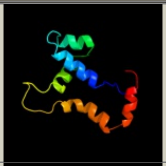
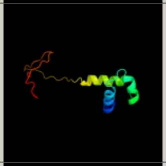
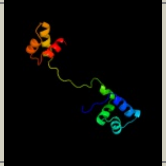
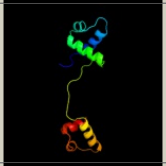
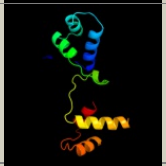
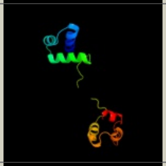
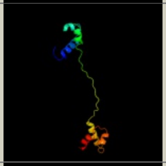
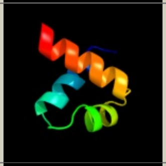
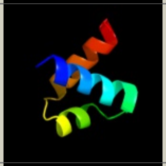
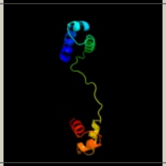
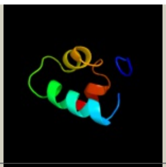
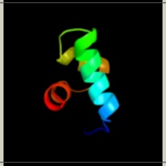
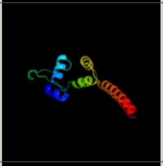
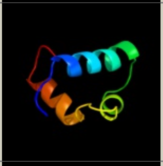
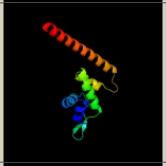
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P19768
Date	Thu Jan 5 11:37:32 GMT 2012
Unique Job ID	3a3fdf6e9ce65683

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2jn6a1	Alignment		99.5	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Cgl2762-like
2	c2rn7A_	Alignment		99.4	24	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**is629 orfa; **PDBTitle:** nmr solution structure of tnpe protein from shigella2 flexneri. northeast structural genomics target sfr125
3	c1u78A_	Alignment		99.0	10	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**transposable element tc3 transposase; **PDBTitle:** structure of the bipartite dna-binding domain of tc32 transposase bound to transposon dna
4	c6paxA_	Alignment		99.0	19	**PDB header:**gene regulation/dna **Chain:** A: **PDB Molecule:**homeobox protein pax-6; **PDBTitle:** crystal structure of the human pax-6 paired domain-dna2 complex reveals a general model for pax protein-dna3 interactions
5	c1hlvA_	Alignment		98.7	16	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**major centromere autoantigen b; **PDBTitle:** crystal structure of cenp-b(1-129) complexed with the cenp-2 b box dna
6	d1pdnc_	Alignment		98.7	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
7	c2k27A_	Alignment		98.1	14	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**paired box protein pax-8; **PDBTitle:** solution structure of human pax8 paired box domain
8	d6paxa1	Alignment		97.9	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
9	d1k78a1	Alignment		97.9	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
10	c3hosA_	Alignment		97.9	10	**PDB header:**transferase, dna binding protein/dna **Chain:** A: **PDB Molecule:**transposable element mariner, complete cds; **PDBTitle:** crystal structure of the mariner mos1 paired end complex with mg
11	d1hlva1	Alignment		97.8	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Centromere-binding

12	d1bw6a_	Alignment		97.8	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Centromere-binding
13	c2elhA_	Alignment		97.7	14	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**cg11849-pa; **PDBTitle:** solution structure of the cenp-b n-terminal dna-binding2 domain of fruit fly distal antenna cg11849-pa
14	d2coba1	Alignment		97.4	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Psq domain
15	c2gloA_	Alignment		97.4	19	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**brinker cg9653-pa; **PDBTitle:** solution structure of the brinker dna binding domain in2 complex with the omb enhancer
16	d1r8da_	Alignment		97.0	12	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**DNA-binding N-terminal domain of transcription activators
17	c2vz4A_	Alignment		96.5	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**hth-type transcriptional activator tipa; **PDBTitle:** the n-terminal domain of merr-like protein tipal bound to2 promoter dna
18	c3hefB_	Alignment		96.4	20	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**gene 1 protein; **PDBTitle:** crystal structure of the bacteriophage sf6 terminase small2 subunit
19	d1q06a_	Alignment		96.3	11	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**DNA-binding N-terminal domain of transcription activators
20	c3hh0C_	Alignment		96.1	7	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**transcriptional regulator, merr family; **PDBTitle:** crystal strucure of a transcriptional regulator, merr family2 from bacillus cereus
21	c3oouA_	Alignment	not modelled	96.1	8	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lin2118 protein; **PDBTitle:** the structure of a protein with unkown function from listeria innocua
22	c2k9sA_	Alignment	not modelled	96.1	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**arabinose operon regulatory protein; **PDBTitle:** solution structure of dna binding domain of e. coli arac
23	c3gpvA_	Alignment	not modelled	96.1	8	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, merr family; **PDBTitle:** crystal structure of a transcriptional regulator, merr2 family from bacillus thuringiensis
24	c3oioA_	Alignment	not modelled	96.0	15	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator (arac-type dna-binding domain- **PDBTitle:** crystal structure of transcriptional regulator (arac-type dna-binding2 domain-containing proteins) from chromobacterium violaceum
25	d1r8ea1	Alignment	not modelled	95.9	10	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**DNA-binding N-terminal domain of transcription activators
26	c3mklB_	Alignment	not modelled	95.7	7	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**hth-type transcriptional regulator gadx; **PDBTitle:** crystal structure of dna-binding transcriptional dual regulator from2 escherichia coli k-12
27	c3lsgD_	Alignment	not modelled	95.4	7	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**two-component response regulator yesn; **PDBTitle:** the crystal structure of the c-terminal domain of the two-2 component response regulator yesn from fusobacterium3 nucleatum subsp. nucleatum atcc 25586
28	c1iufA_	Alignment	not modelled	95.4	16	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**centromere abp1 protein;

28	c1iufA_	Alignment	not modelled	95.4	16	**PDBTitle:** low resolution solution structure of the two dna-binding2 domains in schizosaccharomyces pombe abp1 protein
29	c3gbgA_	Alignment	not modelled	95.3	16	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**tcp pilus virulence regulatory protein; **PDBTitle:** crystal structure of toxt from vibrio cholerae o395
30	c3gp4B_	Alignment	not modelled	95.3	15	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator, merr family; **PDBTitle:** crystal structure of putative merr family transcriptional regulator2 from listeria monocytogenes
31	c2zhhA_	Alignment	not modelled	95.2	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**redox-sensitive transcriptional activator soxr; **PDBTitle:** crystal structure of soxr
32	d2oa4a1	Alignment	not modelled	95.1	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**TrpR-like **Family:**SPO1678-like
33	d1vz0a1	Alignment	not modelled	94.7	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**KorB DNA-binding domain-like **Family:**KorB DNA-binding domain-like
34	c2jmlA_	Alignment	not modelled	94.5	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**dna binding domain/transcriptional regulator; **PDBTitle:** solution structure of the n-terminal domain of cara repressor
35	c2jrtA_	Alignment	not modelled	94.3	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** nmr solution structure of the protein coded by gene2 rhos4_12090 of rhodobacter sphaeroides. northeast3 structural genomics target rhr5
36	d1jhfa1	Alignment	not modelled	94.2	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**LexA repressor, N-terminal DNA-binding domain
37	c2w48D_	Alignment	not modelled	94.1	28	**PDB header:**transcription **Chain:** D: **PDB Molecule:**sorbitol operon regulator; **PDBTitle:** crystal structure of the full-length sorbitol operon2 regulator sorc from klebsiella pneumoniae
38	c3mn2B_	Alignment	not modelled	94.0	12	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**probable arac family transcriptional regulator; **PDBTitle:** the crystal structure of a probable arac family transcriptional2 regulator from rhodopseudomonas palustris cga009
39	d1r1ua_	Alignment	not modelled	93.6	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ArsR-like transcriptional regulators
40	d1fipa_	Alignment	not modelled	93.5	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
41	c1bl0A_	Alignment	not modelled	93.2	14	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**protein (multiple antibiotic resistance protein); **PDBTitle:** multiple antibiotic resistance protein (mara)/dna complex
42	c3qaoA_	Alignment	not modelled	93.1	16	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**merr-like transcriptional regulator; **PDBTitle:** the crystal structure of the n-terminal domain of a merr-like2 transcriptional regulator from listeria monocytogenes egd-e
43	d1ntca_	Alignment	not modelled	92.6	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
44	c2o8xA_	Alignment	not modelled	92.4	20	**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
45	d1rp3a2	Alignment	not modelled	92.4	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
46	c2l0kA_	Alignment	not modelled	92.0	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**stage iii sporulation protein d; **PDBTitle:** nmr solution structure of a transcription factor spoiiid in complex2 with dna
47	c3d6zA_	Alignment	not modelled	92.0	16	**PDB header:**transcription regulator/dna **Chain:** A: **PDB Molecule:**multidrug-efflux transporter 1 regulator; **PDBTitle:** crystal structure of r275e mutant of bmrr bound to dna and rhodamine
48	c2r0qF_	Alignment	not modelled	91.9	13	**PDB header:**recombination/dna **Chain:** F: **PDB Molecule:**putative transposon tn552 dna-invertase bin3; **PDBTitle:** crystal structure of a serine recombinase- dna regulatory2 complex
49	c1d5yD_	Alignment	not modelled	91.7	11	**PDB header:**transcription/dna **Chain:** D: **PDB Molecule:**rob transcription factor; **PDBTitle:** crystal structure of the e. coli rob transcription factor2 in complex with dna
50	c2cg4B_	Alignment	not modelled	91.7	12	**PDB header:**transcription **Chain:** B: **PDB Molecule:**regulatory protein asnc; **PDBTitle:** structure of e.coli asnc
51	d1stza1	Alignment	not modelled	91.6	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Heat-inducible transcription repressor HrcA, N-terminal domain
52	c3e7lD_	Alignment	not modelled	91.4	16	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** crystal structure of sigma54 activator ntrc4's dna binding2 domain
						Fold:DNA/RNA-binding 3-helical bundle

53	d1xsva_	Alignment	not modelled	91.1	14	**Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**YlxM/p13-like
54	d1umqa_	Alignment	not modelled	91.1	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
55	c1umqA_	Alignment	not modelled	91.1	16	**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
56	d1or7a1	Alignment	not modelled	90.8	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
57	d1jhga_	Alignment	not modelled	90.8	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**TrpR-like **Family:**Trp repressor, TrpR
58	d1trra_	Alignment	not modelled	90.8	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**TrpR-like **Family:**Trp repressor, TrpR
59	c1r22B_	Alignment	not modelled	90.7	10	**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
60	c3frwF_	Alignment	not modelled	90.6	22	**PDB header:**structural genomics, unknown function **Chain:** F: **PDB Molecule:**putative trp repressor protein; **PDBTitle:** crystal structure of putative trpr protein from ruminococcus obeum
61	c3hugA_	Alignment	not modelled	90.5	15	**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
62	c2e7xA_	Alignment	not modelled	90.2	19	**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
63	c3korD_	Alignment	not modelled	90.0	18	**PDB header:**transcription **Chain:** D: **PDB Molecule:**possible trp repressor; **PDBTitle:** crystal structure of a putative trp repressor from staphylococcus2 aureus
64	c1or7A_	Alignment	not modelled	90.0	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**rna polymerase sigma-e factor; **PDBTitle:** crystal structure of escherichia coli sigmae with the cytoplasmic2 domain of its anti-sigma rsea
65	c2gm4B_	Alignment	not modelled	89.9	9	**PDB header:**recombination, dna **Chain:** B: **PDB Molecule:**transposon gamma-delta resolvase; **PDBTitle:** an activated, tetrameric gamma-delta resolvase: hin chimaera bound to2 cleaved dna
66	d1etxa_	Alignment	not modelled	89.8	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
67	c3mzyA_	Alignment	not modelled	89.7	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
68	c3i4pA_	Alignment	not modelled	89.4	21	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, asnc family; **PDBTitle:** crystal structure of asnc family transcriptional regulator from2 agrobacterium tumefaciens
69	c2cfxD_	Alignment	not modelled	89.4	14	**PDB header:**transcription **Chain:** D: **PDB Molecule:**hth-type transcriptional regulator lrpc; **PDBTitle:** structure of b.subtilis lrpc
70	c2oqgA_	Alignment	not modelled	89.2	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**possible transcriptional regulator, arsr family protein; **PDBTitle:** arsr-like transcriptional regulator from rhodococcus sp. rha1
71	c3op9A_	Alignment	not modelled	89.0	14	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**pli0006 protein; **PDBTitle:** crystal structure of transcriptional regulator from listeria innocua
72	d1r1ta_	Alignment	not modelled	89.0	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ArsR-like transcriptional regulators
73	c3jthA_	Alignment	not modelled	88.9	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription activator hlyu; **PDBTitle:** crystal structure of a transcriptional regulator hlyu from2 vibrio vulnificus cmcp6
74	d1x57a1	Alignment	not modelled	88.8	8	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**EDF1-like
75	c2kpjA_	Alignment	not modelled	88.7	18	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**sos-response transcriptional repressor, lexa; **PDBTitle:** solution structure of protein sos-response transcriptional2 repressor, lexa from eubacterium rectale. northeast3 structural genomics consortium target err9a
76	d2ezla_	Alignment	not modelled	88.4	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
77	d1ulya_	Alignment	not modelled	88.4	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Hypothetical protein PH1932

78	d1s7oa_	Alignment	not modelled	88.3	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**YlxM/p13-like
79	c1i1gA_	Alignment	not modelled	87.5	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
80	c2p6tH_	Alignment	not modelled	87.5	9	**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
81	c3pqkD_	Alignment	not modelled	87.5	10	**PDB header:**transcription **Chain:** D: **PDB Molecule:**biofilm growth-associated repressor; **PDBTitle:** crystal structure of the transcriptional repressor bigr from xylella2 fastidiosa
82	d1g2ha_	Alignment	not modelled	87.5	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
83	c3f6oB_	Alignment	not modelled	87.3	9	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**probable transcriptional regulator, arsr family **PDBTitle:** crystal structure of arsr family transcriptional regulator,2 rha00566
84	c1rp3G_	Alignment	not modelled	87.0	11	**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
85	d1ijwc_	Alignment	not modelled	87.0	5	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
86	c2jscB_	Alignment	not modelled	86.2	12	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator rv1994c/mt2050; **PDBTitle:** nmr structure of the cadmium metal-sensor cmtr from mycobacterium2 tuberculosis
87	d1y9qa1	Alignment	not modelled	86.2	8	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Probable transcriptional regulator VC1968, N-terminal domain
88	c3b7hA_	Alignment	not modelled	85.9	15	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**prophage lp1 protein 11; **PDBTitle:** crystal structure of the prophage lp1 protein 11
89	d2b5aa1	Alignment	not modelled	85.9	11	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
90	c1rr7A_	Alignment	not modelled	85.7	10	**PDB header:**transcription **Chain:** A: **PDB Molecule:**middle operon regulator; **PDBTitle:** crystal structure of the middle operon regulator protein of2 bacteriophage mu
91	d1rr7a_	Alignment	not modelled	85.7	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Middle operon regulator, Mor
92	d1hcra_	Alignment	not modelled	85.6	5	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
93	c1vz0B_	Alignment	not modelled	85.4	18	**PDB header:**nuclear protein **Chain:** B: **PDB Molecule:**chromosome partitioning protein parb; **PDBTitle:** chromosome segregation protein spo0j from thermus2 thermophilus
94	d2ao9a1	Alignment	not modelled	85.2	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Nanomeric phage protein-like
95	c3omtA_	Alignment	not modelled	85.1	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** putative antitoxin component, chu_2935 protein, from xre family from2 prevotella buccae.
96	c3t76A_	Alignment	not modelled	85.0	16	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator vanug; **PDBTitle:** crystal structure of transcriptional regulator vanug, form ii
97	c3f6vA_	Alignment	not modelled	84.9	10	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**possible transcriptional regulator, arsr family **PDBTitle:** crystal structure of possible transcriptional regulator for2 arsenical resistance
98	c2ia0A_	Alignment	not modelled	84.9	7	**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)
99	d1biaa1	Alignment	not modelled	84.9	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Biotin repressor-like
100	d1i1ga1	Alignment	not modelled	84.7	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
101	c2kkoB_	Alignment	not modelled	84.6	10	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**possible transcriptional regulatory protein **PDBTitle:** solution nmr structure of the homodimeric winged helix-turn-2 helix dna-binding domain (fragment 1-100) mb0332 from3 mycobacterium bovis, a possible arsr-family transcriptional4 regulator. northeast structural genomics consortium target5 mbr242e.

102	c3bs3A_	Alignment	not modelled	84.4	14	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**putative dna-binding protein; **PDBTitle:** crystal structure of a putative dna-binding protein from bacteroides2 fragilis
103	c2l4aA_	Alignment	not modelled	83.9	24	**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
104	c3bd1B_	Alignment	not modelled	83.9	16	**PDB header:**transcription **Chain:** B: **PDB Molecule:**cro protein; **PDBTitle:** structure of the cro protein from putative prophage element xfaso 1 in2 xylella fastidiosa strain ann-1
105	c3fmyA_	Alignment	not modelled	83.7	20	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**hth-type transcriptional regulator mqsa **PDBTitle:** structure of the c-terminal domain of the e. coli protein2 mqsa (ygit/b3021)
106	c3cuoB_	Alignment	not modelled	83.5	10	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**uncharacterized hth-type transcriptional regulator ygav; **PDBTitle:** crystal structure of the predicted dna-binding transcriptional2 regulator from e. coli
107	d1utxa_	Alignment	not modelled	83.2	13	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
108	d1y7ya1	Alignment	not modelled	83.1	11	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
109	c2ewtA_	Alignment	not modelled	83.1	15	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**putative dna-binding protein; **PDBTitle:** crystal structure of the dna-binding domain of bldd
110	d1sq8a_	Alignment	not modelled	83.0	6	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
111	c2dbbA_	Alignment	not modelled	82.5	15	**PDB header:**transcriptional regulator **Chain:** A: **PDB Molecule:**putative hth-type transcriptional regulator ph0061; **PDBTitle:** crystal structure of ph0061
112	c2xcjB_	Alignment	not modelled	82.4	16	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**c protein; **PDBTitle:** crystal structure of p2 c, the immunity repressor of2 temperate e. coli phage p2
113	c2h09A_	Alignment	not modelled	82.3	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator mntr; **PDBTitle:** crystal structure of diphtheria toxin repressor like protein2 from e. coli
114	c3dnvB_	Alignment	not modelled	82.2	5	**PDB header:**transcription/dna **Chain:** B: **PDB Molecule:**hth-type transcriptional regulator hipb; **PDBTitle:** mdt protein
115	c2fjrB_	Alignment	not modelled	82.0	21	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**repressor protein ci; **PDBTitle:** crystal structure of bacteriophage 186
116	d1adra_	Alignment	not modelled	82.0	3	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
117	d2a6ca1	Alignment	not modelled	81.7	14	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**NE1354
118	d1r69a_	Alignment	not modelled	81.2	11	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
119	d2ppxa1	Alignment	not modelled	81.2	10	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
120	c2ppxA_	Alignment	not modelled	81.2	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein atu1735; **PDBTitle:** crystal structure of a hth xre-family like protein from agrobacterium2 tumefaciens