







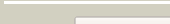



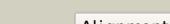

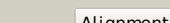






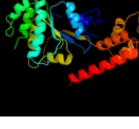


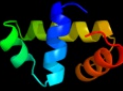








#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3iytG_	 Alignment		99.9	13	PDB header: apoptosis Chain: G: PDB Molecule: apoptotic protease-activating factor 1; PDBTitle: structure of an apoptosome-procaspase-9 card complex
2	c1z6tC_	 Alignment		99.9	14	PDB header: apoptosis Chain: C: PDB Molecule: apoptotic protease activating factor 1; PDBTitle: structure of the apoptotic protease-activating factor 12 bound to adp
3	c2q0oA_	 Alignment		99.9	19	PDB header: transcription Chain: A: PDB Molecule: probable transcriptional activator protein trar; PDBTitle: crystal structure of an anti-activation complex in bacterial quorum2 sensing
4	c3sztB_	 Alignment		99.9	25	PDB header: transcription Chain: B: PDB Molecule: quorum-sensing control repressor; PDBTitle: quorum sensing control repressor, qscr, bound to n-3-oxo-dodecanoyl-l-2 homoserine lactone
5	c1h0mD_	 Alignment		99.9	17	PDB header: transcription/dna Chain: D: PDB Molecule: transcriptional activator protein trar; PDBTitle: three-dimensional structure of the quorum sensing protein2 trar bound to its autoinducer and to its target dna
6	d1hz4a_	 Alignment		99.9	100	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Transcription factor MalT domain III
7	c3qp5C_	 Alignment		99.9	29	PDB header: transcription Chain: C: PDB Molecule: cvir transcriptional regulator; PDBTitle: crystal structure of cvir bound to antagonist chlorolactone (cl)
8	c2a5yB_	 Alignment		99.8	13	PDB header: apoptosis Chain: B: PDB Molecule: ced-4; PDBTitle: structure of a ced-4/ced-9 complex
9	c2fnaA_	 Alignment		99.8	11	PDB header: atp-binding protein Chain: A: PDB Molecule: conserved hypothetical protein; PDBTitle: crystal structure of an archaeal aaa+ atpase (sso1545) from sulfobolbus2 solfataricus p2 at 2.00 a resolution
10	c2qenA_	 Alignment		99.8	13	PDB header: unknown function Chain: A: PDB Molecule: walker-type atpase; PDBTitle: the walker-type atpase paby2304 of pyrococcus abyssi
11	d2fnaa2	 Alignment		99.8	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain

12	c1zljE_	Alignment		99.8	35	PDB header: transcription Chain: E: PDB Molecule: dormancy survival regulator; PDBTitle: crystal structure of the mycobacterium tuberculosis hypoxic2 response regulator dosr c-terminal domain
13	c3c3wB_	Alignment		99.8	36	PDB header: transcription Chain: B: PDB Molecule: two component transcriptional regulatory protein devr; PDBTitle: crystal structure of the mycobacterium tuberculosis hypoxic response2 regulator dosr
14	c3cloC_	Alignment		99.8	30	PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of putative transcriptional regulator containing a2 luxr dna binding domain (np_811094.1) from bacteroides3 thetaiotaomicron vpi-5482 at 2.04 a resolution
15	c2krfB_	Alignment		99.8	26	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulatory protein coma; PDBTitle: nmr solution structure of the dna binding domain of competence protein2 a
16	c3klnC_	Alignment		99.8	26	PDB header: transcription Chain: C: PDB Molecule: transcriptional regulator, luxr family; PDBTitle: vibrio cholerae vpst
17	d1p4wa_	Alignment		99.8	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators)
18	d1l3la1	Alignment		99.8	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators)
19	d1fsea_	Alignment		99.7	34	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators)
20	c1rn1A_	Alignment		99.7	32	PDB header: signal transduction protein Chain: A: PDB Molecule: nitrate/nitrite response regulator protein narl; PDBTitle: the nitrate/nitrite response regulator protein narl from narl
21	c2rnjA_	Alignment	not modelled	99.7	40	PDB header: transcription Chain: A: PDB Molecule: response regulator protein vvar; PDBTitle: nmr structure of the s. aureus vvar dna binding domain
22	d1a04a1	Alignment	not modelled	99.7	30	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators)
23	c1zn2A_	Alignment	not modelled	99.7	45	PDB header: transcription regulator Chain: A: PDB Molecule: response regulatory protein; PDBTitle: low resolution structure of response regulator styr
24	c1x3uA_	Alignment	not modelled	99.7	28	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulatory protein fixj; PDBTitle: solution structure of the c-terminal transcriptional2 activator domain of fixj from sinorhizobium melilot
25	c2jpcA_	Alignment	not modelled	99.7	34	PDB header: dna binding protein Chain: A: PDB Molecule: ssrb; PDBTitle: ssrb dna binding protein
26	c1fnbB_	Alignment	not modelled	99.7	17	PDB header: cell cycle Chain: B: PDB Molecule: cell division control protein 6; PDBTitle: crystal structure of cdc6p from pyrobaculum aerophilum
27	c2qbyB_	Alignment	not modelled	99.7	10	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)
28	d1yioa1	Alignment	not modelled	99.7	45	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators)
						PDB header: replication

29	c2v1uA	Alignment	not modelled	99.7	18	Chain: A: PDB Molecule: cell division control protein 6 homolog; PDBTitle: structure of the aeropyrum pernix orc1 protein in complex2 with dna
30	c2qbyA	Alignment	not modelled	99.6	12	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)
31	d1fnna2	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
32	c1w5sB	Alignment	not modelled	99.4	15	PDB header: replication Chain: B: PDB Molecule: origin recognition complex subunit 2 orc2; PDBTitle: structure of the aeropyrum pernix orc2 protein (adp form)
33	c1in8A	Alignment	not modelled	99.3	22	PDB header: dna binding protein Chain: A: PDB Molecule: holliday junction dna helicase ruvb; PDBTitle: thermotoga maritima ruvb t158v
34	c2chgB	Alignment	not modelled	99.2	12	PDB header: dna-binding protein Chain: B: PDB Molecule: replication factor c small subunit; PDBTitle: replication factor c domains 1 and 2
35	c3pvsA	Alignment	not modelled	99.1	16	PDB header: recombination Chain: A: PDB Molecule: replication-associated recombination protein a; PDBTitle: structure and biochemical activities of escherichia coli mgsa
36	c1sxC	Alignment	not modelled	99.1	18	PDB header: replication Chain: C: PDB Molecule: activator 1 40 kda subunit; PDBTitle: crystal structure of the eukaryotic clamp loader2 (replication factor c, rfc) bound to the dna sliding clamp3 (proliferating cell nuclear antigen, pcna)
37	c3pfiB	Alignment	not modelled	99.1	18	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
38	c2chvE	Alignment	not modelled	99.1	13	PDB header: dna-binding protein Chain: E: PDB Molecule: replication factor c small subunit; PDBTitle: replication factor c adnpn complex
39	d1w5sa2	Alignment	not modelled	99.1	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
40	d1sxd2	Alignment	not modelled	99.0	12	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
41	d1in4a2	Alignment	not modelled	99.0	26	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
42	c3te6A	Alignment	not modelled	99.0	12	PDB header: gene regulation Chain: A: PDB Molecule: regulatory protein sir3; PDBTitle: crystal structure of the s. cerevisiae sir3 aaa+ domain
43	d1iqpa2	Alignment	not modelled	99.0	12	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
44	c1iqpF	Alignment	not modelled	99.0	14	PDB header: replication Chain: F: PDB Molecule: rfcs; PDBTitle: crystal structure of the clamp loader small subunit from2 pyrococcus furiosus
45	d1sxc2	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
46	d1sxb2	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
47	d1r6bx2	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
48	c1hqCB	Alignment	not modelled	98.9	22	PDB header: hydrolase Chain: B: PDB Molecule: ruvb; PDBTitle: structure of ruvb from thermus thermophilus hb8
49	c1sxB	Alignment	not modelled	98.9	18	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)
50	c3u5zM	Alignment	not modelled	98.9	11	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
51	d1njfa	Alignment	not modelled	98.9	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
52	c1xwiA	Alignment	not modelled	98.9	16	PDB header: protein transport Chain: A: PDB Molecule: skd1 protein; PDBTitle: crystal structure of vps4b
53	c2ce7B	Alignment	not modelled	98.9	17	PDB header: cell division protein Chain: B: PDB Molecule: cell division protein ftsH; PDBTitle: edta treated

54	dlsxja2	Alignment	not modelled	98.9	12	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
55	clsxjA	Alignment	not modelled	98.9	13	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)
56	dla5ta2	Alignment	not modelled	98.9	10	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
57	c3d8bB	Alignment	not modelled	98.9	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
58	clsxjD	Alignment	not modelled	98.9	12	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	clxxbB	Alignment	not modelled	98.9	14	PDB header: transferase Chain: B: PDB Molecule: dna polymerase iii subunit gamma; PDBTitle: atpgs bound e. coli clamp loader complex
60	clsxjE	Alignment	not modelled	98.9	13	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)
61	dlsxje2	Alignment	not modelled	98.9	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
62	dlqvra2	Alignment	not modelled	98.9	12	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
63	dlixsb2	Alignment	not modelled	98.9	23	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
64	c3b9pA	Alignment	not modelled	98.8	18	PDB header: hydrolase Chain: A: PDB Molecule: cg5977-pa, isoform a; PDBTitle: spastin
65	c3bosA	Alignment	not modelled	98.8	13	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
66	c2zamA	Alignment	not modelled	98.8	18	PDB header: protein transport Chain: A: PDB Molecule: vacuolar protein sorting-associating protein 4b; PDBTitle: crystal structure of mouse skd1/vps4b apo-form
67	clr6bX	Alignment	not modelled	98.8	12	PDB header: hydrolase Chain: X: PDB Molecule: clpa protein; PDBTitle: high resolution crystal structure of clpa
68	c2dhrC	Alignment	not modelled	98.7	16	PDB header: hydrolase Chain: C: PDB Molecule: ftsh; PDBTitle: whole cytosolic region of atp-dependent metalloprotease2 ftsh (g399l)
69	clkgsA	Alignment	not modelled	98.7	21	PDB header: dna binding protein Chain: A: PDB Molecule: dna binding response regulator d; PDBTitle: crystal structure at 1.50 a of an ompr/phob homolog from thermotoga2 maritima
70	dljbka	Alignment	not modelled	98.7	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
71	c2z4rB	Alignment	not modelled	98.7	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
72	c3hu2C	Alignment	not modelled	98.7	15	PDB header: transport protein Chain: C: PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: structure of p97 n-d1 r86a mutant in complex with atpgs
73	dlixza	Alignment	not modelled	98.6	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
74	c3h4mC	Alignment	not modelled	98.6	17	PDB header: hydrolase Chain: C: PDB Molecule: proteasome-activating nucleotidase; PDBTitle: aaa atpase domain of the proteasome- activating nucleotidase
75	cljr3E	Alignment	not modelled	98.6	11	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
76	d2ce7a2	Alignment	not modelled	98.6	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
77	cliy2A	Alignment	not modelled	98.6	16	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent metalloprotease ftsh; PDBTitle: crystal structure of the ftsh atpase domain from thermus2 thermophilus
78	c2qz4A	Alignment	not modelled	98.5	17	PDB header: hydrolase Chain: A: PDB Molecule: paraplegin; PDBTitle: human paraplegin, aaa domain in complex with adp

79	c1qvrB	Alignment	not modelled	98.5	25	PDB header: chaperone Chain: B: PDB Molecule: clpb protein; PDBTitle: crystal structure analysis of clpb
80	d1r7ra3	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
81	c2p65A	Alignment	not modelled	98.5	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein pf08_0063; PDBTitle: crystal structure of the first nucleotide binding domain of 2 chaperone clpb1, putative, (pv089580) from plasmodium vivax
82	c3pxgA	Alignment	not modelled	98.5	12	PDB header: protein binding Chain: A: PDB Molecule: negative regulator of genetic competence clpc/mecc; PDBTitle: structure of meca121 and clpc1-485 complex
83	c2c9oC	Alignment	not modelled	98.5	11	PDB header: hydrolase Chain: C: PDB Molecule: ruvb-like 1; PDBTitle: 3d structure of the human ruvb-like helicase ruvb1
84	c3eihB	Alignment	not modelled	98.5	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
85	d1l8qa2	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
86	c2r65A	Alignment	not modelled	98.5	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
87	c3cf1C	Alignment	not modelled	98.4	15	PDB header: transport protein Chain: C: PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: structure of p97/vcp in complex with adp/adp.alfx
88	d1tlya	Alignment	not modelled	98.4	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
89	c2kjqA	Alignment	not modelled	98.4	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.
90	c3q9sA	Alignment	not modelled	98.4	28	PDB header: dna binding protein Chain: A: PDB Molecule: dna-binding response regulator; PDBTitle: crystal structure of rra(1-215) from deinococcus radiodurans
91	d1e32a2	Alignment	not modelled	98.4	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
92	c1s3sA	Alignment	not modelled	98.4	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
93	c3gw4B	Alignment	not modelled	98.4	17	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterized protein from deinococcus2 radiodurans. northeast structural genomics consortium target drr162b.
94	d1smyf2	Alignment	not modelled	98.3	27	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
95	d2p7vb1	Alignment	not modelled	98.3	27	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
96	d1r6bx3	Alignment	not modelled	98.3	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
97	c3nbxX	Alignment	not modelled	98.2	14	PDB header: hydrolase Chain: X: PDB Molecule: atpase rava; PDBTitle: crystal structure of e. coli rava (regulatory atpase variant a) in2 complex with adp
98	d1rp3a2	Alignment	not modelled	98.2	27	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
99	c3hteC	Alignment	not modelled	98.2	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
100	c2x8aA	Alignment	not modelled	98.2	13	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
101	c3hugA	Alignment	not modelled	98.2	30	PDB header: transcription/membrane protein Chain: A: PDB Molecule: rna polymerase sigma factor; PDBTitle: crystal structure of mycobacterium tuberculosis anti-sigma factor rsla2 in complex with -35 promoter binding domain of sigl
102	d1or7a1	Alignment	not modelled	98.2	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
103	c3o8vA	Alignment	not modelled	98.1	22	PDB header: transcription Chain: A: PDB Molecule: probable rna polymerase sigma-c factor;

103	c206aA	Alignment	not modelled	98.1	42	PDBTitle: crystal structure of the "-35 element" promoter recognition domain of2 mycobacterium tuberculosis sigc
104	c1ny5A	Alignment	not modelled	98.1	13	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigm54 activator (aaa+ atpase) in the inactive2 state
105	d1xsva	Alignment	not modelled	98.1	26	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: YlxM/p13-like
106	d1ku7a	Alignment	not modelled	98.1	26	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
107	d1d2na	Alignment	not modelled	98.1	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
108	c2hcbC	Alignment	not modelled	98.1	11	PDB header: replication Chain: C: PDB Molecule: chromosomal replication initiator protein dnaa; PDBTitle: structure of amppcp-bound dnaa from aquifex aeolicus
109	d1ny5a2	Alignment	not modelled	98.1	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
110	d1lv7a	Alignment	not modelled	98.1	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
111	c3ulqA	Alignment	not modelled	98.1	9	PDB header: gene regulation/transcription activator Chain: A: PDB Molecule: response regulator aspartate phosphatase f; PDBTitle: crystal structure of the anti-activator rapf complexed with the2 response regulator coma dna binding domain
112	c2ifuA	Alignment	not modelled	98.0	8	PDB header: endocytosis/exocytosis Chain: A: PDB Molecule: gamma-snap; PDBTitle: crystal structure of a gamma-snap from danio rerio
113	c1nsfA	Alignment	not modelled	98.0	15	PDB header: protein transport Chain: A: PDB Molecule: n-ethylmaleimide sensitive factor; PDBTitle: d2 hexamerization domain of n-ethylmaleimide sensitive factor (nsf)
114	d1g41a	Alignment	not modelled	98.0	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
115	d1ku3a	Alignment	not modelled	98.0	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
116	c1rp3G	Alignment	not modelled	98.0	26	PDB header: transcription Chain: G: PDB Molecule: rna polymerase sigma factor sigma-28 (flia); PDBTitle: cocrystal structure of the flagellar sigma/anti-sigma2 complex, sigma-28/flgm
117	c3mzyA	Alignment	not modelled	98.0	28	PDB header: rna binding protein Chain: A: PDB Molecule: rna polymerase sigma-h factor; PDBTitle: the crystal structure of the rna polymerase sigma-h factor from2 fusobacterium nucleatum to 2.5a
118	c3sf4B	Alignment	not modelled	98.0	11	PDB header: signaling protein/protein binding Chain: B: PDB Molecule: g-protein-signaling modulator 2; PDBTitle: crystal structure of the complex between the conserved cell polarity2 proteins inscuteable and lgn
119	c1ojlf	Alignment	not modelled	97.9	15	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
120	d1s7oa	Alignment	not modelled	97.9	26	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: YlxM/p13-like