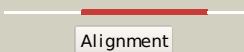

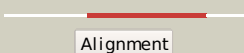

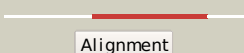

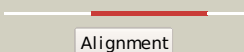
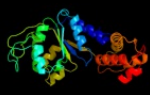
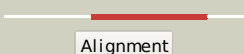

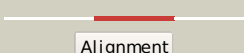

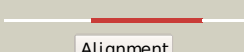



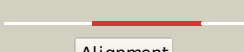














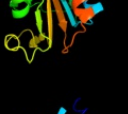
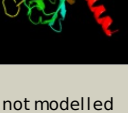


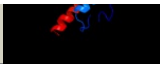



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1ny5A_	 Alignment		100.0	41	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigma54 activator (aaa+ atpase) in the inactive2 state
2	c3dzdA_	 Alignment		100.0	47	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigma54 activator ntrc4 in the inactive2 state
3	c2c99A_	 Alignment		100.0	42	PDB header: transcription regulation Chain: A: PDB Molecule: psp operon transcriptional activator; PDBTitle: structural basis of the nucleotide driven conformational2 changes in the aaa domain of transcription activator pspf
4	d1ny5a2	 Alignment		100.0	45	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
5	c1ojlF_	 Alignment		100.0	52	PDB header: response regulator Chain: F: PDB Molecule: transcriptional regulatory protein zrar; PDBTitle: crystal structure of a sigma54-activator suggests the2 mechanism for the conformational switch necessary for3 sigma54 binding
6	c3co5B_	 Alignment		100.0	24	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
7	d1r6bx3	 Alignment		99.9	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
8	c3pfiB_	 Alignment		99.9	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
9	c1qvrB_	 Alignment		99.8	20	PDB header: chaperone Chain: B: PDB Molecule: clpb protein; PDBTitle: crystal structure analysis of clpb
10	c3pxiB_	 Alignment		99.8	19	PDB header: protein binding Chain: B: PDB Molecule: negative regulator of genetic competence clpc/mecb; PDBTitle: structure of meca108:clpc
11	d1um8a_	 Alignment		99.8	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain

12	c1r6bX_	Alignment		99.8	20	PDB header: hydrolase Chain: X: PDB Molecule: clpa protein; PDBTitle: high resolution crystal structure of clpa
13	c3nbxX_	Alignment		99.8	18	PDB header: hydrolase Chain: X: PDB Molecule: atpase rava; PDBTitle: crystal structure of e. coli rava (regulatory atpase variant a) in2 complex with adp
14	c1n8A_	Alignment		99.8	17	PDB header: dna binding protein Chain: A: PDB Molecule: holliday junction dna helicase ruvb; PDBTitle: thermotoga maritima ruvb t158v
15	d1qvra3	Alignment		99.8	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
16	c3pvsA_	Alignment		99.8	18	PDB header: recombination Chain: A: PDB Molecule: replication-associated recombination protein a; PDBTitle: structure and biochemical activities of escherichia coli mgsa
17	c3trcA_	Alignment		99.7	17	PDB header: transferase Chain: A: PDB Molecule: phosphoenolpyruvate-protein phosphotransferase; PDBTitle: structure of the gaf domain from a phosphoenolpyruvate-protein2 phosphotransferase (ptsp) from coxiella burnetii
18	c3ci6B_	Alignment		99.7	16	PDB header: transferase Chain: B: PDB Molecule: phosphoenolpyruvate-protein phosphotransferase; PDBTitle: crystal structure of the gaf domain from acinetobacter2 phosphoenolpyruvate-protein phosphotransferase
19	c3k1jA_	Alignment		99.7	24	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent protease lon; PDBTitle: crystal structure of lon protease from thermococcus onnurineus na1
20	d1l8qa2	Alignment		99.7	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
21	c3p01C_	Alignment		99.7	15	PDB header: signaling protein Chain: C: PDB Molecule: two-component response regulator; PDBTitle: crystal structure of two-component response regulator from nostoc sp.2 pcc 7120
22	c3k2nB_	Alignment		99.7	18	PDB header: transcription regulator Chain: B: PDB Molecule: sigma-54-dependent transcriptional regulator; PDBTitle: the crystal structure of sigma-54-dependent transcriptional2 regulator domain from chlorobium tepidum t1s
23	c2hbcC_	Alignment	not modelled	99.7	18	PDB header: replication Chain: C: PDB Molecule: chromosomal replication initiator protein dnaa; PDBTitle: structure of amppcp-bound dnaa from aquifex aeolicus
24	d2veaa1	Alignment		99.7	12	Fold: Profilin-like Superfamily: GAF domain-like Family: GAF domain
25	c3e0yA_	Alignment		99.7	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved domain protein; PDBTitle: the crystal structure of a conserved domain from a

					protein of2 geobacter sulfurreducens pca	
26	c1nsfA	Alignment	not modelled	99.7	17	PDB header: protein transport Chain: A: PDB Molecule: n-ethylmaleimide sensitive factor; PDBTitle: d2 hexamerization domain of n-ethylmaleimide sensitive factor (nsf)
27	dlg8pa	Alignment	not modelled	99.6	25	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
28	c3f8tA	Alignment	not modelled	99.6	20	PDB header: hydrolase Chain: A: PDB Molecule: predicted atpase involved in replication control, PDBTitle: crystal structure analysis of a full-length mcm homolog2 from methanopyrus kandleri
29	c3mmhA	Alignment	not modelled	99.6	17	PDB header: oxidoreductase Chain: A: PDB Molecule: methionine-r-sulfoxide reductase; PDBTitle: x-ray structure of free methionine-r-sulfoxide reductase from2 neisseria meningitidis in complex with its substrate
30	c3hteC	Alignment	not modelled	99.6	16	PDB header: motor protein Chain: C: PDB Molecule: atp-dependent clp protease atp-binding subunit clpx; PDBTitle: crystal structure of nucleotide-free hexameric clpx
31	c3ibjB	Alignment	not modelled	99.6	8	PDB header: hydrolase Chain: B: PDB Molecule: cgmp-dependent 3',5'-cyclic phosphodiesterase; PDBTitle: x-ray structure of pde2a
32	c2zmfA	Alignment	not modelled	99.6	13	PDB header: hydrolase Chain: A: PDB Molecule: camp and camp-inhibited cgmp 3',5'-cyclic phosphodiesterase PDBTitle: crystal structure of the c-terminal gaf domain of human2 phosphodiesterase 10a
33	c3p01A	Alignment	not modelled	99.6	15	PDB header: signaling protein Chain: A: PDB Molecule: two-component response regulator; PDBTitle: crystal structure of two-component response regulator from nostoc sp.2 pcc 7120
34	d2o9ca1	Alignment	not modelled	99.6	15	Fold: Profilin-like Superfamily: GAF domain-like Family: GAF domain
35	c3bosA	Alignment	not modelled	99.6	14	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
36	dlvhma	Alignment	not modelled	99.6	13	Fold: Profilin-like Superfamily: GAF domain-like Family: GAF domain
37	c3ksiA	Alignment	not modelled	99.6	13	PDB header: oxidoreductase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: structure of frmrs of staphylococcus aureus (complex with 2-propanol)
38	c1vhmB	Alignment	not modelled	99.6	13	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: protein yebr; PDBTitle: crystal structure of an hypothetical protein
39	c3oovA	Alignment	not modelled	99.6	15	PDB header: signaling protein Chain: A: PDB Molecule: methyl-accepting chemotaxis protein, putative; PDBTitle: crystal structure of a methyl-accepting chemotaxis protein, residues2 122 to 287
40	c3o5yA	Alignment	not modelled	99.6	11	PDB header: transcription regulator Chain: A: PDB Molecule: sensor protein; PDBTitle: the crystal structure of the gaf domain of a two-component sensor2 histidine kinase from bacillus halodurans to 2.45a
41	c1mc0A	Alignment	not modelled	99.6	13	PDB header: hydrolase Chain: A: PDB Molecule: 3',5'-cyclic nucleotide phosphodiesterase 2a; PDBTitle: regulatory segment of mouse 3',5'-cyclic nucleotide phosphodiesterase2 2a, containing the gaf a and gaf b domains
42	c2z4rB	Alignment	not modelled	99.6	14	PDB header: dna binding protein Chain: B: PDB Molecule: chromosomal replication initiator protein dnaa; PDBTitle: crystal structure of domain iii from the thermotoga2 maritima replication initiation protein dnaa
43	c3eeeB	Alignment	not modelled	99.6	15	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: gaf domain/hd domain protein; PDBTitle: the crystal structure of the gaf domain/hd domain protein2 from geobacter sulfurreducens
44	dlntca	Alignment		99.6	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
45	c1hqcb	Alignment	not modelled	99.6	18	PDB header: hydrolase Chain: B: PDB Molecule: ruvb; PDBTitle: structure of ruvb from thermus thermophilus hb8
46	c2r44A	Alignment	not modelled	99.6	13	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
47	dlg41a	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
						PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative two-component sensor histidine

48	c3hcyB_	Alignment	not modelled	99.5	15	kinase protein; PDBTitle: the crystal structure of the domain of putative two-component sensor2 histidine kinase protein from sinorhizobium meliloti 1021
49	c3dbaB_	Alignment	not modelled	99.5	12	PDB header: hydrolase Chain: B: PDB Molecule: cone cgmp-specific 3',5'-cyclic phosphodiesterase subunit PDBTitle: crystal structure of the cgmp-bound gaf a domain from the2 photoreceptor phosphodiesterase 6c
50	c2vjwA_	Alignment	not modelled	99.5	16	PDB header: hydrolase Chain: A: PDB Molecule: gaf family protein; PDBTitle: crystal structure of the second gaf domain of devs from2 mycobacterium smegmatis
51	d2oolal	Alignment	not modelled	99.5	15	Fold: Profilin-like Superfamily: GAF domain-like Family: GAF domain
52	c2c9oC_	Alignment	not modelled	99.5	17	PDB header: hydrolase Chain: C: PDB Molecule: ruvb-like 1; PDBTitle: 3d structure of the human ruvb-like helicase ruvb1
53	c1ykdB_	Alignment	not modelled	99.5	19	PDB header: lyase Chain: B: PDB Molecule: adenylate cyclase; PDBTitle: crystal structure of the tandem gaf domains from a cyanobacterial2 adenyl cyclase: novel modes of ligand-binding and dimerization
54	d1ixsb2	Alignment	not modelled	99.5	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
55	d1ofha_	Alignment	not modelled	99.5	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
56	c2w3gA_	Alignment	not modelled	99.5	15	PDB header: transferase Chain: A: PDB Molecule: two component sensor histidine kinase devs (gaf PDBTitle: air-oxidized structure of the first gaf domain of2 mycobacterium tuberculosis doss
57	d1in4a2	Alignment	not modelled	99.5	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
58	c2qybA_	Alignment	not modelled	99.5	12	PDB header: membrane protein Chain: A: PDB Molecule: membrane protein, putative; PDBTitle: crystal structure of the gaf domain region of putative membrane2 protein from geobacter sulfurreducens pca
59	c3f9vA_	Alignment	not modelled	99.5	19	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
60	d1mc0a1	Alignment	not modelled	99.4	10	Fold: Profilin-like Superfamily: GAF domain-like Family: GAF domain
61	d1fnna2	Alignment	not modelled	99.4	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
62	c3mf0A_	Alignment	not modelled	99.4	9	PDB header: hydrolase Chain: A: PDB Molecule: cgmp-specific 3',5'-cyclic phosphodiesterase; PDBTitle: crystal structure of pde5a gaf domain (89-518)
63	d1sxd2	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
64	d1d2na_	Alignment	not modelled	99.4	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
65	d1etob_	Alignment	not modelled	99.4	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
66	c2lb5A_	Alignment	not modelled	99.4	18	PDB header: transferase Chain: A: PDB Molecule: sensor histidine kinase; PDBTitle: refined structural basis for the photoconversion of a phytochrome to2 the activated far-red light-absorbing form
67	c2dhrC_	Alignment	not modelled	99.4	21	PDB header: hydrolase Chain: C: PDB Molecule: ftsh; PDBTitle: whole cytosolic region of atp-dependent metalloprotease2 ftsh (g399l)
68	d1fipa_	Alignment	not modelled	99.4	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
69	c3e7lD_	Alignment	not modelled	99.3	25	PDB header: transcription regulator Chain: D: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigma54 activator ntrc4's dna binding2 domain
70	c3eihB_	Alignment	not modelled	99.3	20	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
71	d1iqpa2	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
72	d1njfa_	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
73	c2chgB	Alignment	not modelled	99.3	21 PDB header: dna-binding protein Chain: B: PDB Molecule: replication factor c small subunit; PDBTitle: replication factor c domains 1 and 2
74	d1etxa	Alignment	not modelled	99.3	13 Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
75	d1qvra2	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
76	c2k31A	Alignment	not modelled	99.3	10 PDB header: hydrolase Chain: A: PDB Molecule: phosphodiesterase 5a, cgmp-specific; PDBTitle: solution structure of cgmp-binding gaf domain of2 phosphodiesterase 5
77	d1mc0a2	Alignment	not modelled	99.3	14 Fold: Profilin-like Superfamily: GAF domain-like Family: GAF domain
78	c2oolA	Alignment	not modelled	99.3	14 PDB header: signaling protein Chain: A: PDB Molecule: sensor protein; PDBTitle: crystal structure of the chromophore-binding domain of an unusual2 bacteriophytochrome rpbphp3 from r. palustris
79	c1umqA	Alignment	not modelled	99.3	18 PDB header: dna-binding protein Chain: A: PDB Molecule: photosynthetic apparatus regulatory protein; PDBTitle: solution structure and dna binding of the effector domain2 from the global regulator prra(rega) from r. sphaeroides:3 insights into dna binding specificity
80	d1umqa	Alignment	not modelled	99.3	18 Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
81	d2k2na1	Alignment	not modelled	99.3	18 Fold: Profilin-like Superfamily: GAF domain-like Family: GAF domain
82	c2ce7B	Alignment	not modelled	99.3	20 PDB header: cell division protein Chain: B: PDB Molecule: cell division protein ftsh; PDBTitle: edta treated
83	d3c2wa1	Alignment	not modelled	99.3	12 Fold: Profilin-like Superfamily: GAF domain-like Family: GAF domain
84	d1g2ha	Alignment	not modelled	99.3	11 Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
85	c1xwiA	Alignment	not modelled	99.2	18 PDB header: protein transport Chain: A: PDB Molecule: skd1 protein; PDBTitle: crystal structure of vps4b
86	c3c2wB	Alignment	not modelled	99.2	12 PDB header: signaling protein Chain: B: PDB Molecule: bacteriophytochrome; PDBTitle: crystal structure of the photosensory core domain of p.2 aeruginosa bacteriophytochrome pabphp in the pfr state
87	c3b9pA	Alignment	not modelled	99.2	21 PDB header: hydrolase Chain: A: PDB Molecule: cg5977-pa, isoform a; PDBTitle: spastin
88	c2o9bA	Alignment	not modelled	99.2	13 PDB header: transferase Chain: A: PDB Molecule: bacteriophytochrome; PDBTitle: crystal structure of bacteriophytochrome chromophore binding domain
89	c1sxjD	Alignment	not modelled	99.1	17 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)
90	c2p65A	Alignment	not modelled	99.1	17 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
91	d1sxb2	Alignment	not modelled	99.1	13 Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
92	c2kjqA	Alignment	not modelled	99.1	19 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.
93	c3e98B	Alignment	not modelled	99.1	17 PDB header: unknown function Chain: B: PDB Molecule: gaf domain of unknown function; PDBTitle: crystal structure of a gaf domain containing protein that belongs to2 pfam duf484 family (pa5279) from pseudomonas aeruginosa at 2.43 a3 resolution
94	d1f5ma	Alignment	not modelled	99.1	12 Fold: Profilin-like Superfamily: GAF domain-like Family: GAF domain
95	d1sxjc2	Alignment	not modelled	99.1	18 Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
96	c2r65A	Alignment	not modelled	99.1	22 PDB header: hydrolase Chain: A: PDB Molecule: cell division protease ftsh homolog; PDBTitle: crystal structure of helicobacter pylori atp dependent protease, ftsh2 adp complex
97	c2veaA	Alignment	not modelled	99.1	15 PDB header: transferase Chain: A: PDB Molecule: phytochrome-like protein cph1; PDBTitle: the complete sensory module of the cyanobacterial2 phytochrome cph1 in the pr-state.

98	c3h4mC_	Alignment	not modelled	99.1	19	PDB header: hydrolase Chain: C: PDB Molecule: proteasome-activating nucleotidase; PDBTitle: aaa atpase domain of the proteasome- activating nucleotidase
99	c3cf1C_	Alignment	not modelled	99.1	24	PDB header: transport protein Chain: C: PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: structure of p97/vcp in complex with adp/adp.alfx
100	c3u5zM_	Alignment	not modelled	99.1	13	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
101	c3d8bB_	Alignment	not modelled	99.1	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
102	c3hu2C_	Alignment	not modelled	99.1	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
103	d1w5sa2	Alignment	not modelled	99.0	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
104	c2qbyA_	Alignment	not modelled	99.0	16	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)
105	c1xxhB_	Alignment	not modelled	99.0	20	PDB header: transferase Chain: B: PDB Molecule: dna polymerase iii subunit gamma; PDBTitle: atpgs bound e. coli clamp loader complex
106	d2ce7a2	Alignment	not modelled	99.0	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
107	c1fnnB_	Alignment	not modelled	99.0	14	PDB header: cell cycle Chain: B: PDB Molecule: cell division control protein 6; PDBTitle: crystal structure of cdc6p from pyrobaculum aerophilum
108	c2zamA_	Alignment	not modelled	99.0	19	PDB header: protein transport Chain: A: PDB Molecule: vacuolar protein sorting-associated protein 4b; PDBTitle: crystal structure of mouse skd1/vps4b apo-form
109	c1iy2A_	Alignment	not modelled	99.0	23	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent metalloprotease ftsh; PDBTitle: crystal structure of the ftsh atpase domain from thermus2 thermophilus
110	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)
111	d1r6bx2	Alignment	not modelled	99.0	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
112	c1sxC_	Alignment	not modelled	99.0	18	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)
113	c1sxA_	Alignment	not modelled	98.9	11	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	d1ixza_	Alignment	not modelled	98.9	23	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
115	d1sxa2	Alignment	not modelled	98.9	11	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
116	c2xssB_	Alignment	not modelled	98.9	9	PDB header: hydrolase Chain: B: PDB Molecule: cgmp-specific 3', 5'-cyclic phosphodiesterase; PDBTitle: crystal structure of gafb from the human phosphodiesterase 5
117	d1jbka_	Alignment	not modelled	98.9	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
118	c2qz4A_	Alignment	not modelled	98.9	17	PDB header: hydrolase Chain: A: PDB Molecule: paraplegin; PDBTitle: human paraplegin, aaa domain in complex with adp
119	c2v1uA_	Alignment	not modelled	98.9	19	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
120	d1lv7a_	Alignment	not modelled	98.9	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain