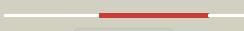
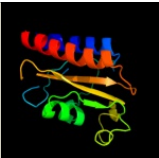


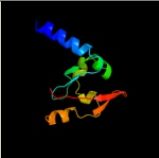
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1ny5A_	 Alignment		100.0	43	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigm54 activator (aaa+ atpase) in the inactive2 state
2	c3dzdA_	 Alignment		100.0	45	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	47	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
5	c1ojlF_	 Alignment		100.0	46	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	25	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	c3pfiB_	 Alignment		99.9	15	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
8	d1r6bx3	 Alignment		99.9	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
9	c1r6bX_	 Alignment		99.8	17	PDB header: hydrolase Chain: X: PDB Molecule: clpa protein; PDBTitle: high resolution crystal structure of clpa
10	c1qvrB_	 Alignment		99.8	19	PDB header: chaperone Chain: B: PDB Molecule: clpb protein; PDBTitle: crystal structure analysis of clpb
11	d1um8a_	 Alignment		99.8	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain

12	c3pxiB_	Alignment		99.8	17	PDB header: protein binding Chain: B: PDB Molecule: negative regulator of genetic competence clpc/meccb; PDBTitle: structure of meca108:clpc
13	clin8A_	Alignment		99.8	18	PDB header: dna binding protein Chain: A: PDB Molecule: holliday junction dna helicase ruvb; PDBTitle: thermotoga maritima ruvb t158v
14	c3nbxX_	Alignment		99.8	19	PDB header: hydrolase Chain: X: PDB Molecule: atpase rava; PDBTitle: crystal structure of e. coli rava (regulatory atpase variant a) in2 complex with adp
15	dlqvra3	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	24	PDB header: recombination Chain: A: PDB Molecule: replication-associated recombination protein a; PDBTitle: structure and biochemical activities of escherichia coli mgsa
17	c3k1jA_	Alignment		99.8	24	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent protease lon; PDBTitle: crystal structure of lon protease from thermococcus onnurineus na1
18	dl18qa2	Alignment		99.7	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
19	c3f8tA_	Alignment		99.7	13	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
20	c2hcbC_	Alignment		99.7	15	PDB header: replication Chain: C: PDB Molecule: chromosomal replication initiator protein dnaa; PDBTitle: structure of amppcp-bound dnaa from aquifex aeolicus
21	clnsfA_	Alignment	not modelled	99.6	19	PDB header: protein transport Chain: A: PDB Molecule: n-ethylmaleimide sensitive factor; PDBTitle: d2 hexamerization domain of n-ethylmaleimide sensitive factor (nsf)
22	dlg41a_	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
23	dlg8pa_	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
24	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
25	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
26	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
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	clhqcb_	Alignment	not modelled	99.6	18	PDB header: hydrolase Chain: B: PDB Molecule: ruvb;

					PDBTitle: structure of ruvb from thermus thermophilus hb8
29	c2c9oC_	Alignment	not modelled	99.5	19 PDB header: hydrolase Chain: C: PDB Molecule: ruvb-like 1; PDBTitle: 3d structure of the human ruvb-like helicase ruvbl1
30	c3f9vA_	Alignment	not modelled	99.5	14 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
31	d1ofha_	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
32	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
33	d1ixsb2	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
34	d1ntca_	Alignment		99.5	28 Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
35	d1fnna2	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
36	d1sxd2	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
37	d1d2na_	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
38	d1etob_	Alignment	not modelled	99.4	25 Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
39	d1iqpa2	Alignment	not modelled	99.3	20 Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
40	d1fipa_	Alignment	not modelled	99.3	24 Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
41	c2chgB_	Alignment	not modelled	99.3	23 PDB header: dna-binding protein Chain: B: PDB Molecule: replication factor c small subunit; PDBTitle: replication factor c domains 1 and 2
42	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
43	d1g2ha_	Alignment	not modelled	99.3	17 Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
44	c2dhrC_	Alignment	not modelled	99.3	21 PDB header: hydrolase Chain: C: PDB Molecule: ftsh; PDBTitle: whole cytosolic region of atp-dependent metalloprotease2 ftsh (g399l)
45	c3b9pA_	Alignment	not modelled	99.3	21 PDB header: hydrolase Chain: A: PDB Molecule: cg5977-pa, isoform a; PDBTitle: spastin
46	d1etxa_	Alignment	not modelled	99.3	25 Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
47	c2ce7B_	Alignment	not modelled	99.2	24 PDB header: cell division protein Chain: B: PDB Molecule: cell division protein ftsh; PDBTitle: edta treated
48	d1sxb2	Alignment	not modelled	99.2	17 Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
49	d1umqa_	Alignment	not modelled	99.2	15 Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
50	c1umqA_	Alignment	not modelled	99.2	15 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
51	c3eihB_	Alignment	not modelled	99.2	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
52	c3e7ID_	Alignment	not modelled	99.2	33 PDB header: transcription regulator Chain: D: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigma54 activator ntrc4's dna binding2 domain

53	c2kjqA	Alignment	not modelled	99.2	23	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.
54	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
55	c3h4mC	Alignment	not modelled	99.2	16	PDB header: hydrolase Chain: C: PDB Molecule: proteasome-activating nucleotidase; PDBTitle: aaa atpase domain of the proteasome- activating nucleotidase
56	d1w5sa2	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
57	c2w1rA	Alignment		99.1	14	PDB header: transcription Chain: A: PDB Molecule: stage v sporulation protein t; PDBTitle: crystal structure of the c-terminal domain of b. subtilis2 spovt
58	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
59	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
60	c1xxhB	Alignment	not modelled	99.1	20	PDB header: transferase Chain: B: PDB Molecule: dna polymerase iii subunit gamma; PDBTitle: atpgs bound e. coli clamp loader complex
61	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
62	c1xwiA	Alignment	not modelled	99.1	19	PDB header: protein transport Chain: A: PDB Molecule: skd1 protein; PDBTitle: crystal structure of vps4b
63	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
64	c1sxjD	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)
65	c3u5zM	Alignment	not modelled	99.1	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
66	c2r65A	Alignment	not modelled	99.0	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
67	c1fnbB	Alignment	not modelled	99.0	11	PDB header: cell cycle Chain: B: PDB Molecule: cell division control protein 6; PDBTitle: crystal structure of cdc6p from pyrobaculum aerophilum
68	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
69	c1sxjB	Alignment	not modelled	99.0	19	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)
70	d1lv7a	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
71	c2qbyB	Alignment	not modelled	99.0	16	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)
72	c2v1uA	Alignment	not modelled	99.0	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
73	c3cf1C	Alignment	not modelled	99.0	22	PDB header: transport protein Chain: C: PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: structure of p97/vcp in complex with adp/adp.alfx
74	c2qbyA	Alignment	not modelled	99.0	15	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)
75	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
76	c1iy2A	Alignment	not modelled	98.9	22	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent metalloprotease ftsh; PDBTitle: crystal structure of the ftsh atpase domain from thermus2 thermophilus

77	c3p01C_	Alignment		98.9	11	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
78	c3mmhA_	Alignment		98.9	14	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
79	c1sxjC_	Alignment	not modelled	98.9	16	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)
80	c3o5yA_	Alignment		98.9	13	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
81	c2qz4A_	Alignment	not modelled	98.9	16	PDB header: hydrolase Chain: A: PDB Molecule: paraplegin; PDBTitle: human paraplegin, aaa domain in complex with adp
82	d1ixza_	Alignment	not modelled	98.9	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
83	c2chvE_	Alignment	not modelled	98.9	23	PDB header: dna-binding protein Chain: E: PDB Molecule: replication factor c small subunit; PDBTitle: replication factor c adnpn complex
84	c3ksiA_	Alignment		98.9	11	PDB header: oxidoreductase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: structure of frmrs of staphylococcus aureus (complex with 2-propanol)
85	d1sxje2	Alignment	not modelled	98.9	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
86	c2zamA_	Alignment	not modelled	98.9	23	PDB header: protein transport Chain: A: PDB Molecule: vacuolar protein sorting-associating protein 4b; PDBTitle: crystal structure of mouse skd1/vps4b apo-form
87	d1e32a2	Alignment	not modelled	98.9	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
88	c3hu2C_	Alignment	not modelled	98.9	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
89	c1iqpF_	Alignment	not modelled	98.9	22	PDB header: replication Chain: F: PDB Molecule: rfcs; PDBTitle: crystal structure of the clamp loader small subunit from2 pyrococcus furiosus
90	c2x8aA_	Alignment	not modelled	98.8	12	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
91	c3trcA_	Alignment	not modelled	98.8	12	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
92	c3p01A_	Alignment		98.8	11	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
93	d1vhma_	Alignment	not modelled	98.8	7	Fold: Profilin-like Superfamily: GAF domain-like Family: GAF domain
94	c1sxjA_	Alignment	not modelled	98.8	15	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)
95	c1vhmB_	Alignment	not modelled	98.8	7	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: protein yebr; PDBTitle: crystal structure of an hypothetical protein
96	d1jbka_	Alignment	not modelled	98.8	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
97	c3oosB_	Alignment	not modelled	98.8	16	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: gaf domain/hd domain protein;

97	c3eeab	Alignment	not modelled	98.8	10	PDBTitle: the crystal structure of the gaf domain/hd domain protein2 from geobacter sulfurreducens Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
98	d1e94e	Alignment	not modelled	98.7	18	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)
99	c1sxE	Alignment	not modelled	98.7	19	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
100	c1mc0A	Alignment	not modelled	98.7	14	PDB header: hydrolase Chain: B: PDB Molecule: cgmp-dependent 3',5'-cyclic phosphodiesterase; PDBTitle: x-ray structure of pde2a
101	c3ibjB	Alignment		98.7	16	PDB header: transferase, cell adhesion Chain: A: PDB Molecule: nph1-1, ras-related c3 botulinum toxin substrate PDBTitle: structure of a photoactivatable rac1 containing the lov22 c450a mutant
102	c2wkqA	Alignment		98.6	17	Fold: Profilin-like Superfamily: GAF domain-like Family: GAF domain
103	d2veaa1	Alignment	not modelled	98.6	10	Fold: Profilin-like Superfamily: GAF domain-like Family: GAF domain
104	d1f5ma	Alignment	not modelled	98.6	14	PDB header: hydrolase Chain: A: PDB Molecule: cgmp-specific 3',5'-cyclic phosphodiesterase; PDBTitle: crystal structure of pde5a gaf domain (89-518)
105	c3mf0A	Alignment	not modelled	98.6	14	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
106	c1s3sA	Alignment	not modelled	98.6	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
107	d1r7ra3	Alignment	not modelled	98.6	22	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
108	c3dbaB	Alignment	not modelled	98.6	11	Fold: Profilin-like Superfamily: GAF domain-like Family: GAF domain
109	d2o9ca1	Alignment	not modelled	98.5	11	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative two-component sensor histidine kinase protein; PDBTitle: the crystal structure of the domain of putative two-component sensor2 histidine kinase protein from sinorhizobium meliloti 1021
110	c3hcyB	Alignment	not modelled	98.5	10	PDB header: replication Chain: A: PDB Molecule: dna replication protein dnac; PDBTitle: crystal structure of the dnac helicase loader
111	c3ec2A	Alignment	not modelled	98.5	17	PDB header: hydrolase Chain: A: PDB Molecule: gaf family protein; PDBTitle: crystal structure of the second gaf domain of devs from2 mycobacterium smegmatis
112	c2vjwA	Alignment	not modelled	98.5	9	PDB header: transferase Chain: E: PDB Molecule: dna polymerase iii, delta' subunit; PDBTitle: crystal structure of the processivity clamp loader gamma2 complex of e. coli dna polymerase iii
113	c1jr3E	Alignment	not modelled	98.5	15	PDB header: transcription Chain: A: PDB Molecule: sensory box/ggdef family protein; PDBTitle: crystal structure of the sensory box domain of the sensory-2 box/ggdef protein so_1695 from shewanella oneidensis,3 northeast structural genomics consortium target sor288b
114	c3mfxA	Alignment		98.5	13	PDB header: transferase Chain: B: PDB Molecule: phosphoenolpyruvate-protein phosphotransferase; PDBTitle: crystal structure of the gaf domain from acinetobacter2 phosphoenolpyruvate-protein phosphotransferase
115	c3ci6B	Alignment		98.5	11	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
116	c2qybA	Alignment	not modelled	98.4	12	PDB header: transcription Chain: B: PDB Molecule: transcription regulator tyrr; PDBTitle: n-terminal domain of tyrr transcription factor (residues 1 -2 190)
117	c2jheB	Alignment		98.4	14	
		Alignment				

118	c3oovA_	 Alignment	not modelled	98.4	13	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
119	c3pxgA_	 Alignment	not modelled	98.4	20	PDB header: protein binding Chain: A: PDB Molecule: negative regulator of genetic competence clpc/mecb; PDBTitle: structure of meca121 and clpc1-485 complex
120	c2w3gA_	 Alignment	not modelled	98.4	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