	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
51	c3u5zM_	Alignment	not modelled	99.6	19	**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
52	c2hcbC_	Alignment	not modelled	99.6	18	**PDB header:**replication **Chain:** C: **PDB Molecule:**chromosomal replication initiator protein dnaa; **PDBTitle:** structure of amppcp-bound dnaa from aquifex aeolicus
53	c2chgB_	Alignment	not modelled	99.6	21	**PDB header:**dna-binding protein **Chain:** B: **PDB Molecule:**replication factor c small subunit; **PDBTitle:** replication factor c domains 1 and 2
54	c1xxhB_	Alignment	not modelled	99.6	29	**PDB header:**transferase **Chain:** B: **PDB Molecule:**dna polymerase iii subunit gamma; **PDBTitle:** atpgs bound e. coli clamp loader complex

55	d1jbka_	Alignment	not modelled	99.6	26	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
56	c1sxjA_	Alignment	not modelled	99.5	16	**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)
57	d1sxjb2	Alignment	not modelled	99.5	22	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
58	d1w5sa2	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
59	d1sxje2	Alignment	not modelled	99.5	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
60	d1r6bx2	Alignment	not modelled	99.5	22	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
61	d1iqpa2	Alignment	not modelled	99.5	28	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
62	d1sxja2	Alignment	not modelled	99.5	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
63	c3f8tA_	Alignment	not modelled	99.5	19	**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
64	d1gvnb_	Alignment	not modelled	99.5	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Plasmid maintenance system epsilon/zeta, toxin zeta subunit
65	c1sxjB_	Alignment	not modelled	99.5	21	**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)
66	c1sxjC_	Alignment	not modelled	99.5	21	**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)
67	c1sxjE_	Alignment	not modelled	99.5	19	**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)
68	d1qvra2	Alignment	not modelled	99.5	27	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
69	c2chvE_	Alignment	not modelled	99.5	24	**PDB header:**dna-binding protein **Chain:** E: **PDB Molecule:**replication factor c small subunit; **PDBTitle:** replication factor c adpnp complex
70	c1sxjD_	Alignment	not modelled	99.5	26	**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)
71	c2p5tD_	Alignment	not modelled	99.4	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
72	c3bosA_	Alignment	not modelled	99.4	20	**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
73	d1sxjc2	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
74	c1iqpF_	Alignment	not modelled	99.4	27	**PDB header:**replication **Chain:** F: **PDB Molecule:**rfcs; **PDBTitle:** crystal structure of the clamp loader small subunit from2 pyrococcus furiosus
75	d1njfa_	Alignment	not modelled	99.4	26	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
76	d1oz4a3	Alignment	not modelled	99.4	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
77	c2z4rB_	Alignment	not modelled	99.4	22	**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
						Fold:P-loop containing nucleoside triphosphate hydrolases

78	d1fnna2	Alignment	not modelled	99.4	17	**Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
79	c2p65A_	Alignment	not modelled	99.4	25	**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
80	d1a5ta2	Alignment	not modelled	99.4	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
81	c1jr3E_	Alignment	not modelled	99.3	22	**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
82	c3te6A_	Alignment	not modelled	99.3	21	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**regulatory protein sir3; **PDBTitle:** crystal structure of the s. cerevisiae sir3 aaa+ domain
83	d1sxjd2	Alignment	not modelled	99.3	22	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
84	c3pxgA_	Alignment	not modelled	99.2	26	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**negative regulator of genetic competence clpc/mecb; **PDBTitle:** structure of meca121 and clpc1-485 complex
85	c3f9vA_	Alignment	not modelled	99.2	17	**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
86	c3co5B_	Alignment	not modelled	99.1	22	**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
87	c1fnnB_	Alignment	not modelled	99.1	15	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**cell division control protein 6; **PDBTitle:** crystal structure of cdc6p from pyrobaculum aerophilum
88	c2qbyB_	Alignment	not modelled	99.0	20	**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)
89	c2v1uA_	Alignment	not modelled	99.0	24	**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
90	c3ec2A_	Alignment	not modelled	98.9	17	**PDB header:**replication **Chain:** A: **PDB Molecule:**dna replication protein dnac; **PDBTitle:** crystal structure of the dnac helicase loader
91	c2ds8A_	Alignment		98.9	100	**PDB header:**metal binding protein, protein binding **Chain:** A: **PDB Molecule:**atp-dependent clp protease atp-binding subunit **PDBTitle:** structure of the zbd-xb complex
92	c1w5sB_	Alignment	not modelled	98.9	21	**PDB header:**replication **Chain:** B: **PDB Molecule:**origin recognition complex subunit 2 orc2; **PDBTitle:** structure of the aeropyrum pernix orc2 protein (adp form)
93	c2qbyA_	Alignment	not modelled	98.8	19	**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)
94	d2gnoa2	Alignment	not modelled	98.8	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
95	c2w58B_	Alignment	not modelled	98.7	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**primosome component (helicase loader); **PDBTitle:** crystal structure of the dnai
96	c2kjqA_	Alignment	not modelled	98.7	16	**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.
97	d2ds5a1	Alignment		98.7	100	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**ClpX chaperone zinc binding domain
98	c1ovxB_	Alignment		98.7	100	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**atp-dependent clp protease atp-binding subunit clpx; **PDBTitle:** nmr structure of the e. coli clpx chaperone zinc binding domain dimer
99	c3qmzA_	Alignment	not modelled	98.4	17	**PDB header:**motor protein **Chain:** A: **PDB Molecule:**cytoplasmic dynein heavy chain; **PDBTitle:** crystal structure of the cytoplasmic dynein heavy chain motor domain
						Fold:P-loop containing nucleoside triphosphate hydrolases

100	d1kaga_	Alignment	not modelled	98.3	42	**Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Shikimate kinase (AroK)
101	d1lw7a2	Alignment	not modelled	98.3	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
102	d1ye8a1	Alignment	not modelled	98.3	23	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
103	c3trfB_	Alignment	not modelled	98.3	41	**PDB header:**transferase **Chain:** B: **PDB Molecule:**shikimate kinase; **PDBTitle:** structure of a shikimate kinase (arok) from coxiella burnetii
104	c2gxaA_	Alignment	not modelled	98.3	13	**PDB header:**replication/dna **Chain:** A: **PDB Molecule:**replication protein e1; **PDBTitle:** crystal structure of papillomavirus e1 hexameric helicase2 with ssdna and mgadp
105	c3be4A_	Alignment	not modelled	98.2	30	**PDB header:**transferase **Chain:** A: **PDB Molecule:**adenylate kinase; **PDBTitle:** crystal structure of cryptosporidium parvum adenylate kinase cgd5_3360
106	c3tlxA_	Alignment	not modelled	98.2	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**adenylate kinase 2; **PDBTitle:** crystal structure of pf10_0086, adenylate kinase from plasmodium2 falciparum
107	d2iyva1	Alignment	not modelled	98.2	35	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Shikimate kinase (AroK)
108	d1svma_	Alignment	not modelled	98.2	25	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
109	c2qgzA_	Alignment	not modelled	98.2	19	**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
110	c1zuiA_	Alignment	not modelled	98.2	38	**PDB header:**transferase **Chain:** A: **PDB Molecule:**shikimate kinase; **PDBTitle:** structural basis for shikimate-binding specificity of helicobacter2 pylori shikimate kinase
111	d1e6ca_	Alignment	not modelled	98.1	33	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Shikimate kinase (AroK)
112	d1viaa_	Alignment	not modelled	98.1	50	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Shikimate kinase (AroK)
113	c2og2A_	Alignment	not modelled	98.1	23	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**putative signal recognition particle receptor; **PDBTitle:** crystal structure of chloroplast ftsy from arabidopsis2 thaliana
114	c1lw7A_	Alignment	not modelled	98.1	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**transcriptional regulator nadr; **PDBTitle:** nadr protein from haemophilus influenzae
115	c2ak3B_	Alignment	not modelled	98.1	16	**PDB header:**transferase (phosphotransferase) **Chain:** B: **PDB Molecule:**adenylate kinase isoenzyme-3; **PDBTitle:** the three-dimensional structure of the complex between2 mitochondrial matrix adenylate kinase and its substrate3 amp at 1.85 angstroms resolution
116	d1qhxa_	Alignment	not modelled	98.1	26	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Chloramphenicol phosphotransferase
117	d2ak3a1	Alignment	not modelled	98.1	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
118	d2i3ba1	Alignment	not modelled	98.1	38	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
119	c2iy3A_	Alignment	not modelled	98.1	15	**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
120	c2ar7A_	Alignment	not modelled	98.1	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**adenylate kinase 4; **PDBTitle:** crystal structure of human adenylate kinase 4, ak4