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Description	P0AFP2
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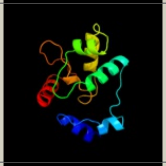
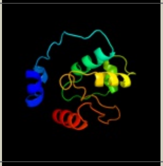
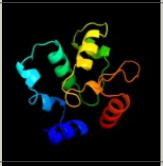
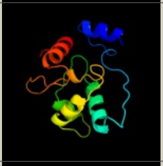
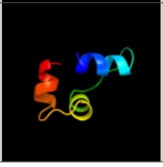
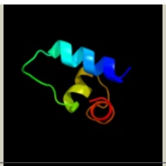
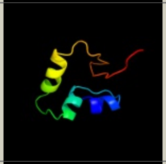
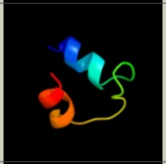
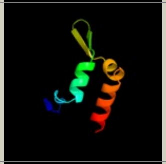
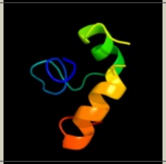
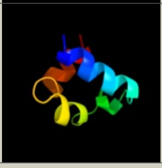
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2kimA_	Alignment		100.0	52	**PDB header:**transferase **Chain:** A: **PDB Molecule:**o6-methylguanine-dna methyltransferase; **PDBTitle:** 1.7-mm microcryoprobe solution nmr structure of an o6-2 methylguanine dna methyltransferase family protein from3 vibrio parahaemolyticus. northeast structural genomics4 consortium target vpr247.
2	c3gx4X_	Alignment		100.0	42	**PDB header:**dna binding protein/dna **Chain:** X: **PDB Molecule:**alkyltransferase-like protein 1; **PDBTitle:** crystal structure analysis of s. pombe atl in complex with dna
3	c1sfeA_	Alignment		100.0	27	**PDB header:**dna-binding protein **Chain:** A: **PDB Molecule:**ada o6-methylguanine-dna methyltransferase; **PDBTitle:** ada o6-methylguanine-dna methyltransferase from escherichia coli
4	c1t39A_	Alignment		100.0	26	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**methylated-dna--protein-cysteine **PDBTitle:** human o6-alkylguanine-dna alkyltransferase covalently2 crosslinked to dna
5	c1mgtA_	Alignment		100.0	28	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein (o6-methylguanine-dna methyltransferase); **PDBTitle:** crystal structure of o6-methylguanine-dna methyltransferase from2 hyperthermophilic archaeon pyrococcus kodakaraensis strain kod1
6	c1wrjA_	Alignment		100.0	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methylated-dna--protein-cysteine **PDBTitle:** crystal structure of o6-methylguanine methyltransferase2 from sulfolobus tokodaii
7	d1qnta1	Alignment		100.0	33	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Methylated DNA-protein cysteine methyltransferase, C-terminal domain **Family:**Methylated DNA-protein cysteine methyltransferase, C-terminal domain
8	d1sfea1	Alignment		100.0	31	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Methylated DNA-protein cysteine methyltransferase, C-terminal domain **Family:**Methylated DNA-protein cysteine methyltransferase, C-terminal domain
9	c2g7hA_	Alignment		100.0	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methylated-dna--protein-cysteine **PDBTitle:** structure of an o6-methylguanine dna methyltransferase from2 methanococcus jannaschii (mj1529)
10	d1mgta1	Alignment		100.0	35	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Methylated DNA-protein cysteine methyltransferase, C-terminal domain **Family:**Methylated DNA-protein cysteine methyltransferase, C-terminal domain
11	d2gxba1	Alignment		55.8	31	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Z-DNA binding domain

12	d1qgpa_	Alignment		53.4	28	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Z-DNA binding domain
13	d1qbjc_	Alignment		49.4	30	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Z-DNA binding domain
14	c2y9xC_	Alignment		40.3	17	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**polyphenol oxidase; **PDBTitle:** crystal structure of ppo3, a tyrosinase from agaricus bisporus, in2 deoxy-form that contains additional unknown lectin-like subunit,3 with inhibitor tropolone
15	d1s6la1	Alignment		36.7	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MerB N-terminal domain-like
16	d1cf7b_	Alignment		35.8	29	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Cell cycle transcription factor e2f-dp
17	c2l01A_	Alignment		32.6	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of protein bvu3908 from bacteroides vulgatus,2 northeast structural genomics consortium target bvr153
18	d1qb7a_	Alignment		30.1	16	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
19	c2l02B_	Alignment		26.3	17	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of protein bt2368 from bacteroides2 thetaiotaomicron, northeast structural genomics consortium target3 btr375
20	d2cyya1	Alignment		25.2	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
21	d1bw6a_	Alignment	not modelled	24.7	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Centromere-binding
22	c3chmA_	Alignment	not modelled	24.6	10	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**cop9 signalosome complex subunit 7; **PDBTitle:** crystal structure of pci domain from a. thaliana cop9 signalosome2 subunit 7 (csn7)
23	d1dpua_	Alignment	not modelled	22.2	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**C-terminal domain of RPA32
24	c1dpuA_	Alignment	not modelled	22.2	10	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**replication protein a (rpa32) c-terminal domain; **PDBTitle:** solution structure of the c-terminal domain of human rpa322 complexed with ung2(73-88)
25	c1i1gA_	Alignment	not modelled	21.2	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator lrpa; **PDBTitle:** crystal structure of the lrp-like transcriptional regulator from the2 archaeon pyrococcus furiosus
26	c1nh1A_	Alignment	not modelled	19.3	17	**PDB header:**avirulence protein **Chain:** A: **PDB Molecule:**avirulence b protein; **PDBTitle:** crystal structure of the type iii effector avrb from2 pseudomonas syringae.
27	d1nh1a_	Alignment	not modelled	19.3	17	**Fold:**Antivirulence factor **Superfamily:**Antivirulence factor **Family:**Antivirulence factor
28	c1js8A_	Alignment	not modelled	18.7	16	**PDB header:**oxygen storage/transport **Chain:** A: **PDB Molecule:**hemocyanin; **PDBTitle:** structure of a functional unit from octopus hemocyanin

29	c1x3uA_	Alignment	not modelled	18.4	19	**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
30	c2cfxD_	Alignment	not modelled	17.5	7	**PDB header:**transcription **Chain:** D: **PDB Molecule:**hth-type transcriptional regulator lrpc; **PDBTitle:** structure of b.subtilis lrpc
31	c2j6aA_	Alignment	not modelled	17.1	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein trm112; **PDBTitle:** crystal structure of s. cerevisiae ynr046w, a zinc finger2 protein from the erf1 methyltransferase complex.
32	d1or7a1	Alignment	not modelled	16.6	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
33	c2p3xA_	Alignment	not modelled	16.2	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**polyphenol oxidase, chloroplast; **PDBTitle:** crystal structure of grenache (vitis vinifera) polyphenol2 oxidase
34	d1g47a1	Alignment	not modelled	15.4	29	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
35	c3l6wB_	Alignment	not modelled	14.0	16	**PDB header:**oxygen binding **Chain:** B: **PDB Molecule:**hemocyanin 1; **PDBTitle:** structure of the collar functional unit (klh1-h) of keyhole2 limpet hemocyanin
36	d2hs5a1	Alignment	not modelled	13.8	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**GntR-like transcriptional regulators
37	c2xzm8_	Alignment	not modelled	13.4	13	**PDB header:**ribosome **Chain:** 8: **PDB Molecule:**rps25e,; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1
38	c2e1cA_	Alignment	not modelled	13.0	11	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**putative hth-type transcriptional regulator ph1519; **PDBTitle:** structure of putative hth-type transcriptional regulator ph1519/dna2 complex
39	c3k2zA_	Alignment	not modelled	12.9	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lexa repressor; **PDBTitle:** crystal structure of a lexa protein from thermotoga maritima
40	d1uxca_	Alignment	not modelled	12.5	16	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
41	d1mkma1	Alignment	not modelled	11.1	7	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Transcriptional regulator IclR, N-terminal domain
42	c2dbbA_	Alignment	not modelled	11.1	13	**PDB header:**transcriptional regulator **Chain:** A: **PDB Molecule:**putative hth-type transcriptional regulator ph0061; **PDBTitle:** crystal structure of ph0061
43	c3i4pA_	Alignment	not modelled	10.8	15	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, asnc family; **PDBTitle:** crystal structure of asnc family transcriptional regulator from2 agrobacterium tumefaciens
44	d1mzva_	Alignment	not modelled	10.4	19	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
45	c3r1fO_	Alignment	not modelled	10.2	14	**PDB header:**transcription **Chain:** O: **PDB Molecule:**esx-1 secretion-associated regulator espr; **PDBTitle:** crystal structure of a key regulator of virulence in mycobacterium2 tuberculosis
46	c2cg4B_	Alignment	not modelled	9.9	11	**PDB header:**transcription **Chain:** B: **PDB Molecule:**regulatory protein asnc; **PDBTitle:** structure of e.coli asnc
47	d1s7oa_	Alignment	not modelled	9.6	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**YlxM/p13-like
48	d1tnsa_	Alignment	not modelled	9.5	18	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**Excisionase-like
49	d1biaa1	Alignment	not modelled	9.3	8	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Biotin repressor-like
50	d1bt3a_	Alignment	not modelled	9.2	14	**Fold:**Di-copper centre-containing domain **Superfamily:**Di-copper centre-containing domain **Family:**Catechol oxidase
51	c1zx4B_	Alignment	not modelled	8.9	17	**PDB header:**translation **Chain:** B: **PDB Molecule:**plasmid partition par b protein; **PDBTitle:** structure of parb bound to dna
52	d2cfxa1	Alignment	not modelled	8.8	5	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
53	d1stza1	Alignment	not modelled	8.8	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Heat-inducible transcription repressor HrcA, N-terminal domain
54	d2cg4a1	Alignment	not modelled	8.5	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain

55	d1jhfa1	Alignment	not modelled	8.4	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**LexA repressor, N-terminal DNA-binding domain
56	d1j3ma_	Alignment	not modelled	8.4	33	**Fold:**TBP-like **Superfamily:**TT1751-like **Family:**TT1751-like
57	c2l4aA_	Alignment	not modelled	8.2	10	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**leucine responsive regulatory protein; **PDBTitle:** nmr structure of the dna-binding domain of e.coli lrp
58	d1lcda_	Alignment	not modelled	8.2	32	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
59	c2krfB_	Alignment	not modelled	7.9	19	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulatory protein coma; **PDBTitle:** nmr solution structure of the dna binding domain of competence protein2 a
60	d1xsva_	Alignment	not modelled	7.9	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**YlxM/p13-like
61	c2o8xA_	Alignment	not modelled	7.9	23	**PDB header:**transcription **Chain:** A: **PDB Molecule:**probable rna polymerase sigma-c factor; **PDBTitle:** crystal structure of the "-35 element" promoter recognition domain of2 mycobacterium tuberculosis sigc
62	c2ia0A_	Alignment	not modelled	7.8	8	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative hth-type transcriptional regulator pf0864; **PDBTitle:** transcriptional regulatory protein pf0864 from pyrococcus furiosus a2 member of the asnc family (pf0864)
63	d2hsga1	Alignment	not modelled	7.6	32	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
64	d1uxda_	Alignment	not modelled	7.3	16	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
65	d1hlva1	Alignment	not modelled	7.3	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Centromere-binding
66	c3fmsA_	Alignment	not modelled	7.2	13	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, gntr family; **PDBTitle:** crystal structure of tm0439, a gntr transcriptional2 regulator
67	c1mkmA_	Alignment	not modelled	7.2	7	**PDB header:**transcription **Chain:** A: **PDB Molecule:**iclr transcriptional regulator; **PDBTitle:** crystal structure of the thermotoga maritima iclr
68	c3hugA_	Alignment	not modelled	6.9	23	**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
69	d2j85a1	Alignment	not modelled	6.8	18	**Fold:**STIV B116-like **Superfamily:**STIV B116-like **Family:**STIV B116-like
70	c3mkyP_	Alignment	not modelled	6.8	6	**PDB header:**dna binding protein/dna **Chain:** P: **PDB Molecule:**protein sopb; **PDBTitle:** structure of sopb(155-323)-18mer dna complex, i23 form
71	d1efaa1	Alignment	not modelled	6.8	32	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
72	c3uo9B_	Alignment	not modelled	6.3	14	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** B: **PDB Molecule:**glutaminase kidney isoform, mitochondrial; **PDBTitle:** crystal structure of human gac in complex with glutamate and bptes
73	c3ss4C_	Alignment	not modelled	6.3	14	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**glutaminase c; **PDBTitle:** crystal structure of mouse glutaminase c, phosphate-bound form
74	c2e7xA_	Alignment	not modelled	6.1	13	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**150aa long hypothetical transcriptional regulator; **PDBTitle:** structure of the lrp/asnc like transcriptional regulator from2 sulfolobus tokodaii 7 complexed with its cognate ligand
75	c3mzyA_	Alignment	not modelled	6.0	14	**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
76	d1qpza1	Alignment	not modelled	5.8	32	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
77	c3m6zA_	Alignment	not modelled	5.8	27	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**topoisomerase v; **PDBTitle:** crystal structure of an n-terminal 44 kda fragment of topoisomerase v2 in the presence of guanidium hydrochloride
78	c2p6tH_	Alignment	not modelled	5.8	13	**PDB header:**transcription **Chain:** H: **PDB Molecule:**transcriptional regulator, lrp/asnc family; **PDBTitle:** crystal structure of transcriptional regulator nmb0573 and l-leucine2 complex from neisseria meningitidis
79	d1xmka1	Alignment	not modelled	5.8	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Z-DNA binding domain
80	d1i1ga1	Alignment	not modelled	5.6	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain

						Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
81	d1rp3a2	Alignment	not modelled	5.6	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
82	c2gqqB_	Alignment	not modelled	5.5	9	**PDB header:**transcription **Chain:** B: **PDB Molecule:**leucine-responsive regulatory protein; **PDBTitle:** crystal structure of e. coli leucine-responsive regulatory protein2 (lrp)
83	c2vbzA_	Alignment	not modelled	5.5	23	**PDB header:**dna-binding protein **Chain:** A: **PDB Molecule:**transcriptional regulatory protein; **PDBTitle:** feast or famine regulatory protein (rv3291c)from m.2 tuberculosis complexed with l-tryptophan
84	c3go5A_	Alignment	not modelled	5.4	11	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**multidomain protein with s1 rna-binding domains; **PDBTitle:** crystal structure of a multidomain protein with nucleic acid binding2 domains (sp_0946) from streptococcus pneumoniae tigr4 at 1.40 a3 resolution
85	c3g5oA_	Alignment	not modelled	5.4	16	**PDB header:**toxin/antitoxin **Chain:** A: **PDB Molecule:**uncharacterized protein rv2865; **PDBTitle:** the crystal structure of the toxin-antitoxin complex relbe2 (rv2865-2 2866) from mycobacterium tuberculosis
86	d1q9ua_	Alignment	not modelled	5.4	26	**Fold:**TBP-like **Superfamily:**TT1751-like **Family:**TT1751-like
87	c3db0B_	Alignment	not modelled	5.3	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**lin2891 protein; **PDBTitle:** crystal structure of putative pyridoxamine 5'-phosphate oxidase2 (np_472219.1) from listeria innocua at 2.00 a resolution
88	c1vftA_	Alignment	not modelled	5.2	22	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**alanine racemase; **PDBTitle:** crystal structure of l-cycloserine-bound form of alanine2 racemase from d-cycloserine-producing streptomyces3 lavendulae