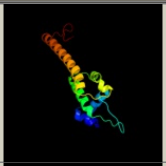
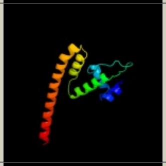
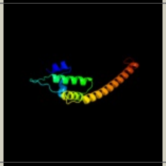
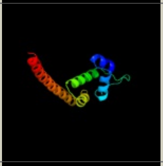
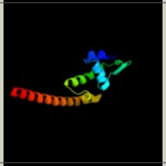
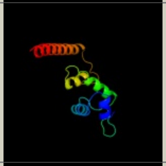
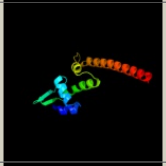
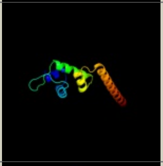
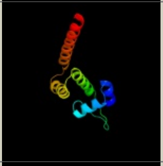
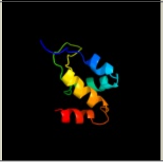
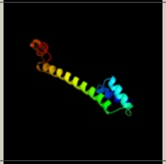
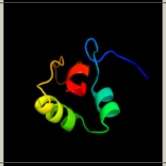
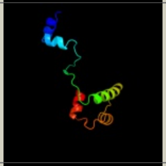
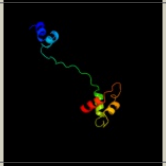
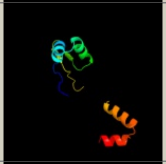
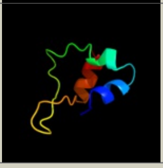
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P0ACS2
Date	Thu Jan 5 11:18:53 GMT 2012
Unique Job ID	001cfe4ab09f72df

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2zhhA_	Alignment		100.0	100	**PDB header:**transcription **Chain:** A: **PDB Molecule:**redox-sensitive transcriptional activator soxr; **PDBTitle:** crystal structure of soxr
2	c3gp4B_	Alignment		99.9	27	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator, merr family; **PDBTitle:** crystal structure of putative merr family transcriptional regulator2 from listeria monocytogenes
3	d1q06a_	Alignment		99.9	26	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**DNA-binding N-terminal domain of transcription activators
4	c3gpvA_	Alignment		99.9	22	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, merr family; **PDBTitle:** crystal structure of a transcriptional regulator, merr2 family from bacillus thuringiensis
5	c3d6zA_	Alignment		99.9	24	**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
6	c3hh0C_	Alignment		99.9	20	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**transcriptional regulator, merr family; **PDBTitle:** crystal strucure of a transcriptional regulator, merr family2 from bacillus cereus
7	d1r8ea1	Alignment		99.9	24	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**DNA-binding N-terminal domain of transcription activators
8	c3qaoA_	Alignment		99.9	20	**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
9	d1r8da_	Alignment		99.8	22	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**DNA-binding N-terminal domain of transcription activators
10	c2vz4A_	Alignment		99.8	24	**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
11	c2jmlA_	Alignment		99.6	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**dna binding domain/transcriptional regulator; **PDBTitle:** solution structure of the n-terminal domain of cara repressor

12	c2dg6A_	Alignment		99.6	28	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** crystal structure of the putative transcriptional regulator sco55502 from streptomyces coelicolor a3(2)
13	d1q08a_	Alignment		99.4	18	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**DNA-binding N-terminal domain of transcription activators
14	c1z4hA_	Alignment		96.6	11	**PDB header:**protein binding, dna binding protein **Chain:** A: **PDB Molecule:**tor inhibition protein; **PDBTitle:** the response regulator tori belongs to a new family of2 atypical excisionase
15	c2ev2B_	Alignment		96.1	10	**PDB header:**lyase **Chain:** B: **PDB Molecule:**hypothetical protein rv1264/mt1302; **PDBTitle:** structure of rv1264n, the regulatory domain of the mycobacterial2 adenylyl cylcase rv1264, at ph 8.5
16	c2kfsA_	Alignment		95.2	17	**PDB header:**dna-binding protein **Chain:** A: **PDB Molecule:**conserved hypothetical regulatory protein; **PDBTitle:** nmr structure of rv2175c
17	c1hlvA_	Alignment		94.8	18	**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
18	c1u78A_	Alignment		94.3	9	**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
19	c3by6C_	Alignment		93.9	17	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**predicted transcriptional regulator; **PDBTitle:** crystal structure of a transcriptional regulator from oenococcus oeni
20	c3ezfA_	Alignment		93.7	19	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**para; **PDBTitle:** partition protein
21	c3neuA_	Alignment	not modelled	92.7	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lin1836 protein; **PDBTitle:** the crystal structure of a functionally-unknown protein lin1836 from2 listeria innocua clip11262
22	c2wusR_	Alignment	not modelled	92.4	13	**PDB header:**structural protein **Chain:** R: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** bacterial actin mreb assembles in complex with cell shape2 protein rodz
23	c3op9A_	Alignment	not modelled	92.0	16	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**pli0006 protein; **PDBTitle:** crystal structure of transcriptional regulator from listeria innocua
24	c3cuoB_	Alignment	not modelled	91.6	26	**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
25	c6paxA_	Alignment	not modelled	91.6	14	**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
26	d1j9ia_	Alignment	not modelled	91.0	13	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**Terminase gpNU1 subunit domain
27	d1biaa1	Alignment	not modelled	90.9	8	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Biotin repressor-like
28	d1ku9a_	Alignment	not modelled	90.9	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**DNA-binding protein Mj223

29	d1pdnc_	Alignment	not modelled	89.9	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
30	c3jthA_	Alignment	not modelled	89.2	26	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription activator hlyu; **PDBTitle:** crystal structure of a transcriptional regulator hlyu from2 vibrio vulnificus cmcp6
31	d2ofya1	Alignment	not modelled	89.0	21	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
32	c3b7hA_	Alignment	not modelled	88.9	20	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**prophage lp1 protein 11; **PDBTitle:** crystal structure of the prophage lp1 protein 11
33	c3kxaD_	Alignment	not modelled	88.8	23	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of ngo0477 from neisseria gonorrhoeae
34	d2ppxa1	Alignment	not modelled	88.0	21	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
35	c2ppxA_	Alignment	not modelled	88.0	21	**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
36	c3clcC_	Alignment	not modelled	88.0	16	**PDB header:**transcription regulator/dna **Chain:** C: **PDB Molecule:**regulatory protein; **PDBTitle:** crystal structure of the restriction-modification controller protein2 c.esp1396i tetramer in complex with its natural 35 base-pair operator
37	c2du9A_	Alignment	not modelled	87.9	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**predicted transcriptional regulators; **PDBTitle:** crystal structure of the transcriptional factor from c.glutamicum
38	d1j5ya1	Alignment	not modelled	87.9	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Biotin repressor-like
39	d1stza1	Alignment	not modelled	87.6	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Heat-inducible transcription repressor HrcA, N-terminal domain
40	d1utxa_	Alignment	not modelled	87.5	29	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
41	c2oqgA_	Alignment	not modelled	87.5	23	**PDB header:**transcription **Chain:** A: **PDB Molecule:**possible transcriptional regulator, arsr family protein; **PDBTitle:** arsr-like transcriptional regulator from rhodococcus sp. rha1
42	c3fmyA_	Alignment	not modelled	87.3	37	**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)
43	d2jn6a1	Alignment	not modelled	87.3	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Cgl2762-like
44	c3fymA_	Alignment	not modelled	87.1	21	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** the 1a structure of ymfm, a putative dna-binding membrane2 protein from staphylococcus aureus
45	d2d1ha1	Alignment	not modelled	86.8	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**TrmB-like
46	d1r1ua_	Alignment	not modelled	85.9	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ArsR-like transcriptional regulators
47	d2b5aa1	Alignment	not modelled	85.8	24	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
48	c1r22B_	Alignment	not modelled	85.6	25	**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
49	c3kjxD_	Alignment	not modelled	85.5	32	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**transcriptional regulator, laci family; **PDBTitle:** crystal structure of a transcriptional regulator, lacl2 family protein from silicibacter pomeroyi
50	d1y7ya1	Alignment	not modelled	85.4	27	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
51	c3f52A_	Alignment	not modelled	85.3	24	**PDB header:**transcription activator **Chain:** A: **PDB Molecule:**clp gene regulator (clgr); **PDBTitle:** crystal structure of the clp gene regulator clgr from c. glutamicum
52	d1r1ta_	Alignment	not modelled	85.2	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ArsR-like transcriptional regulators
53	c3h5tA_	Alignment	not modelled	85.2	10	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, laci family; **PDBTitle:** crystal structure of a transcriptional regulator, lacl2 family protein from corynebacterium glutamicum
54	c2kkoB_	Alignment	not modelled	85.0	16	**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.
55	d2coba1	Alignment	not modelled	83.9	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Psq domain
56	d1uxca_	Alignment	not modelled	83.7	20	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
57	d1mkma1	Alignment	not modelled	83.7	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Transcriptional regulator IclR, N-terminal domain
58	c3bs3A_	Alignment	not modelled	83.5	15	**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
59	c2kpjA_	Alignment	not modelled	83.4	24	**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
60	c3f6vA_	Alignment	not modelled	82.8	23	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**possible transcriptional regulator, arsr family **PDBTitle:** crystal structure of possible transcriptional regulator for2 arsenical resistance
61	d2hsga1	Alignment	not modelled	82.6	20	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
62	c3f6wE_	Alignment	not modelled	82.1	22	**PDB header:**dna binding protein **Chain:** E: **PDB Molecule:**xre-family like protein; **PDBTitle:** xre-family like protein from pseudomonas syringae pv. tomato str.2 dc3000
63	c3bd1B_	Alignment	not modelled	81.9	24	**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
64	d1r69a_	Alignment	not modelled	81.5	26	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
65	c1b0nA_	Alignment	not modelled	80.6	36	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**protein (sinr protein); **PDBTitle:** sinr protein/sini protein complex
66	c3omtA_	Alignment	not modelled	80.4	6	**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.
67	c3t76A_	Alignment	not modelled	80.2	22	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator vanug; **PDBTitle:** crystal structure of transcriptional regulator vanug, form ii
68	d1adra_	Alignment	not modelled	80.0	26	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
69	d1x57a1	Alignment	not modelled	79.8	25	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**EDF1-like
70	d1uxda_	Alignment	not modelled	79.3	20	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
71	c2rn7A_	Alignment	not modelled	79.3	17	**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
72	d1lcda_	Alignment	not modelled	79.2	25	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
73	d1sq8a_	Alignment	not modelled	79.0	33	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
74	d1b0na2	Alignment	not modelled	78.8	33	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
75	c3dnvB_	Alignment	not modelled	78.8	26	**PDB header:**transcription/dna **Chain:** B: **PDB Molecule:**hth-type transcriptional regulator hipb; **PDBTitle:** mdt protein
76	c1zljE_	Alignment	not modelled	78.8	32	**PDB header:**transcription **Chain:** E: **PDB Molecule:**dormancy survival regulator; **PDBTitle:** crystal structure of the mycobacterium tuberculosis hypoxic2 response regulator dosr c-terminal domain
77	c2bnoA_	Alignment	not modelled	78.4	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**epoxidase; **PDBTitle:** the structure of hydroxypropylphosphonic acid epoxidase2 from s. wedmorenis.
78	d2r1jl1	Alignment	not modelled	77.7	26	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
79	d1qpza1	Alignment	not modelled	77.6	32	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
						PDB header:dna binding protein

80	c3trbA_	Alignment	not modelled	77.6	7	**Chain:** A: **PDB Molecule:**virulence-associated protein i; **PDBTitle:** structure of an addiction module antidote protein of a higa (higa)2 family from coxiella burnetii
81	c3r0aB_	Alignment	not modelled	77.5	12	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** possible transcriptional regulator from methanosarcina mazei go1 (gi2 21227196)
82	c3pqkD_	Alignment	not modelled	77.4	15	**PDB header:**transcription **Chain:** D: **PDB Molecule:**biofilm growth-associated repressor; **PDBTitle:** crystal structure of the transcriptional repressor bigr from xylella2 fastidiosa
83	c2ef8A_	Alignment	not modelled	77.2	33	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**putative transcription factor; **PDBTitle:** crystal structure of c.ecot38is
84	d1jt6a1	Alignment	not modelled	76.8	30	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
85	c1bdhA_	Alignment	not modelled	76.4	32	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**protein (purine repressor); **PDBTitle:** purine repressor mutant-hypoxanthine-palindromic operator2 complex
86	d1pm6a_	Alignment	not modelled	76.3	13	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**Excisionase-like
87	d2o7ta1	Alignment	not modelled	76.0	35	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
88	d1yioa1	Alignment	not modelled	76.0	20	**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)
89	d2bjca1	Alignment	not modelled	76.0	30	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
90	d2htja1	Alignment	not modelled	75.9	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**FaeA-like
91	c1y9qA_	Alignment	not modelled	75.8	21	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, hth_3 family; **PDBTitle:** crystal structure of hth_3 family transcriptional regulator2 from vibrio cholerae
92	d1efaa1	Alignment	not modelled	75.8	25	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
93	d1t56a1	Alignment	not modelled	75.7	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
94	c1stzB_	Alignment	not modelled	74.9	22	**PDB header:**transcription **Chain:** B: **PDB Molecule:**heat-inducible transcription repressor hrca homolog; **PDBTitle:** crystal structure of a hypothetical protein at 2.2 a resolution
95	c2dg7A_	Alignment	not modelled	74.9	25	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** crystal structure of the putative transcriptional regulator sco03372 from streptomyces coelicolor a3(2)
96	c2l8nA_	Alignment	not modelled	74.8	21	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional repressor cytr; **PDBTitle:** nmr structure of the cytidine repressor dna binding domain in presence2 of operator half-site dna
97	c3gn5B_	Alignment	not modelled	74.6	37	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**hth-type transcriptional regulator mqsa (ygit/b3021); **PDBTitle:** structure of the e. coli protein mqsa (ygit/b3021)
98	c2zkzC_	Alignment	not modelled	74.3	14	**PDB header:**transcription **Chain:** C: **PDB Molecule:**transcriptional repressor pagr; **PDBTitle:** crystal structure of the transcriptional repressor pagr of bacillus2 anthracis
99	c1bjzA_	Alignment	not modelled	74.2	25	**PDB header:**transcription regulation **Chain:** A: **PDB Molecule:**tetracycline repressor; **PDBTitle:** tetracycline chelated mg2+-ion initiates helix unwinding for tet2 repressor induction
100	c2x48B_	Alignment	not modelled	74.2	22	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**cag38821; **PDBTitle:** orf 55 from sulfolobus islandicus rudivirus 1
101	d2fbqa1	Alignment	not modelled	74.2	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
102	c3cecA_	Alignment	not modelled	74.0	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative antidote protein of plasmid maintenance system; **PDBTitle:** crystal structure of a putative antidote protein of plasmid2 maintenance system (npun_f2943) from nostoc punctiforme pcc 73102 at3 1.60 a resolution
103	c1y6uA_	Alignment	not modelled	74.0	14	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**excisionase from transposon tn916; **PDBTitle:** the structure of the excisionase (xis) protein from2 conjugative transposon tn916 provides insights into the3 regulation of heterobivalent tyrosine recombinases
104	c2ebyA_	Alignment	not modelled	73.9	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative hth-type transcriptional regulator ybaq; **PDBTitle:** crystal structure of a hypothetical protein from e. coli
105	c2xcjB_	Alignment	not modelled	73.8	27	**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
106	d1fsea_	Alignment	not modelled	73.6	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)
107	c1x3uA_	Alignment	not modelled	73.4	9	**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
108	d1rp3a2	Alignment	not modelled	73.3	36	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
109	c2jvlA_	Alignment	not modelled	73.2	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**trmbf1; **PDBTitle:** nmr structure of the c-terminal domain of mbf1 of trichoderma reesei
110	c2krfB_	Alignment	not modelled	73.2	15	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulatory protein coma; **PDBTitle:** nmr solution structure of the dna binding domain of competence protein2 a
111	c2nx4A_	Alignment	not modelled	73.1	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**transcriptional regulator, tetr family protein; **PDBTitle:** the crystal structure of athe putative tetr-family transcriptional2 regulator rha06780 from rhodococcus sp. rha1.
112	d1ulya_	Alignment	not modelled	73.1	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Hypothetical protein PH1932
113	c1zvvA_	Alignment	not modelled	73.1	20	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**glucose-resistance amylase regulator; **PDBTitle:** crystal structure of a ccpa-crh-dna complex
114	d2icta1	Alignment	not modelled	72.9	12	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
115	d1llib_	Alignment	not modelled	72.8	12	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
116	c2o8xA_	Alignment	not modelled	72.6	17	**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
117	c2d6yA_	Alignment	not modelled	72.5	10	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**putative tetr family regulatory protein; **PDBTitle:** crystal structure of transcriptional factor sco4008 from streptomyces2 coelicolor a3(2)
118	d2vkva1	Alignment	not modelled	72.4	30	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
119	d2croa_	Alignment	not modelled	72.2	30	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
120	d1sfxa_	Alignment	not modelled	72.2	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**TrmB-like