Phyre2

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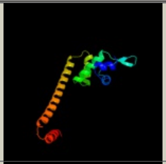
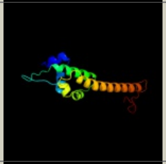
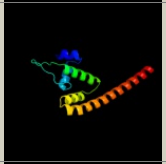
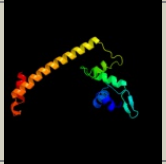
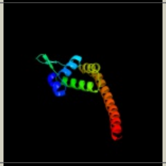
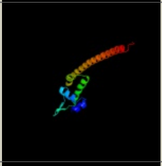
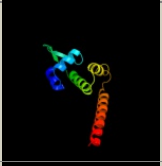
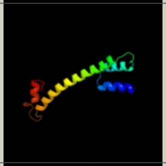
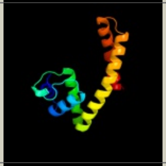
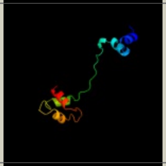
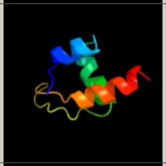
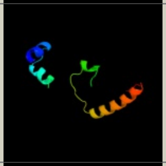
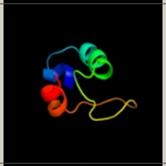
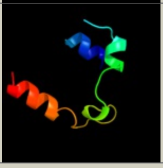
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1q06a_	Alignment		99.9	38	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**DNA-binding N-terminal domain of transcription activators
2	c2zhhA_	Alignment		99.9	25	**PDB header:**transcription **Chain:** A: **PDB Molecule:**redox-sensitive transcriptional activator soxr; **PDBTitle:** crystal structure of soxr
3	c3gp4B_	Alignment		99.9	28	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator, merr family; **PDBTitle:** crystal structure of putative merr family transcriptional regulator2 from listeria monocytogenes
4	c3hh0C_	Alignment		99.9	24	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**transcriptional regulator, merr family; **PDBTitle:** crystal strucure of a transcriptional regulator, merr family2 from bacillus cereus
5	c3gpvA_	Alignment		99.9	23	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, merr family; **PDBTitle:** crystal structure of a transcriptional regulator, merr2 family from bacillus thuringiensis
6	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
7	d1r8da_	Alignment		99.9	25	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**DNA-binding N-terminal domain of transcription activators
8	c3qaoA_	Alignment		99.9	23	**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	d1r8ea1	Alignment		99.9	22	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**DNA-binding N-terminal domain of transcription activators
10	c2vz4A_	Alignment		99.9	28	**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		99.7	16	**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	29	**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		99.6	100	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**DNA-binding N-terminal domain of transcription activators
14	c2ev2B_	Alignment		96.8	9	**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
15	c3ezfA_	Alignment		95.8	12	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**para; **PDBTitle:** partition protein
16	c1u78A_	Alignment		95.6	15	**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
17	c1z4hA_	Alignment		95.1	8	**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
18	c1hlvA_	Alignment		94.8	19	**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
19	d1j9ia_	Alignment		94.0	16	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**Terminase gpNU1 subunit domain
20	d1stza1	Alignment		93.9	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Heat-inducible transcription repressor HrcA, N-terminal domain
21	c3cuoB_	Alignment	not modelled	92.4	11	**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
22	c2wusR_	Alignment	not modelled	92.3	18	**PDB header:**structural protein **Chain:** R: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** bacterial actin mreb assembles in complex with cell shape2 protein rodz
23	d1j5ya1	Alignment	not modelled	91.6	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Biotin repressor-like
24	c3by6C_	Alignment	not modelled	90.9	19	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**predicted transcriptional regulator; **PDBTitle:** crystal structure of a transcriptional regulator from oenococcus oeni
25	c2kfsA_	Alignment	not modelled	90.8	16	**PDB header:**dna-binding protein **Chain:** A: **PDB Molecule:**conserved hypothetical regulatory protein; **PDBTitle:** nmr structure of rv2175c
26	c1stzB_	Alignment	not modelled	90.7	20	**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
27	c3jthA_	Alignment	not modelled	90.6	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription activator hlyu; **PDBTitle:** crystal structure of a transcriptional regulator hlyu from2 vibrio vulnificus cmcp6
28	d1r1ua_	Alignment	not modelled	90.3	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain

						Family: ArsR-like transcriptional regulators
29	d1biaa1	Alignment	not modelled	90.0	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Biotin repressor-like
30	c3op9A_	Alignment	not modelled	90.0	22	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**pli0006 protein; **PDBTitle:** crystal structure of transcriptional regulator from listeria innocua
31	c3clcC_	Alignment	not modelled	89.8	24	**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
32	c1r22B_	Alignment	not modelled	89.7	17	**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
33	c6paxA_	Alignment	not modelled	89.5	10	**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
34	d2jn6a1	Alignment	not modelled	89.4	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Cgl2762-like
35	d1utxa_	Alignment	not modelled	88.9	33	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
36	d1r1ta_	Alignment	not modelled	88.3	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ArsR-like transcriptional regulators
37	c2ppxA_	Alignment	not modelled	88.2	18	**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
38	d2ppxa1	Alignment	not modelled	88.2	18	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
39	d2ofya1	Alignment	not modelled	88.1	28	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
40	c3fymA_	Alignment	not modelled	87.9	10	**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
41	c3neuA_	Alignment	not modelled	87.5	26	**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
42	c3fmyA_	Alignment	not modelled	87.1	18	**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	d2b5aa1	Alignment	not modelled	87.0	28	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
44	c2kkoB_	Alignment	not modelled	86.8	13	**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.
45	d2d1ha1	Alignment	not modelled	86.6	7	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**TrmB-like
46	c2kpjA_	Alignment	not modelled	86.1	32	**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
47	d1pdnc_	Alignment	not modelled	85.5	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
48	c2oqgA_	Alignment	not modelled	85.4	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**possible transcriptional regulator, arsr family protein; **PDBTitle:** arsr-like transcriptional regulator from rhodococcus sp. rha1
49	d2hsga1	Alignment	not modelled	85.0	18	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
50	d2coba1	Alignment	not modelled	84.9	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Psq domain
51	d2htja1	Alignment	not modelled	84.3	31	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**FaeA-like
52	c3f6vA_	Alignment	not modelled	84.1	10	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**possible transcriptional regulator, arsr family **PDBTitle:** crystal structure of possible transcriptional regulator for2 arsenical resistance

53	c3bs3A_	Alignment	not modelled	82.8	18	**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
54	c3omtA_	Alignment	not modelled	82.7	9	**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.
55	c2ebyA_	Alignment	not modelled	82.6	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative hth-type transcriptional regulator ybaq; **PDBTitle:** crystal structure of a hypothetical protein from e. coli
56	c2du9A_	Alignment	not modelled	82.4	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**predicted transcriptional regulators; **PDBTitle:** crystal structure of the transcriptional factor from c.glutamicum
57	d1ulya_	Alignment	not modelled	81.9	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Hypothetical protein PH1932
58	c3pqkD_	Alignment	not modelled	81.9	13	**PDB header:**transcription **Chain:** D: **PDB Molecule:**biofilm growth-associated repressor; **PDBTitle:** crystal structure of the transcriptional repressor bigr from xylella2 fastidiosa
59	c3b7hA_	Alignment	not modelled	81.7	18	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**prophage lp1 protein 11; **PDBTitle:** crystal structure of the prophage lp1 protein 11
60	d1r69a_	Alignment	not modelled	81.7	27	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
61	c2rn7A_	Alignment	not modelled	81.4	32	**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
62	d1x57a1	Alignment	not modelled	81.2	27	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**EDF1-like
63	d1adra_	Alignment	not modelled	80.9	32	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
64	d1sq8a_	Alignment	not modelled	80.5	27	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
65	c2zkzC_	Alignment	not modelled	80.5	8	**PDB header:**transcription **Chain:** C: **PDB Molecule:**transcriptional repressor pagr; **PDBTitle:** crystal structure of the transcriptional repressor pagr of bacillus2 anthracis
66	c1zljE_	Alignment	not modelled	79.9	14	**PDB header:**transcription **Chain:** E: **PDB Molecule:**dormancy survival regulator; **PDBTitle:** crystal structure of the mycobacterium tuberculosis hypoxic2 response regulator dosr c-terminal domain
67	c1b0nA_	Alignment	not modelled	79.9	32	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**protein (sinr protein); **PDBTitle:** sinr protein/sini protein complex
68	d1ku9a_	Alignment	not modelled	79.8	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**DNA-binding protein Mj223
69	d1uxca_	Alignment	not modelled	79.4	30	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
70	c3dnvB_	Alignment	not modelled	79.3	32	**PDB header:**transcription/dna **Chain:** B: **PDB Molecule:**hth-type transcriptional regulator hipb; **PDBTitle:** mdt protein
71	c3kxaD_	Alignment	not modelled	79.3	24	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of ngo0477 from neisseria gonorrhoeae
72	d1qpza1	Alignment	not modelled	79.2	20	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
73	c3f52A_	Alignment	not modelled	79.1	27	**PDB header:**transcription activator **Chain:** A: **PDB Molecule:**clp gene regulator (clgr); **PDBTitle:** crystal structure of the clp gene regulator clgr from c. glutamicum
74	c1bdhA_	Alignment	not modelled	78.9	21	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**protein (purine repressor); **PDBTitle:** purine repressor mutant-hypoxanthine-palindromic operator2 complex
75	c3t76A_	Alignment	not modelled	78.7	27	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator vanug; **PDBTitle:** crystal structure of transcriptional regulator vanug, form ii
76	d2r1jl1	Alignment	not modelled	78.5	32	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
77	d1b0na2	Alignment	not modelled	78.4	32	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
78	d1y7ya1	Alignment	not modelled	78.2	14	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
79	c2xcjB_	Alignment	not modelled	77.7	32	**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

80	d1jt6a1	Alignment	not modelled	77.6	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
81	c3h5tA_	Alignment	not modelled	77.4	14	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, laci family; **PDBTitle:** crystal structure of a transcriptional regulator, lacI2 family protein from corynebacterium glutamicum
82	c3mlfC_	Alignment	not modelled	77.1	32	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**transcriptional regulator; **PDBTitle:** putative transcriptional regulator from staphylococcus aureus.
83	d1yioa1	Alignment	not modelled	76.8	10	**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)
84	c2o8xA_	Alignment	not modelled	76.8	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
85	c3gn5B_	Alignment	not modelled	76.5	18	**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)
86	c1j5yA_	Alignment	not modelled	76.3	25	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, biotin repressor family; **PDBTitle:** crystal structure of transcriptional regulator (tm1602) from2 thermotoga maritima at 2.3 a resolution
87	c1y9qA_	Alignment	not modelled	76.3	14	**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
88	d2icta1	Alignment	not modelled	75.7	23	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
89	d1uxda_	Alignment	not modelled	75.6	30	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
90	d1fsea_	Alignment	not modelled	75.2	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)
91	c2x48B_	Alignment	not modelled	75.2	23	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**cag38821; **PDBTitle:** orf 55 from sulfolobus islandicus rudivirus 1
92	c3trbA_	Alignment	not modelled	75.1	14	**PDB header:**dna binding protein **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
93	d2o7ta1	Alignment	not modelled	74.7	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
94	d1llib_	Alignment	not modelled	74.5	14	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
95	d1t56a1	Alignment	not modelled	74.5	30	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
96	c1x3uA_	Alignment	not modelled	74.4	14	**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	c2ef8A_	Alignment	not modelled	74.3	23	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**putative transcription factor; **PDBTitle:** crystal structure of c.ecot38is
98	c2krfB_	Alignment	not modelled	74.1	18	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulatory protein coma; **PDBTitle:** nmr solution structure of the dna binding domain of competence protein2 a
99	c3f6oB_	Alignment	not modelled	74.0	10	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**probable transcriptional regulator, arsr family **PDBTitle:** crystal structure of arsr family transcriptional regulator,2 rha00566
100	d2fbqa1	Alignment	not modelled	73.9	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
101	c2jvlA_	Alignment	not modelled	73.8	32	**PDB header:**transcription **Chain:** A: **PDB Molecule:**trmbf1; **PDBTitle:** nmr structure of the c-terminal domain of mbf1 of trichoderma reesei
102	d1rp3a2	Alignment	not modelled	73.7	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
103	d1y9qa1	Alignment	not modelled	73.5	14	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Probable transcriptional regulator VC1968, N-terminal domain
104	c3f6wE_	Alignment	not modelled	73.5	18	**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
105	c2bnoA_	Alignment	not modelled	73.3	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**epoxidase; **PDBTitle:** the structure of hydroxypropylphosphonic acid epoxidase2 from s. wedmorenis.

106	c3cecA_	Alignment	not modelled	73.3	18	**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
107	c3kjxD_	Alignment	not modelled	73.3	11	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**transcriptional regulator, laci family; **PDBTitle:** crystal structure of a transcriptional regulator, lacI2 family protein from silicibacter pomeroyi
108	d1p4wa_	Alignment	not modelled	72.5	27	**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)
109	d1lcda_	Alignment	not modelled	72.2	20	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
110	d1a04a1	Alignment	not modelled	72.2	15	**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)
111	d1mkma1	Alignment	not modelled	72.1	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Transcriptional regulator IclR, N-terminal domain
112	d2vkva1	Alignment	not modelled	72.0	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
113	d1l3la1	Alignment	not modelled	71.6	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)
114	d2croa_	Alignment	not modelled	71.5	32	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
115	c3e7lD_	Alignment	not modelled	71.4	11	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** crystal structure of sigma54 activator ntrc4's dna binding2 domain
116	d2bjca1	Alignment	not modelled	71.3	20	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
117	d1jhfa1	Alignment	not modelled	71.1	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**LexA repressor, N-terminal DNA-binding domain
118	c2auwB_	Alignment	not modelled	71.1	14	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**hypothetical protein ne0471; **PDBTitle:** crystal structure of putative dna binding protein ne0471 from2 nitrosomonas europaea atcc 19718
119	c2l8nA_	Alignment	not modelled	70.9	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
120	d1sfxa_	Alignment	not modelled	70.8	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**TrmB-like