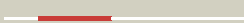
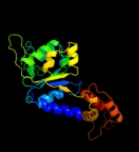
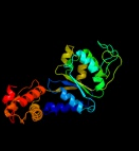
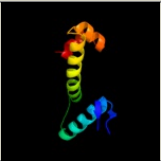


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1ny5A_	 Alignment		100.0	31	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigm54 activator (aaa+ atpase) in the inactive2 state
2	c3dzdA_	 Alignment		100.0	33	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigma54 activator ntrc4 in the inactive2 state
3	c2pjuD_	 Alignment		100.0	94	PDB header: transcription Chain: D: PDB Molecule: propionate catabolism operon regulatory protein; PDBTitle: crystal structure of propionate catabolism operon2 regulatory protein prpr
4	d2pjua1	 Alignment		100.0	99	Fold: Chelatase-like Superfamily: PrpR receptor domain-like Family: PrpR receptor domain-like
5	c2c99A_	 Alignment		100.0	41	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
6	d1ny5a2	 Alignment		100.0	42	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
7	c1ojlF_	 Alignment		100.0	48	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
8	c2q5cA_	 Alignment		100.0	23	PDB header: transcription Chain: A: PDB Molecule: ntrc family transcriptional regulator; PDBTitle: crystal structure of ntrc family transcriptional regulator from2 clostridium acetobutylicum
9	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
10	c1qvrB_	 Alignment		99.9	16	PDB header: chaperone Chain: B: PDB Molecule: clpb protein; PDBTitle: crystal structure analysis of clpb
11	c1r6bX_	 Alignment		99.9	17	PDB header: hydrolase Chain: X: PDB Molecule: clpa protein; PDBTitle: high resolution crystal structure of clpa

12	c3pxiB_	Alignment		99.9	16	PDB header: protein binding Chain: B: PDB Molecule: negative regulator of genetic competence clpc/mecc; PDBTitle: structure of meca108:clpc
13	d1r6bx3	Alignment		99.9	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
14	c3pfiB_	Alignment		99.9	20	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
15	c1in8A_	Alignment		99.8	17	PDB header: dna binding protein Chain: A: PDB Molecule: holliday junction dna helicase ruvb; PDBTitle: thermotoga maritima ruvb t158v
16	c3nbxX_	Alignment		99.8	17	PDB header: hydrolase Chain: X: PDB Molecule: atpase rava; PDBTitle: crystal structure of e. coli rava (regulatory atpase variant a) in2 complex with adp
17	d1um8a_	Alignment		99.8	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
18	d1qvra3	Alignment		99.8	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
19	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
20	d1l8qa2	Alignment		99.8	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
21	c3k1jA_	Alignment	not modelled	99.8	22	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent protease lon; PDBTitle: crystal structure of lon protease from thermococcus onnurineus na1
22	c2hcbC_	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
23	c1nsfA_	Alignment	not modelled	99.7	19	PDB header: protein transport Chain: A: PDB Molecule: n-ethylmaleimide sensitive factor; PDBTitle: d2 hexamerization domain of n-ethylmaleimide sensitive factor (nsf)
24	d1g41a_	Alignment	not modelled	99.7	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
25	c1hqcb_	Alignment	not modelled	99.6	18	PDB header: hydrolase Chain: B: PDB Molecule: ruvb; PDBTitle: structure of ruvb from thermus thermophilus hb8
26	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
27	c3hteC_	Alignment	not modelled	99.6	17	PDB header: motor protein Chain: C: PDB Molecule: atp-dependent clp protease atp-binding subunit clpx; PDBTitle: crystal structure of nucleotide-free hexameric clpx
28	c2z4rB_	Alignment	not modelled	99.6	12	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

29	d1g8pa_	Alignment	not modelled	99.6	23	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
30	c3f8tA_	Alignment	not modelled	99.6	21	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
31	d1ofha_	Alignment	not modelled	99.6	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
32	c3bosA_	Alignment	not modelled	99.6	17	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
33	d1in4a2	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
34	c2c9oC_	Alignment	not modelled	99.5	20	PDB header: hydrolase Chain: C: PDB Molecule: ruvb-like 1; PDBTitle: 3d structure of the human ruvb-like helicase ruvb1
35	d1ixsb2	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
36	d1fnna2	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
37	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
38	c3f9vA_	Alignment	not modelled	99.4	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
39	d1sxjd2	Alignment	not modelled	99.4	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
40	c2dhrC_	Alignment	not modelled	99.4	25	PDB header: hydrolase Chain: C: PDB Molecule: ftsh; PDBTitle: whole cytosolic region of atp-dependent metalloprotease2 ftsh (g399l)
41	c3eihB_	Alignment	not modelled	99.4	19	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
42	c2chgB_	Alignment	not modelled	99.3	18	PDB header: dna-binding protein Chain: B: PDB Molecule: replication factor c small subunit; PDBTitle: replication factor c domains 1 and 2
43	d1njfa_	Alignment	not modelled	99.3	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
44	c3b9pA_	Alignment	not modelled	99.3	24	PDB header: hydrolase Chain: A: PDB Molecule: cg5977-pa, isoform a; PDBTitle: spastin
45	c2ce7B_	Alignment	not modelled	99.3	26	PDB header: cell division protein Chain: B: PDB Molecule: cell division protein ftsh; PDBTitle: edta treated
46	d1ntca_	Alignment		99.2	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
47	c1xwiA_	Alignment	not modelled	99.2	21	PDB header: protein transport Chain: A: PDB Molecule: skd1 protein; PDBTitle: crystal structure of vps4b
48	d1iqpa2	Alignment	not modelled	99.2	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
49	c3hu2C_	Alignment	not modelled	99.2	21	PDB header: transport protein Chain: C: PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: structure of p97 n-d1 r86a mutant in complex with atpgs
50	d1sxjc2	Alignment	not modelled	99.2	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
51	d1sxb2	Alignment	not modelled	99.1	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
52	c2kjqA_	Alignment	not modelled	99.1	17	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.

53	c1xxhB	Alignment	not modelled	99.1	17	PDB header: transferase Chain: B: PDB Molecule: dna polymerase iii subunit gamma; PDBTitle: atpgs bound e. coli clamp loader complex
54	d1qvra2	Alignment	not modelled	99.1	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
55	d2ce7a2	Alignment	not modelled	99.1	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
56	d1w5sa2	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
57	c3cf1C	Alignment	not modelled	99.1	23	PDB header: transport protein Chain: C: PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: structure of p97/vcp in complex with adp/adp.alfx
58	c1sxD	Alignment	not modelled	99.1	15	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)
59	c1sxB	Alignment	not modelled	99.1	17	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)
60	c3d8bB	Alignment	not modelled	99.1	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
61	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
62	c3u5zM	Alignment	not modelled	99.1	15	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
63	c2zamA	Alignment	not modelled	99.1	21	PDB header: protein transport Chain: A: PDB Molecule: vacuolar protein sorting-associating protein 4b; PDBTitle: crystal structure of mouse skd1/vps4b apo-form
64	c2r65A	Alignment	not modelled	99.1	28	PDB header: hydrolase Chain: A: PDB Molecule: cell division protease ftsh homolog; PDBTitle: crystal structure of helicobacter pylori atp dependent protease, ftsh2 adp complex
65	d1etob	Alignment		99.1	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
66	c1sxC	Alignment	not modelled	99.0	20	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	c1umqA	Alignment	not modelled	99.0	22	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
68	d1umqa	Alignment	not modelled	99.0	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
69	c3h4mC	Alignment	not modelled	99.0	25	PDB header: hydrolase Chain: C: PDB Molecule: proteasome-activating nucleotidase; PDBTitle: aaa atpase domain of the proteasome- activating nucleotidase
70	c1fnnB	Alignment	not modelled	99.0	15	PDB header: cell cycle Chain: B: PDB Molecule: cell division control protein 6; PDBTitle: crystal structure of cdc6p from pyrobaculum aerophilum
71	d1e32a2	Alignment	not modelled	99.0	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
72	d1sxja2	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
73	c2qz4A	Alignment	not modelled	99.0	27	PDB header: hydrolase Chain: A: PDB Molecule: paraplegin; PDBTitle: human paraplegin, aaa domain in complex with adp
74	c2qbyB	Alignment	not modelled	99.0	15	PDB header: replication/dna Chain: B: PDB Molecule: cell division control protein 6 homolog 3; PDBTitle: crystal structure of a heterodimer of cdc6/crc1 initiators2 bound to origin dna (from s. solfataricus)
75	d1sxje2	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
76	d1fipa	Alignment	not modelled	99.0	26	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like

77	cliqpF_	Alignment	not modelled	99.0	21	PDB header: replication Chain: F: PDB Molecule: rfcs; PDBTitle: crystal structure of the clamp loader small subunit from2 pyrococcus furiosus
78	dlr6bx2	Alignment	not modelled	99.0	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
79	c2chvE_	Alignment	not modelled	98.9	19	PDB header: dna-binding protein Chain: E: PDB Molecule: replication factor c small subunit; PDBTitle: replication factor c adpnp complex
80	dlixza_	Alignment	not modelled	98.9	25	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
81	c2v1uA_	Alignment	not modelled	98.9	17	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
82	clsxjA_	Alignment	not modelled	98.9	14	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)
83	cls3sA_	Alignment	not modelled	98.9	20	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
84	cliy2A_	Alignment	not modelled	98.9	24	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent metalloprotease ftsh; PDBTitle: crystal structure of the ftsh atpase domain from thermus2 thermophilus
85	dl1v7a_	Alignment	not modelled	98.9	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
86	dl1etxa_	Alignment	not modelled	98.9	26	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
87	c2qbyA_	Alignment	not modelled	98.9	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)
88	clsxjE_	Alignment	not modelled	98.8	16	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)
89	dlg2ha_	Alignment	not modelled	98.8	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
90	c3e7lD_	Alignment	not modelled	98.8	16	PDB header: transcription regulator Chain: D: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigma54 activator ntrc4's dna binding2 domain
91	dljbka_	Alignment	not modelled	98.8	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
92	c2x8aA_	Alignment	not modelled	98.7	16	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
93	dlr7ra3	Alignment	not modelled	98.6	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
94	dl1e94e_	Alignment	not modelled	98.6	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
95	c3ec2A_	Alignment	not modelled	98.6	18	PDB header: replication Chain: A: PDB Molecule: dna replication protein dnac; PDBTitle: crystal structure of the dnac helicase loader
96	c2qgzA_	Alignment	not modelled	98.5	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
97	cljr3E_	Alignment	not modelled	98.3	20	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
98	clw5sB_	Alignment	not modelled	98.3	13	PDB header: replication Chain: B: PDB Molecule: origin recognition complex subunit 2 orc2; PDBTitle: structure of the aeropyrum pernix orc2 protein (adp form)
99	c3pxgA_	Alignment	not modelled	98.1	16	PDB header: protein binding Chain: A: PDB Molecule: negative regulator of genetic competence clpc/mecc; PDBTitle: structure of meca121 and clpc1-485 complex
100	c2w58B_	Alignment	not modelled	98.1	14	PDB header: hydrolase Chain: B: PDB Molecule: primosome component (helicase loader); PDBTitle: crystal structure of the dna1
101	dl1oz4a3	Alignment	not modelled	98.1	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain

102	d1a5ta2	Alignment	not modelled	98.0	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
103	c3te6A	Alignment	not modelled	98.0	8	PDB header: gene regulation Chain: A: PDB Molecule: regulatory protein sir3; PDBTitle: crystal structure of the s. cerevisiae sir3 aaa+ domain
104	d2gnoa2	Alignment	not modelled	98.0	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
105	c3m6aC	Alignment	not modelled	97.9	17	PDB header: hydrolase Chain: C: PDB Molecule: atp-dependent protease la 1; PDBTitle: crystal structure of bacillus subtilis lon c-terminal domain
106	c3n70F	Alignment	not modelled	97.7	25	PDB header: transport protein Chain: F: PDB Molecule: transport activator; PDBTitle: the crystal structure of the p-loop ntpase domain of the sigma-542 transport activator from e. coli to 2.8a
107	d1gvnb	Alignment	not modelled	97.4	25	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Plasmid maintenance system epsilon/zeta, toxin zeta subunit
108	c3e1sA	Alignment	not modelled	97.0	21	PDB header: hydrolase Chain: A: PDB Molecule: exodeoxyribonuclease v, subunit recd; PDBTitle: structure of an n-terminal truncation of deinococcus radiodurans recd2
109	c2p5tD	Alignment	not modelled	97.0	19	PDB header: transcription regulator Chain: D: PDB Molecule: pez2; PDBTitle: molecular and structural characterization of the pezat chromosomal2 toxin-antitoxin system of the human pathogen streptococcus pneumoniae
110	c3qmzA	Alignment	not modelled	96.6	15	PDB header: motor protein Chain: A: PDB Molecule: cytoplasmic dynein heavy chain; PDBTitle: crystal structure of the cytoplasmic dynein heavy chain motor domain
111	d1svma	Alignment	not modelled	96.1	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
112	c2fnaA	Alignment	not modelled	96.0	21	PDB header: atp-binding protein Chain: A: PDB Molecule: conserved hypothetical protein; PDBTitle: crystal structure of an archaeal aaa+ atpase (sso1545) from sulfobolus2 solfataricus p2 at 2.00 a resolution
113	d1tuea	Alignment	not modelled	96.0	11	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
114	d2fnaa2	Alignment	not modelled	95.8	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
115	c2gnoA	Alignment	not modelled	95.8	15	PDB header: replication Chain: A: PDB Molecule: dna polymerase iii, gamma subunit-related protein; PDBTitle: crystal structure of a dna polymerase iii, gamma subunit-related2 protein (tm0771) from thermotoga maritima msb8 at 2.00 a resolution
116	c2qenA	Alignment	not modelled	95.7	15	PDB header: unknown function Chain: A: PDB Molecule: walker-type atpase; PDBTitle: the walker-type atpase paby2304 of pyrococcus abyssi
117	c1xxiF	Alignment	not modelled	95.7	18	PDB header: transferase Chain: F: PDB Molecule: dna polymerase iii, delta subunit; PDBTitle: adp bound e. coli clamp loader complex
118	d1ye8a1	Alignment	not modelled	95.6	33	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
119	d1g6oa	Alignment	not modelled	95.5	23	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
120	d2i3ba1	Alignment	not modelled	95.5	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)