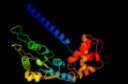
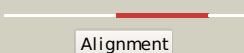
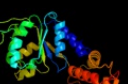
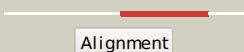
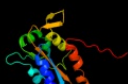


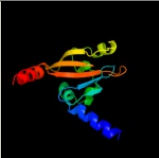
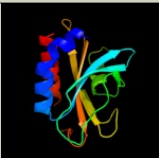
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1ny5A_	 Alignment		100.0	29	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigm54 activator (aaa+ atpase) in the inactive2 state
2	c3dzdA_	 Alignment		100.0	27	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	27	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	33	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
5	c1ojlF_	 Alignment		100.0	32	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	22	PDB header: transcription regulator Chain: B: PDB Molecule: putative two-component system transcriptional response PDBTitle: crystal structure of sigma-54 interaction domain of putative2 transcriptional response regulator from neisseria gonorrhoeae
7	c3pfiB_	 Alignment		99.9	14	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	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
9	c1qvrB_	 Alignment		99.9	21	PDB header: chaperone Chain: B: PDB Molecule: clpb protein; PDBTitle: crystal structure analysis of clpb
10	d1um8a_	 Alignment		99.8	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
11	c1r6bX_	 Alignment		99.8	18	PDB header: hydrolase Chain: X: PDB Molecule: clpa protein; PDBTitle: high resolution crystal structure of clpa

12	clin8A_	Alignment		99.8	17	PDB header: dna binding protein Chain: A: PDB Molecule: holliday junction dna helicase ruvb; PDBTitle: thermotoga maritima ruvb t158v
13	d1qvra3	Alignment		99.8	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
14	c3pxiB_	Alignment		99.8	17	PDB header: protein binding Chain: B: PDB Molecule: negative regulator of genetic competence clpc/mecb; PDBTitle: structure of meca108:clpc
15	c3kljA_	Alignment		99.8	20	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent protease lon; PDBTitle: crystal structure of lon protease from thermococcus onnurineus na1
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	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
18	c3f8tA_	Alignment		99.8	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
19	d1l8qa2	Alignment		99.8	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
20	d1g8pa_	Alignment		99.7	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
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	c1hqcb_	Alignment	not modelled	99.7	14	PDB header: hydrolase Chain: B: PDB Molecule: ruvb; PDBTitle: structure of ruvb from thermus thermophilus hb8
23	c2r44A_	Alignment	not modelled	99.7	10	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
24	c2hcbC_	Alignment	not modelled	99.7	16	PDB header: replication Chain: C: PDB Molecule: chromosomal replication initiator protein dnaa; PDBTitle: structure of amppcp-bound dnaa from aquifex aeolicus
25	c3hteC_	Alignment	not modelled	99.7	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	c2z4rB_	Alignment	not modelled	99.7	13	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	d1ntca_	Alignment		99.6	30	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
28	c1nsfA_	Alignment	not modelled	99.6	21	PDB header: protein transport Chain: A: PDB Molecule: n-ethylmaleimide sensitive factor; PDBTitle: d2 hexamerization domain of n-ethylmaleimide sensitive factor (nsf)
29	c2c9oC_	Alignment	not modelled	99.6	13	PDB header: hydrolase Chain: C: PDB Molecule: ruvb-like 1; PDBTitle: 3d structure of the human ruvb-like helicase ruvbl1
30	d1g41a_	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
31	d1fnna2_	Alignment	not modelled	99.6	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
32	d1ofha_	Alignment	not modelled	99.6	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
33	d1ixsb2_	Alignment	not modelled	99.6	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
34	d1in4a2_	Alignment	not modelled	99.6	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
35	c3f9vA_	Alignment	not modelled	99.6	15	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
36	d1sxd2_	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	c2chgB_	Alignment	not modelled	99.5	17	PDB header: dna-binding protein Chain: B: PDB Molecule: replication factor c small subunit; PDBTitle: replication factor c domains 1 and 2
38	c2dhrC_	Alignment	not modelled	99.5	21	PDB header: hydrolase Chain: C: PDB Molecule: ftsh; PDBTitle: whole cytosolic region of atp-dependent metalloprotease2 ftsh (g399l)
39	d1etob_	Alignment	not modelled	99.5	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
40	d1fipa_	Alignment	not modelled	99.5	26	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
41	d1etxa_	Alignment	not modelled	99.5	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
42	d1iqpa2_	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
43	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
44	d1njfa_	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
45	d1umqa_	Alignment	not modelled	99.4	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
46	c1umqA_	Alignment	not modelled	99.4	19	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
47	c2ce7B_	Alignment	not modelled	99.4	17	PDB header: cell division protein Chain: B: PDB Molecule: cell division protein ftsh; PDBTitle: edta treated
48	c3eihB_	Alignment	not modelled	99.4	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
49	c1xxhB_	Alignment	not modelled	99.3	17	PDB header: transferase Chain: B: PDB Molecule: dna polymerase iii subunit gamma; PDBTitle: atpgs bound e. coli clamp loader complex
50	c2kjqA_	Alignment	not modelled	99.3	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. Fold: P-loop containing nucleoside triphosphate hydrolases

51	d1sxjc2	Alignment	not modelled	99.3	16	Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
52	d1sxb2	Alignment	not modelled	99.3	11	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
53	c3e7ID	Alignment	not modelled	99.3	21	PDB header: transcription regulator Chain: D: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigma54 activator ntrc4's dna binding2 domain
54	c3b9pA	Alignment	not modelled	99.3	18	PDB header: hydrolase Chain: A: PDB Molecule: cg5977-pa, isoform a; PDBTitle: spastin
55	c1xwiA	Alignment	not modelled	99.3	13	PDB header: protein transport Chain: A: PDB Molecule: skd1 protein; PDBTitle: crystal structure of vps4b
56	d1g2ha	Alignment	not modelled	99.3	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
57	c2r65A	Alignment	not modelled	99.2	20	PDB header: hydrolase Chain: A: PDB Molecule: cell division protease ftsh homolog; PDBTitle: crystal structure of helicobacter pylori atp dependent protease, ftsh2 adp complex
58	c3cf1C	Alignment	not modelled	99.2	20	PDB header: transport protein Chain: C: PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: structure of p97/vcp in complex with adp/adp.alfx
59	c3hu2C	Alignment	not modelled	99.2	17	PDB header: transport protein Chain: C: PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: structure of p97 n-d1 r86a mutant in complex with atpgs
60	c1fnnB	Alignment	not modelled	99.2	15	PDB header: cell cycle Chain: B: PDB Molecule: cell division control protein 6; PDBTitle: crystal structure of cdc6p from pyrobaculum aerophilum
61	c3u5zM	Alignment	not modelled	99.2	10	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
62	d1w5sa2	Alignment	not modelled	99.2	12	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
63	c1sxD	Alignment	not modelled	99.2	13	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)
64	d1sxja2	Alignment	not modelled	99.2	11	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
65	c1sxjB	Alignment	not modelled	99.2	13	PDB header: replication Chain: B: PDB Molecule: activator 1 37 kda subunit; PDBTitle: crystal structure of the eukaryotic clamp loader2 (replication factor c, rfc) bound to the dna sliding clamp3 (proliferating cell nuclear antigen, pcna)
66	c3h4mC	Alignment	not modelled	99.2	17	PDB header: hydrolase Chain: C: PDB Molecule: proteasome-activating nucleotidase; PDBTitle: aaa atpase domain of the proteasome- activating nucleotidase
67	c1sxjC	Alignment	not modelled	99.2	15	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)
68	d1qvra2	Alignment	not modelled	99.2	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
69	c2chvE	Alignment	not modelled	99.2	16	PDB header: dna-binding protein Chain: E: PDB Molecule: replication factor c small subunit; PDBTitle: replication factor c adpnp complex
70	c3d8bB	Alignment	not modelled	99.2	13	PDB header: hydrolase Chain: B: PDB Molecule: fidgetin-like protein 1; PDBTitle: crystal structure of human fidgetin-like protein 1 in complex with adp
71	c1sxjA	Alignment	not modelled	99.1	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)
72	c2qbyB	Alignment	not modelled	99.1	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)
73	d1r6bx2	Alignment	not modelled	99.1	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
74	c2qbyA	Alignment	not modelled	99.1	10	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	c2v1uA	Alignment	not modelled	99.1	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
						PDB header: protein transport

76	c2zamA	Alignment	not modelled	99.1	14	Chain: A: PDB Molecule: vacuolar protein sorting-associating protein 4b; PDBTitle: crystal structure of mouse skd1/vps4b apo-form
77	c1iqpF	Alignment	not modelled	99.1	16	PDB header: replication Chain: F: PDB Molecule: rfcs; PDBTitle: crystal structure of the clamp loader small subunit from2 pyrococcus furiosus
78	d2ce7a2	Alignment	not modelled	99.1	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
79	c2p65A	Alignment	not modelled	99.1	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein pf08_0063; PDBTitle: crystal structure of the first nucleotide binding domain of2 chaperone clpb1, putative, (pv089580) from plasmodium vivax
80	c1iy2A	Alignment	not modelled	99.1	27	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent metalloprotease ftsh; PDBTitle: crystal structure of the ftsh atpase domain from thermus2 thermophilus
81	d1sxje2	Alignment	not modelled	99.0	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
82	d1ixza	Alignment	not modelled	99.0	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
83	c1sxjE	Alignment	not modelled	99.0	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)
84	d1lv7a	Alignment	not modelled	99.0	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
85	c2qz4A	Alignment	not modelled	99.0	19	PDB header: hydrolase Chain: A: PDB Molecule: paraplegin; PDBTitle: human paraplegin, aaa domain in complex with adp
86	c2x8aA	Alignment	not modelled	99.0	15	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
87	c1s3sA	Alignment	not modelled	99.0	19	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
88	d1e32a2	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
89	c2wkqA	Alignment		98.9	13	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
90	d1jbka	Alignment	not modelled	98.8	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
91	c1jr3E	Alignment	not modelled	98.8	18	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
92	c3b33A	Alignment		98.7	14	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
93	d1r7ra3	Alignment	not modelled	98.7	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
94	c1w5sB	Alignment	not modelled	98.7	12	PDB header: replication Chain: B: PDB Molecule: origin recognition complex subunit 2 orc2; PDBTitle: structure of the aeropyrum pernix orc2 protein (adp form)
95	d1e94e	Alignment	not modelled	98.7	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
96	c3ec2A	Alignment	not modelled	98.6	16	PDB header: replication Chain: A: PDB Molecule: dna replication protein dnac; PDBTitle: crystal structure of the dnac helicase loader
97	c3pxgA	Alignment	not modelled	98.6	21	PDB header: protein binding Chain: A: PDB Molecule: negative regulator of genetic competence clpc/mecb; PDBTitle: structure of meca121 and clpc1-485 complex
98	c3te6A	Alignment	not modelled	98.5	11	PDB header: gene regulation Chain: A: PDB Molecule: regulatory protein sir3; PDBTitle: crystal structure of the s. cerevisiae sir3 aaa+ domain
99	d2gnoa2	Alignment	not modelled	98.5	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases

					Family: Extended AAA-ATPase domain
100	c2w58B_	Alignment	not modelled	98.5	17 PDB header: hydrolase Chain: B: PDB Molecule: primosome component (helicase loader); PDBTitle: crystal structure of the dnaI
101	c2qgzA_	Alignment	not modelled	98.4	15 PDB header: hydrolase Chain: A: PDB Molecule: putative primosome component; PDBTitle: crystal structure of a putative primosome component from <i>Streptococcus pyogenes</i> serotype M3. Northeast structural genomics target dr58
102	c2jheB_	Alignment		98.4	14 PDB header: transcription Chain: B: PDB Molecule: transcription regulator tyrr; PDBTitle: n-terminal domain of tyrr transcription factor (residues 1-2190)
103	d1a5ta2	Alignment	not modelled	98.4	15 Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
104	c3oloB_	Alignment		98.3	7 PDB header: transferase Chain: B: PDB Molecule: two-component sensor histidine kinase; PDBTitle: crystal structure of a pas domain from two-component sensor histidine kinase
105	c1v9yA_	Alignment		98.3	14 PDB header: signaling protein Chain: A: PDB Molecule: heme pas sensor protein; PDBTitle: crystal structure of the heme pas sensor domain of EcDds (ferric form)
106	d1v9ya_	Alignment		98.3	14 Fold: Profilin-like Superfamily: PYP-like sensor domain (PAS domain) Family: Heme-binding PAS domain
107	c3mfxA_	Alignment	not modelled	98.3	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 <i>Shewanella oneidensis</i> , 3 northeast structural genomics consortium target sor288b
108	d1nwza_	Alignment	not modelled	98.2	15 Fold: Profilin-like Superfamily: PYP-like sensor domain (PAS domain) Family: PYP-like
109	d1oz4a3	Alignment	not modelled	98.2	23 Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
110	c2pr6A_	Alignment	not modelled	98.2	11 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)
111	c3n70F_	Alignment	not modelled	98.1	26 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 <i>E. coli</i> to 2.8 Å
112	d1mzua_	Alignment	not modelled	98.1	13 Fold: Profilin-like Superfamily: PYP-like sensor domain (PAS domain) Family: PYP-like
113	d1lotda_	Alignment	not modelled	98.1	14 Fold: Profilin-like Superfamily: PYP-like sensor domain (PAS domain) Family: PYP-like
114	c3m6aC_	Alignment	not modelled	98.1	12 PDB header: hydrolase Chain: C: PDB Molecule: atp-dependent protease Iα1; PDBTitle: crystal structure of <i>Bacillus subtilis</i> lon c-terminal domain
115	c3mjgB_	Alignment	not modelled	98.1	10 PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the pas domain of q24qt8_deshy protein from <i>Desulfitobacterium hafniense</i> . Northeast structural genomics3 consortium target dhr85c.
116	c3r4kD_	Alignment		98.1	21 PDB header: dna binding protein Chain: D: PDB Molecule: transcriptional regulator, IclR family; PDBTitle: crystal structure of a putative IclR transcriptional regulator2 (tm1040_3717) from <i>Silicibacter</i> sp. tm1040 at 2.46 Å resolution
117	c3lyxA_	Alignment	not modelled	98.0	11 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 <i>Colwellia psychrerythraea</i> . Northeast structural genomics consortium target id_csr222b
118	d1tf1a_	Alignment		98.0	14 Fold: Profilin-like Superfamily: GAF domain-like Family: IclR ligand-binding domain-like

119	c3bwlA_	Alignment	not modelled	98.0	15	PDB header: transferase Chain: A: PDB Molecule: sensor protein; PDBTitle: crystal structure of pas domain of htr-like protein from haloarcula2 marismortui
120	c3a0vA_	Alignment	not modelled	98.0	13	PDB header: transferase Chain: A: PDB Molecule: sensor protein; PDBTitle: pas domain of histidine kinase thka (tm1359) (semet,2 f486m/f489m)