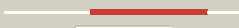
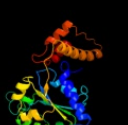
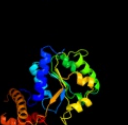
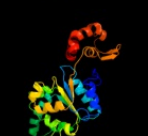
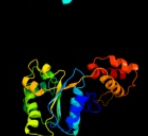


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1ny5A_	 Alignment		100.0	41	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigm54 activator (aaa+ atpase) in the inactive2 state
2	c3dzdA_	 Alignment		100.0	44	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	37	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	44	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
5	c1ojlF_	 Alignment		100.0	41	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	23	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	c2jheB_	 Alignment		100.0	95	PDB header: transcription Chain: B: PDB Molecule: transcription regulator tyrr; PDBTitle: n-terminal domain of tyrr transcription factor (residues 1-2 190)
8	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
9	d1r6bx3	 Alignment		99.9	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
10	c3pxiB_	 Alignment		99.8	18	PDB header: protein binding Chain: B: PDB Molecule: negative regulator of genetic competence clpc/meqb; PDBTitle: structure of meca108:clpc
11	c1qvrB_	 Alignment		99.8	19	PDB header: chaperone Chain: B: PDB Molecule: clpb protein; PDBTitle: crystal structure analysis of clpb

12	d1um8a_	Alignment		99.8	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
13	c1r6bX_	Alignment		99.8	18	PDB header: hydrolase Chain: X: PDB Molecule: clpa protein; PDBTitle: high resolution crystal structure of clpa
14	c3pvsA_	Alignment		99.8	14	PDB header: recombination Chain: A: PDB Molecule: replication-associated recombination protein a; PDBTitle: structure and biochemical activities of escherichia coli mgsa
15	c1in8A_	Alignment		99.8	15	PDB header: dna binding protein Chain: A: PDB Molecule: holliday junction dna helicase ruvb; PDBTitle: thermotoga maritima ruvb t158v
16	d1qvra3	Alignment		99.8	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
17	c3nbxX_	Alignment		99.8	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
18	d1l8qa2	Alignment		99.8	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
19	c3k1jA_	Alignment		99.7	23	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent protease lon; PDBTitle: crystal structure of lon protease from thermococcus onnurineus na1
20	c2hcbC_	Alignment		99.7	20	PDB header: replication Chain: C: PDB Molecule: chromosomal replication initiator protein dnaa; PDBTitle: structure of amppcp-bound dnaa from aquifex aeolicus
21	c3bosA_	Alignment	not modelled	99.7	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
22	c1nsfA_	Alignment	not modelled	99.6	18	PDB header: protein transport Chain: A: PDB Molecule: n-ethylmaleimide sensitive factor; PDBTitle: d2 hexamerization domain of n-ethylmaleimide sensitive factor (nsf)
23	c2z4rB_	Alignment	not modelled	99.6	16	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
24	c3f8tA_	Alignment	not modelled	99.6	16	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
25	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
26	c2r44A_	Alignment	not modelled	99.6	14	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	c1hqcb_	Alignment	not modelled	99.6	13	PDB header: hydrolase Chain: B: PDB Molecule: ruvb; PDBTitle: structure of ruvb from thermus thermophilus hb8
						PDB header: hydrolase

28	c2c9oC	Alignment	not modelled	99.5	18	Chain: C: PDB Molecule: ruvb-like 1; PDBTitle: 3d structure of the human ruvb-like helicase ruvb1
29	dlg41a	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
30	c2wkqA	Alignment	not modelled	99.5	12	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
31	dlg8pa	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
32	d1ntca	Alignment		99.5	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
33	dlixsb2	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
34	dlin4a2	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
35	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
36	c3f9vA	Alignment	not modelled	99.5	18	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
37	d1fnna2	Alignment	not modelled	99.5	11	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
38	d1d2na	Alignment	not modelled	99.4	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
39	d1etob	Alignment	not modelled	99.4	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
40	c3mfxA	Alignment	not modelled	99.4	11	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
41	c3e7ID	Alignment	not modelled	99.3	15	PDB header: transcription regulator Chain: D: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigma54 activator ntrc4's dna binding2 domain
42	d1g2ha	Alignment	not modelled	99.3	54	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
43	c2dhrC	Alignment	not modelled	99.3	18	PDB header: hydrolase Chain: C: PDB Molecule: ftsh; PDBTitle: whole cytosolic region of atp-dependent metalloprotease2 ftsh (g399l)
44	d1iqpa2	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
45	c2chgB	Alignment	not modelled	99.3	19	PDB header: dna-binding protein Chain: B: PDB Molecule: replication factor c small subunit; PDBTitle: replication factor c domains 1 and 2
46	d1fipa	Alignment	not modelled	99.3	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
47	d1sxjd2	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
48	c3mxqC	Alignment	not modelled	99.3	11	PDB header: transferase Chain: C: PDB Molecule: sensor protein; PDBTitle: crystal structure of sensory box sensor histidine kinase from vibrio2 cholerae
49	c3b33A	Alignment	not modelled	99.3	22	PDB header: transferase Chain: A: PDB Molecule: sensor protein; PDBTitle: crystal structure of the pas domain of nitrogen regulation protein2 nr(ii) from vibrio parahaemolyticus
50	c3eihB	Alignment	not modelled	99.3	15	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
51	c3oloB	Alignment	not modelled	99.3	14	PDB header: transferase Chain: B: PDB Molecule: two-component sensor histidine kinase; PDBTitle: crystal structure of a pas domain from two-component sensor histidine2 kinase
						Fold: DNA/RNA-binding 3-helical bundle

52	d1etxa_	Alignment	not modelled	99.3	17	Superfamily: Homeodomain-like Family: FIS-like
53	c3caxA_	Alignment	not modelled	99.3	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein pf0695; PDBTitle: crystal structure of uncharacterized protein pf0695
54	d1njfa_	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	c1xwiA_	Alignment	not modelled	99.2	16	PDB header: protein transport Chain: A: PDB Molecule: skd1 protein; PDBTitle: crystal structure of vps4b
56	c3b9pA_	Alignment	not modelled	99.2	19	PDB header: hydrolase Chain: A: PDB Molecule: cg5977-pa, isoform a; PDBTitle: spastin
57	c2kjqA_	Alignment	not modelled	99.2	20	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.
58	c2gj3A_	Alignment	not modelled	99.2	17	PDB header: transferase Chain: A: PDB Molecule: nitrogen fixation regulatory protein; PDBTitle: crystal structure of the fad-containing pas domain of the2 protein nifl from azotobacter vinelandii.
59	d1nwza_	Alignment	not modelled	99.2	10	Fold: Profilin-like Superfamily: PYP-like sensor domain (PAS domain) Family: PYP-like
60	c3hu2C_	Alignment	not modelled	99.2	19	PDB header: transport protein Chain: C: PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: structure of p97 n-d1 r86a mutant in complex with atpgs
61	c1v9yA_	Alignment	not modelled	99.2	14	PDB header: signaling protein Chain: A: PDB Molecule: heme pas sensor protein; PDBTitle: crystal structure of the heme pas sensor domain of ec dos (ferric2 form)
62	d1v9ya_	Alignment	not modelled	99.2	14	Fold: Profilin-like Superfamily: PYP-like sensor domain (PAS domain) Family: Heme-binding PAS domain
63	c3lyxA_	Alignment	not modelled	99.2	16	PDB header: transcription Chain: A: PDB Molecule: sensory box/ggdef domain protein; PDBTitle: crystal structure of the pas domain of the protein cps_12912 from colwellia psychrerythraea. northeast structural3 genomics consortium target id csr222b
64	c2ce7B_	Alignment	not modelled	99.2	19	PDB header: cell division protein Chain: B: PDB Molecule: cell division protein ftsh; PDBTitle: edta treated
65	c3mqoB_	Alignment	not modelled	99.2	13	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, luxr family; PDBTitle: the crystal structure of the pas domain in complex with isopropanol of2 a transcriptional regulator in the luxr family from burkholderia3 thailandensis to 1.7a
66	d2ce7a2	Alignment	not modelled	99.2	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
67	c2v1bA_	Alignment	not modelled	99.2	11	PDB header: transferase Chain: A: PDB Molecule: nph1-1; PDBTitle: n- and c-terminal helices of oat lov2 (404-546) are2 involved in light-induced signal transduction (room3 temperature (293k) light structure of lov2 (404-546))
68	c3luqC_	Alignment	not modelled	99.2	8	PDB header: transferase Chain: C: PDB Molecule: sensor protein; PDBTitle: the crystal structure of a pas domain from a sensory box2 histidine kinase regulator from geobacter sulfurreducens to3 2.5a
69	c2r78D_	Alignment	not modelled	99.1	21	PDB header: transferase Chain: D: PDB Molecule: sensor protein; PDBTitle: crystal structure of a domain of the sensory box sensor2 histidine kinase/response regulator from geobacter3 sulfurreducens
70	c3bwlA_	Alignment	not modelled	99.1	14	PDB header: transferase Chain: A: PDB Molecule: sensor protein; PDBTitle: crystal structure of pas domain of htr-like protein from haloarcula2 marismortui
71	c3h4mC_	Alignment	not modelled	99.1	15	PDB header: hydrolase Chain: C: PDB Molecule: proteasome-activating nucleotidase; PDBTitle: aaa atpase domain of the proteasome- activating nucleotidase
72	c3mjgB_	Alignment	not modelled	99.1	11	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the pas domain of q24qt8_deshy protein from2 desulfitobacterium hafniense. northeast structural genomics3 consortium target dhr85c.
73	c2r65A_	Alignment	not modelled	99.1	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
74	c3fg8B_	Alignment	not modelled	99.1	11	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein rha05790; PDBTitle: crystal structure of pas domain of rha05790
75	c2w0nA_	Alignment	not modelled	99.1	18	PDB header: transferase Chain: A: PDB Molecule: sensor protein dcus; PDBTitle: plasticity of pas domain and potential role for signal2 transduction in the histidine-kinase dcus
76	c3cf1C_	Alignment	not modelled	99.1	18	PDB header: transport protein Chain: C: PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: structure of p97/vcp in complex with adp/adp.alfx

77	d1ew0a_	Alignment	not modelled	99.1	12	Fold: Profilin-like Superfamily: PYP-like sensor domain (PAS domain) Family: Heme-binding PAS domain
78	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
79	c1umqA_	Alignment	not modelled	99.1	14	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	99.1	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
81	d1sxc2	Alignment	not modelled	99.1	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
82	d1w5sa2	Alignment	not modelled	99.1	11	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
83	d1qvra2	Alignment	not modelled	99.1	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
84	c3d8bB_	Alignment	not modelled	99.0	18	PDB header: hydrolase Chain: B: PDB Molecule: fidgetin-like protein 1; PDBTitle: crystal structure of human fidgetin-like protein 1 in complex with adp
85	dlixza_	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
86	cliy2A_	Alignment	not modelled	99.0	21	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent metalloprotease ftsh; PDBTitle: crystal structure of the ftsh atpase domain from thermus2 thermophilus
87	c2zamA_	Alignment	not modelled	99.0	19	PDB header: protein transport Chain: A: PDB Molecule: vacuolar protein sorting-associating protein 4b; PDBTitle: crystal structure of mouse skd1/vps4b apo-form
88	c3u5zM_	Alignment	not modelled	99.0	14	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
89	c2pr6A_	Alignment	not modelled	99.0	14	PDB header: flavoprotein, signaling protein Chain: A: PDB Molecule: blue-light photoreceptor; PDBTitle: structural basis for light-dependent signaling in the dimeric lov2 photosensor ytvA (light structure)
90	c3a0vA_	Alignment	not modelled	99.0	13	PDB header: transferase Chain: A: PDB Molecule: sensor protein; PDBTitle: pas domain of histidine kinase thka (tm1359) (semet,2 f486m/f489m)
91	c1fnnB_	Alignment	not modelled	99.0	10	PDB header: cell cycle Chain: B: PDB Molecule: cell division control protein 6; PDBTitle: crystal structure of cdc6p from pyrobaculum aerophilum
92	c2p65A_	Alignment	not modelled	99.0	16	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
93	d1otda_	Alignment	not modelled	99.0	10	Fold: Profilin-like Superfamily: PYP-like sensor domain (PAS domain) Family: PYP-like
94	d1mzua_	Alignment	not modelled	99.0	13	Fold: Profilin-like Superfamily: PYP-like sensor domain (PAS domain) Family: PYP-like
95	d1lv7a_	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
96	c3a0rA_	Alignment	not modelled	99.0	12	PDB header: transferase Chain: A: PDB Molecule: sensor protein; PDBTitle: crystal structure of histidine kinase thka (tm1359) in complex with2 response regulator protein trra (tm1360)
97	d1y28a_	Alignment	not modelled	99.0	12	Fold: Profilin-like Superfamily: PYP-like sensor domain (PAS domain) Family: Heme-binding PAS domain
98	c1xxbB_	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
99	d1r6bx2	Alignment	not modelled	98.9	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
100	c2chvE_	Alignment	not modelled	98.9	17	PDB header: dna-binding protein Chain: E: PDB Molecule: replication factor c small subunit; PDBTitle: replication factor c adpnp complex
101	c1sxC_	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)
102	c2x1vA_	Alignment	not modelled	98.9	17	PDB header: replication Chain: A: PDB Molecule: cell division control protein 6 homolog;

102	c2v1uA	Alignment	not modelled	98.9	17	PDBTitle: structure of the aeropyrum pernix orc1 protein in complex2 with dna PDB header: nuclear protein
103	c2x8aA	Alignment	not modelled	98.9	14	Chain: A: PDB Molecule: nuclear valosin-containing protein-like; PDBTitle: human nuclear valosin containing protein like (nvl), c-2 terminal aaa-atpase domain
104	c2qbyA	Alignment	not modelled	98.9	13	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	c1sxiB	Alignment	not modelled	98.9	19	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)
106	c3k3dA	Alignment	not modelled	98.9	9	PDB header: signaling protein Chain: A: PDB Molecule: protein rv1364c/mt1410; PDBTitle: the n-terminal pas domain crystal structure of rv1364c from2 mycobacterium tuberculosis at 2.3 angstrom
107	c1sxiB	Alignment	not modelled	98.9	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)
108	c3fc7B	Alignment	not modelled	98.9	14	PDB header: transferase Chain: B: PDB Molecule: htr-like protein; PDBTitle: the crystal structure of a domain of htr-like protein from haloarcula2 marismortui atcc 43049
109	d1xj3a1	Alignment	not modelled	98.9	13	Fold: Profilin-like Superfamily: PYP-like sensor domain (PAS domain) Family: Heme-binding PAS domain
110	c2l4rA	Alignment	not modelled	98.9	12	PDB header: transport protein Chain: A: PDB Molecule: potassium voltage-gated channel subfamily h member 2; PDBTitle: nmr solution structure of the n-terminal pas domain of herg
111	c2qkpD	Alignment	not modelled	98.9	9	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of c-terminal domain of smu_1151c from streptococcus2 mutans
112	c3kx0X	Alignment	not modelled	98.9	15	PDB header: signaling protein Chain: X: PDB Molecule: uncharacterized protein rv1364c/mt1410; PDBTitle: crystal structure of the pas domain of rv1364c
113	c2qbyB	Alignment	not modelled	98.9	19	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)
114	c2qz4A	Alignment	not modelled	98.9	17	PDB header: hydrolase Chain: A: PDB Molecule: paraplegin; PDBTitle: human paraplegin, aaa domain in complex with adp
115	c2vlgD	Alignment	not modelled	98.9	3	PDB header: transferase Chain: D: PDB Molecule: sporulation kinase a; PDBTitle: kina pas-a domain, homodimer
116	d1n9la	Alignment	not modelled	98.9	13	Fold: Profilin-like Superfamily: PYP-like sensor domain (PAS domain) Family: Flavin-binding PAS domain
117	d1sxiA2	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
118	c1sxiD	Alignment	not modelled	98.8	14	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)
119	d1bywa	Alignment	not modelled	98.8	12	Fold: Profilin-like Superfamily: PYP-like sensor domain (PAS domain) Family: Flavin-binding PAS domain
120	c1s3sA	Alignment	not modelled	98.8	18	PDB header: protein binding Chain: A: PDB Molecule: transitional endoplasmic reticulum atpase (ter PDBTitle: crystal structure of aaa atpase p97/vcp nd1 in complex with2 p47 c