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Description	P0AFH0
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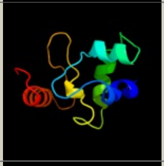
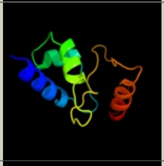
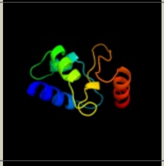
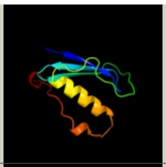
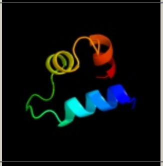
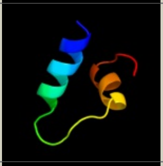
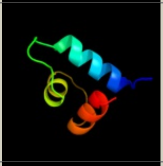
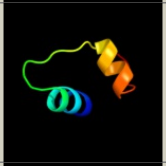
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1sfeA_	Alignment		100.0	32	**PDB header:**dna-binding protein **Chain:** A: **PDB Molecule:**ada o6-methylguanine-dna methyltransferase; **PDBTitle:** ada o6-methylguanine-dna methyltransferase from escherichia coli
2	c1wrjA_	Alignment		100.0	31	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methylated-dna--protein-cysteine **PDBTitle:** crystal structure of o6-methylguanine methyltransferase2 from sulfolobus tokodaii
3	c1t39A_	Alignment		100.0	35	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**methylated-dna--protein-cysteine **PDBTitle:** human o6-alkylguanine-dna alkyltransferase covalently2 crosslinked to dna
4	c1mgtA_	Alignment		100.0	30	**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
5	c2g7hA_	Alignment		100.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methylated-dna--protein-cysteine **PDBTitle:** structure of an o6-methylguanine dna methyltransferase from2 methanococcus jannaschii (mj1529)
6	d1sfea1	Alignment		100.0	52	**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
7	d1qnta1	Alignment		100.0	50	**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	c3gx4X_	Alignment		100.0	34	**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
9	d1mgta1	Alignment		100.0	44	**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
10	c2kimA_	Alignment		100.0	31	**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.
11	d1sfea2	Alignment		99.0	12	**Fold:**Ribonuclease H-like motif **Superfamily:**Methylated DNA-protein cysteine methyltransferase domain **Family:**Methylated DNA-protein cysteine methyltransferase domain

12	d1qnta2	Alignment		96.2	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Methylated DNA-protein cysteine methyltransferase domain **Family:**Methylated DNA-protein cysteine methyltransferase domain
13	c1dpuA_	Alignment		68.8	19	**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)
14	d1dpua_	Alignment		68.8	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**C-terminal domain of RPA32
15	d2gxba1	Alignment		64.6	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Z-DNA binding domain
16	d1qgpa_	Alignment		58.3	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Z-DNA binding domain
17	d1stza1	Alignment		57.8	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Heat-inducible transcription repressor HrcA, N-terminal domain
18	d1qbjc_	Alignment		54.2	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Z-DNA binding domain
19	d1jhfa1	Alignment		40.7	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**LexA repressor, N-terminal DNA-binding domain
20	c3k69A_	Alignment		37.9	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative transcription regulator; **PDBTitle:** crystal structure of a putative transcriptional regulator (lp_0360)2 from lactobacillus plantarum at 1.95 a resolution
21	d1tnsa_	Alignment	not modelled	35.3	22	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**Excisionase-like
22	c3lwfD_	Alignment	not modelled	33.1	16	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** crystal structure of putative transcriptional regulator (np_470886.1)2 from listeria innocua at 2.06 a resolution
23	d1cf7b_	Alignment	not modelled	23.1	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Cell cycle transcription factor e2f-dp
24	c2l01A_	Alignment	not modelled	22.8	10	**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
25	d2cyya1	Alignment	not modelled	21.7	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
26	d1bw6a_	Alignment	not modelled	20.5	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Centromere-binding
27	c3c8lB_	Alignment	not modelled	19.9	40	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**ftsz-like protein of unknown function; **PDBTitle:** crystal structure of a ftsz-like protein of unknown function2 (npun_r1471) from nostoc punctiforme pcc 73102 at 1.22 a resolution
28	d1ub9a_	Alignment	not modelled	17.8	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators

29	d1or7a1	Alignment	not modelled	17.6	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
30	c2l02B_	Alignment	not modelled	17.4	27	**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
31	c2o8xA_	Alignment	not modelled	17.2	14	**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
32	c3k2zA_	Alignment	not modelled	16.8	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lexa repressor; **PDBTitle:** crystal structure of a lexa protein from thermotoga maritima
33	d1u0ma2	Alignment	not modelled	16.7	13	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
34	d1mkma1	Alignment	not modelled	15.8	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Transcriptional regulator IclR, N-terminal domain
35	c2cfxD_	Alignment	not modelled	15.6	7	**PDB header:**transcription **Chain:** D: **PDB Molecule:**hth-type transcriptional regulator lrpc; **PDBTitle:** structure of b.subtilis lrpc
36	c3g5oA_	Alignment	not modelled	15.2	13	**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
37	c3fvcA_	Alignment	not modelled	14.2	29	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**glycoprotein gp110; **PDBTitle:** crystal structure of a trimeric variant of the epstein-barr virus2 glycoprotein b
38	c2iv1J_	Alignment	not modelled	14.1	16	**PDB header:**lyase **Chain:** J: **PDB Molecule:**cyanate hydratase; **PDBTitle:** site directed mutagenesis of key residues involved in the2 catalytic mechanism of cyanase
39	d1dwka1	Alignment	not modelled	12.7	16	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Cyanase N-terminal domain
40	d2cfxa1	Alignment	not modelled	12.3	7	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
41	d1ku7a_	Alignment	not modelled	12.3	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
42	c2da5A_	Alignment	not modelled	12.3	13	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**zinc fingers and homeoboxes protein 3; **PDBTitle:** solution structure of the second homeobox domain of zinc2 fingers and homeoboxes protein 3 (triple homeobox 13 protein)
43	c3r0aB_	Alignment	not modelled	12.2	18	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** possible transcriptional regulator from methanosarcina mazei go1 (gi2 21227196)
44	c3hugA_	Alignment	not modelled	12.2	17	**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
45	d1s6la1	Alignment	not modelled	11.9	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MerB N-terminal domain-like
46	c3t72o_	Alignment	not modelled	11.6	13	**PDB header:**transcription/dna **Chain:** O: **PDB Molecule:**pho box dna (strand 1); **PDBTitle:** phob(e)-sigma70(4)-(rnap-betha-flap-tip-helix)-dna transcription2 activation sub-complex
47	c2dbbA_	Alignment	not modelled	11.5	15	**PDB header:**transcriptional regulator **Chain:** A: **PDB Molecule:**putative hth-type transcriptional regulator ph0061; **PDBTitle:** crystal structure of ph0061
48	d1s7oa_	Alignment	not modelled	11.5	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**YlxM/p13-like
49	d1ku3a_	Alignment	not modelled	11.3	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
50	c2e1cA_	Alignment	not modelled	11.1	10	**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
51	d1dhsa_	Alignment	not modelled	11.0	18	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Deoxyhypusine synthase, DHS
52	d1biaa1	Alignment	not modelled	10.9	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Biotin repressor-like
53	c1mkmA_	Alignment	not modelled	10.2	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**iclr transcriptional regulator; **PDBTitle:** crystal structure of the thermotoga maritima iclr
54	c1i1gA_	Alignment	not modelled	9.7	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator lrpa;

54	c1i1gA_	Alignment	not modelled	9.7	15	**PDBTitle:** crystal structure of the lrp-like transcriptional regulator from the2 archaeon pyrococcus furiosus
55	c3narA_	Alignment	not modelled	9.4	25	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc fingers and homeoboxes protein 1; **PDBTitle:** crystal structure of zhx1 hd4 (zinc-fingers and homeoboxes protein 1,2 homeodomain 4)
56	c2y75F_	Alignment	not modelled	9.2	10	**PDB header:**transcription **Chain:** F: **PDB Molecule:**hth-type transcriptional regulator cymr; **PDBTitle:** the structure of cymr (yrzc) the global cysteine regulator2 of b. subtilis
57	d1rp3a2	Alignment	not modelled	9.2	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
58	d1xmka1	Alignment	not modelled	9.1	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Z-DNA binding domain
59	d2guma1	Alignment	not modelled	8.9	20	**Fold:**Viral glycoprotein ectodomain-like **Superfamily:**Viral glycoprotein ectodomain-like **Family:**Glycoprotein B-like
60	c3nw8B_	Alignment	not modelled	8.8	20	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**envelope glycoprotein b; **PDBTitle:** glycoprotein b from herpes simplex virus type 1, y179s mutant, high-ph
61	c2inpD_	Alignment	not modelled	8.7	38	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**phenol hydroxylase component phl; **PDBTitle:** structure of the phenol hydroxylase-regulatory protein2 complex
62	c3i4pA_	Alignment	not modelled	8.7	13	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, asnc family; **PDBTitle:** crystal structure of asnc family transcriptional regulator from2 agrobacterium tumefaciens
63	d2cg4a1	Alignment	not modelled	8.6	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
64	d2f3ci1	Alignment	not modelled	8.6	56	**Fold:**Kazal-type serine protease inhibitors **Superfamily:**Kazal-type serine protease inhibitors **Family:**Ovomucoid domain III-like
65	d2p7vb1	Alignment	not modelled	8.5	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
66	d2hs5a1	Alignment	not modelled	8.4	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**GntR-like transcriptional regulators
67	d1xsva_	Alignment	not modelled	8.4	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**YlxM/p13-like
68	c2ia0A_	Alignment	not modelled	8.3	15	**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)
69	d1wh5a_	Alignment	not modelled	8.3	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
70	d1s7ea1	Alignment	not modelled	8.0	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
71	c3ee6A_	Alignment	not modelled	7.9	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tripeptidyl-peptidase 1; **PDBTitle:** crystal structure analysis of tripeptidyl peptidase -i
72	d1i1ga1	Alignment	not modelled	7.8	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
73	d3ctaa1	Alignment	not modelled	7.5	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
74	d2ecba1	Alignment	not modelled	7.5	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
75	d2hi3a1	Alignment	not modelled	7.5	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
76	d1ku2a1	Alignment	not modelled	7.4	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma3 domain
77	d1xd7a_	Alignment	not modelled	7.4	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Transcriptional regulator Rrf2
78	c1rr7A_	Alignment	not modelled	7.4	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**middle operon regulator; **PDBTitle:** crystal structure of the middle operon regulator protein of2 bacteriophage mu
79	d1rr7a_	Alignment	not modelled	7.4	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Middle operon regulator, Mor
80	d1smyf2	Alignment	not modelled	7.3	8	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain

81	c3qmlC_	Alignment	not modelled	7.3	21	**PDB header:**chaperone/protein transport **Chain:** C: **PDB Molecule:**nucleotide exchange factor sil1; **PDBTitle:** the structural analysis of sil1-bip complex reveals the mechanism for2 sil1 to function as a novel nucleotide exchange factor
82	d1nffa_	Alignment	not modelled	7.2	11	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
83	c1r22B_	Alignment	not modelled	7.2	22	**PDB header:**transcription repressor **Chain:** B: **PDB Molecule:**transcriptional repressor smtb; **PDBTitle:** crystal structure of the cyanobacterial metallothionein2 repressor smtb (c14s/c61s/c121s mutant) in the zn2alpha5-3 form
84	d1ttya_	Alignment	not modelled	7.2	7	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
85	c2e7xA_	Alignment	not modelled	7.2	10	**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
86	c2l4aA_	Alignment	not modelled	7.1	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
87	d1ig6a_	Alignment	not modelled	6.9	8	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**ARID-like **Family:**ARID domain
88	c3eusB_	Alignment	not modelled	6.8	26	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**dna-binding protein; **PDBTitle:** the crystal structure of the dna binding protein from silicibacter2 pomeroyi
89	c3a01A_	Alignment	not modelled	6.8	16	**PDB header:**gene regulation/dna **Chain:** A: **PDB Molecule:**homeodomain-containing protein; **PDBTitle:** crystal structure of aristaless and clawless homeodomains bound to dna
90	c3sztB_	Alignment	not modelled	6.7	17	**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
91	c2kxxA_	Alignment	not modelled	6.6	36	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**small protein a; **PDBTitle:** nmr structure of escherichia coli bame, a lipoprotein component of the2 beta-barrel assembly machinery complex
92	d1t1ea2	Alignment	not modelled	6.4	6	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Subtilase propeptides/inhibitors
93	d1hlva1	Alignment	not modelled	6.4	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Centromere-binding
94	d1rg6a_	Alignment	not modelled	6.4	21	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
95	d1p2fa1	Alignment	not modelled	6.3	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**PhoB-like
96	c1x3uA_	Alignment	not modelled	6.1	16	**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
97	c3frwF_	Alignment	not modelled	6.0	14	**PDB header:**structural genomics, unknown function **Chain:** F: **PDB Molecule:**putative trp repressor protein; **PDBTitle:** crystal structure of putative trpr protein from ruminococcus obeum
98	c2oqgA_	Alignment	not modelled	6.0	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**possible transcriptional regulator, arsr family protein; **PDBTitle:** arsr-like transcriptional regulator from rhodococcus sp. rha1
99	c3mq0A_	Alignment	not modelled	6.0	13	**PDB header:**transcription repressor **Chain:** A: **PDB Molecule:**transcriptional repressor of the blcabc operon; **PDBTitle:** crystal structure of agobacterium tumefaciens repressor blcr