Phyre^2

Email	l.a.kelley@imperial.ac.uk
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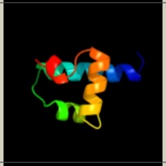
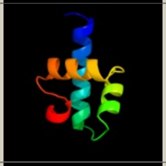
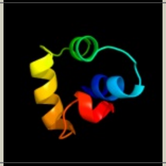
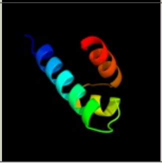
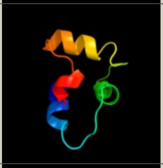
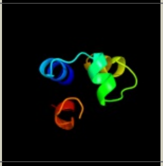
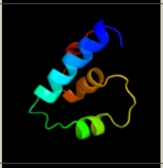
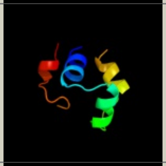
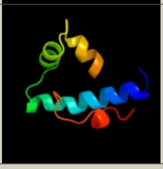
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3gbgA_	Alignment		99.8	16	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**tcp pilus virulence regulatory protein; **PDBTitle:** crystal structure of toxt from vibrio cholerae o395
2	c1d5yD_	Alignment		99.6	10	**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
3	c2k9sA_	Alignment		99.6	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**arabinose operon regulatory protein; **PDBTitle:** solution structure of dna binding domain of e. coli arac
4	c3mklB_	Alignment		99.5	16	**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
5	c3oioA_	Alignment		99.5	26	**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
6	c1bl0A_	Alignment		99.5	14	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**protein (multiple antibiotic resistance protein); **PDBTitle:** multiple antibiotic resistance protein (mara)/dna complex
7	c3oouA_	Alignment		99.5	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lin2118 protein; **PDBTitle:** the structure of a protein with unkown function from listeria innocua
8	c3mn2B_	Alignment		99.5	25	**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
9	d1bl0a2	Alignment		99.4	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**AraC type transcriptional activator
10	d1d5ya2	Alignment		99.4	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**AraC type transcriptional activator
11	c3lsgD_	Alignment		99.2	14	**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

12	c1zgwA_	Alignment		98.2	11	**PDB header:**transcription regulator/dna **Chain:** A: **PDB Molecule:**ada polyprotein; **PDBTitle:** nmr structure of e. coli ada protein in complex with dna
13	d1bl0a1	Alignment		97.4	8	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**AraC type transcriptional activator
14	d1d5ya1	Alignment		97.4	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**AraC type transcriptional activator
15	d2jn6a1	Alignment		85.8	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Cgl2762-like
16	d2croa_	Alignment		83.5	17	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
17	d1sq8a_	Alignment		82.1	20	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
18	d1lmb3_	Alignment		81.2	19	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
19	c2ewtA_	Alignment		78.4	15	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**putative dna-binding protein; **PDBTitle:** crystal structure of the dna-binding domain of bldd
20	d1llib_	Alignment		73.7	12	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
21	d2r1jl1	Alignment	not modelled	69.1	22	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
22	d1rioa_	Alignment	not modelled	67.5	19	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
23	c3clcC_	Alignment	not modelled	63.8	18	**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
24	c3t76A_	Alignment	not modelled	60.2	16	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator vanug; **PDBTitle:** crystal structure of transcriptional regulator vanug, form ii
25	c3bdnB_	Alignment	not modelled	57.1	9	**PDB header:**transcription/dna **Chain:** B: **PDB Molecule:**lambda repressor; **PDBTitle:** crystal structure of the lambda repressor
26	c3omtA_	Alignment	not modelled	55.7	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.
27	c3f6wE_	Alignment	not modelled	54.9	12	**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
28	d2hsga1	Alignment	not modelled	48.2	13	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator

29	c3gziA_	Alignment	not modelled	47.6	8	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, tetr family; **PDBTitle:** crystal structure of a transcriptional regulator of the tetr family2 (shew_3567) from shewanella loihica pv-4 at 2.05 a resolution
30	c3f52A_	Alignment	not modelled	47.5	12	**PDB header:**transcription activator **Chain:** A: **PDB Molecule:**clp gene regulator (clgr); **PDBTitle:** crystal structure of the clp gene regulator clgr from c. glutamicum
31	c2wgbB_	Alignment	not modelled	47.5	12	**PDB header:**transcription **Chain:** B: **PDB Molecule:**tetr family transcriptional repressor lfrr; **PDBTitle:** crystal structure of the tetr-like transcriptional2 regulator lfrr from mycobacterium smegmatis
32	d1b0na2	Alignment	not modelled	47.3	13	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
33	c3f1bA_	Alignment	not modelled	46.6	12	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**tetr-like transcriptional regulator; **PDBTitle:** the crystal structure of a tetr-like transcriptional regulator from2 rhodococcus sp. rha1.
34	d1r69a_	Alignment	not modelled	43.9	17	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
35	c2qtqB_	Alignment	not modelled	42.8	8	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator, tetr family; **PDBTitle:** crystal structure of a predicted dna-binding transcriptional regulator2 (saro_1072) from novosphingobium aromaticivorans dsm at 1.85 a3 resolution
36	c3ppbB_	Alignment	not modelled	41.7	13	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**putative tetr family transcription regulator; **PDBTitle:** crystal structure of a putative tetr family transcription regulator2 (shew_3104) from shewanella sp. pv-4 at 2.10 a resolution
37	c2kpjA_	Alignment	not modelled	41.2	9	**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
38	c3mvpA_	Alignment	not modelled	41.1	8	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**tetr/acrr transcriptional regulator; **PDBTitle:** crystal structure of a tetr/acrr transcriptional regulator from2 streptococcus mutans to 1.85a
39	c1vi0B_	Alignment	not modelled	40.7	13	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator; **PDBTitle:** crystal structure of a transcriptional regulator
40	d2i10a1	Alignment	not modelled	39.9	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
41	d2b5aa1	Alignment	not modelled	39.6	11	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
42	c1jumB_	Alignment	not modelled	39.2	11	**PDB header:**transcription **Chain:** B: **PDB Molecule:**hypothetical transcriptional regulator in qaca **PDBTitle:** crystal structure of the multidrug binding transcriptional2 repressor qacr bound to the natural drug berberine
43	c2nx4A_	Alignment	not modelled	38.3	13	**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.
44	d1qpza1	Alignment	not modelled	37.7	10	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
45	c2f07A_	Alignment	not modelled	37.4	5	**PDB header:**transcription **Chain:** A: **PDB Molecule:**yvdt; **PDBTitle:** crystal structure of yvdt from bacillus subtilis
46	c1ui6B_	Alignment	not modelled	37.2	5	**PDB header:**antibiotic **Chain:** B: **PDB Molecule:**a-factor receptor homolog; **PDBTitle:** crystal structure of gamma-butyrolactone receptor (arpa-like protein)
47	d1utxa_	Alignment	not modelled	36.9	12	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
48	c3bniA_	Alignment	not modelled	36.6	8	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**putative tetr-family transcriptional regulator; **PDBTitle:** crystal structure of tetr-family transcriptional regulator from2 streptomyces coelicolor
49	d2fx0a1	Alignment	not modelled	36.5	8	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
50	c2ibdB_	Alignment	not modelled	34.7	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**possible transcriptional regulator; **PDBTitle:** crystal structure of probable transcriptional regulatory protein2 rha5900
51	c2g7gA_	Alignment	not modelled	34.7	8	**PDB header:**transcription **Chain:** A: **PDB Molecule:**rha04620, putative transcriptional regulator; **PDBTitle:** the crystal structure of the putative transcriptional regulator2 rha04620 from rhodococcus sp. rha1
52	d2bjca1	Alignment	not modelled	34.4	10	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator

53	d1u2wa1	Alignment	not modelled	34.4	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ArsR-like transcriptional regulators
54	d2icta1	Alignment	not modelled	33.5	11	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
55	c3nnrA_	Alignment	not modelled	33.4	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, tetr family; **PDBTitle:** crystal structure of a tetr-family transcriptional regulator2 (maqu_3571) from marinobacter aquaeolei vt8 at 2.49 a resolution
56	d1nera_	Alignment	not modelled	33.4	20	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
57	c3anpD_	Alignment	not modelled	32.4	13	**PDB header:**transcription **Chain:** D: **PDB Molecule:**transcriptional repressor, tetr family; **PDBTitle:** crystal structure of thermus thermophilus fadr, a tetr familly2 transcriptional repressor, in complex with lauroyl-coa.
58	d1r1ua_	Alignment	not modelled	32.3	6	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ArsR-like transcriptional regulators
59	c1y9qA_	Alignment	not modelled	31.9	15	**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
60	c2raeA_	Alignment	not modelled	31.9	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, acrr family protein; **PDBTitle:** crystal structure of a tetr/acrr family transcriptional regulator from2 rhodococcus sp. rha1
61	c3he0A_	Alignment	not modelled	31.9	8	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, tetr family; **PDBTitle:** the structure of a putative transcriptional regulator tetr family2 protein from vibrio parahaemolyticus.
62	c2rasB_	Alignment	not modelled	31.3	8	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator, tetr family; **PDBTitle:** crystal structure of a putative tetr/acrr family transcriptional2 regulator (saro_0558) from novosphingobium aromaticivorans dsm at3 1.80 a resolution
63	d1efaa1	Alignment	not modelled	31.2	13	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
64	d1jhfa1	Alignment	not modelled	31.2	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**LexA repressor, N-terminal DNA-binding domain
65	c2eh3A_	Alignment	not modelled	30.8	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator; **PDBTitle:** crystal structure of aq_1058, a transcriptional regulator (terr/acrr2 family) from aquifex aeolicus vf5
66	c3bcgA_	Alignment	not modelled	30.4	13	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**hth-type transcriptional regulator acrr; **PDBTitle:** conformational changes of the acrr regulator reveal a2 mechanism of induction
67	c3cjdB_	Alignment	not modelled	30.1	5	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator, tetr family; **PDBTitle:** crystal structure of putative tetr transcriptional regulator2 (yp_510936.1) from jannaschia sp. ccs1 at 1.79 a resolution
68	c3o60A_	Alignment	not modelled	30.0	8	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lin0861 protein; **PDBTitle:** the crystal structure of lin0861 from listeria innocua to 2.8a
69	c2i10A_	Alignment	not modelled	29.9	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative tetr transcriptional regulator; **PDBTitle:** putative tetr transcriptional regulator from rhodococcus sp. rha1
70	c2wuiA_	Alignment	not modelled	29.8	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator; **PDBTitle:** crystal structure of mexz, a key repressor responsible for2 antibiotic resistance in pseudomonas aeruginosa.
71	c3dcfB_	Alignment	not modelled	29.6	8	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator of the tetr/acrr **PDBTitle:** crystal structure of transcriptional regulator of the2 tetr/acrr family (yp_290855.1) from thermobifida fusca yx-3 er1 at 2.50 a resolution
72	c3bs3A_	Alignment	not modelled	29.3	11	**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
73	c3bruA_	Alignment	not modelled	29.2	8	**PDB header:**transcription **Chain:** A: **PDB Molecule:**regulatory protein, tetr family; **PDBTitle:** crystal structure of regulatory protein tetr from rhodobacter2 sphaeroides
74	c2jk3A_	Alignment	not modelled	29.2	8	**PDB header:**transcription **Chain:** A: **PDB Molecule:**hemolysin ii regulatory protein; **PDBTitle:** crystal structure of the hlyiir mutant protein with2 residues 169-186 substituted by gssgssg linker
75	c2fq4A_	Alignment	not modelled	29.0	14	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, tetr family; **PDBTitle:** the crystal structure of the transcriptional regulator (tetr family)2 from bacillus cereus
76	c3pasA_	Alignment	not modelled	28.9	18	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**tetr family transcription regulator; **PDBTitle:** crystal structure of a tetr family transcription regulator (maqu_1417)2 from marinobacter aquaeolei vt8 at 1.90 a resolution
77	c3b81A_	Alignment	not modelled	28.6	13	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, acrr family; **PDBTitle:** crystal structure of predicted dna-binding transcriptional regulator2 of tetr/acrr family (np_350189.1) from clostridium

					acetobutylicum at3 2.10 a resolution
78	c2genA_	Alignment	not modelled	28.6	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**probable transcriptional regulator; **PDBTitle:** structural genomics, the crystal structure of a probable2 transcriptional regulator from pseudomonas aeruginosa pao1
79	c2fbqA_	Alignment	not modelled	28.4	5	**PDB header:**transcription **Chain:** A: **PDB Molecule:**probable transcriptional regulator; **PDBTitle:** the crystal structure of transcriptional regulator pa3006
80	c3dewA_	Alignment	not modelled	28.4	13	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, tetr family; **PDBTitle:** the structure of a putative tetr family transcriptional regulator from2 geobacter sulfurreducens pca.
81	c2hytA_	Alignment	not modelled	28.4	5	**PDB header:**transcription **Chain:** A: **PDB Molecule:**tetr-family transcriptional regulator; **PDBTitle:** crystal structure of a tetr-family transcriptional regulator (eca1819)2 from pectobacterium atrosepticum at 1.64 a resolution
82	c3on4D_	Alignment	not modelled	27.8	11	**PDB header:**transcription **Chain:** D: **PDB Molecule:**transcriptional regulator, tetr family; **PDBTitle:** crystal structure of tetr transcriptional regulator from legionella2 pneumophila
83	c3qkxB_	Alignment	not modelled	27.7	8	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**uncharacterized hth-type transcriptional regulator hi_0893; **PDBTitle:** crystal structure of a tetr-family transcriptional regulator (hi0893)2 from haemophilus influenzae rd at 2.35 a resolution
84	c3lwjA_	Alignment	not modelled	27.5	3	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**putative tetr-family transcriptional regulator; **PDBTitle:** crystal structure of putative tetr-family transcriptional regulator2 (yp_752756.1) from syntrophomonas wolfei str. goettingen at 2.07 a3 resolution
85	d1adra_	Alignment	not modelled	27.5	16	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
86	d1j5ya1	Alignment	not modelled	27.4	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Biotin repressor-like
87	c3s5rA_	Alignment	not modelled	27.3	13	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**transcriptional regulator tetr family; **PDBTitle:** crystal structure of a putative transcriptional regulator of the tetr2 family (syn_02108) from syntrophus aciditrophicus at 2.60 a3 resolution
88	c2gfnA_	Alignment	not modelled	27.3	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**hth-type transcriptional regulator pksa related protein; **PDBTitle:** crystal structure of hth-type transcriptional regulator pksa related2 protein from rhodococcus sp. rha1
89	d1y9qa1	Alignment	not modelled	27.3	14	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Probable transcriptional regulator VC1968, N-terminal domain
90	c2dg7A_	Alignment	not modelled	26.7	11	**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)
91	c3qbmA_	Alignment	not modelled	25.5	11	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**tetr transcriptional regulator; **PDBTitle:** crystal structure of a tetr transcriptional regulator (caur_2221) from2 chloroflexus aurantiacus j-10-fl at 1.80 a resolution
92	c2kz3A_	Alignment	not modelled	25.4	14	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein rad51l3; **PDBTitle:** backbone 1h, 13c, and 15n chemical shift assignments for human rad51d2 from 1 to 83
93	c3nxcA_	Alignment	not modelled	25.3	19	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**hth-type protein slma; **PDBTitle:** molecular mechanism by which the escherichia coli nucleoid occlusion2 factor, slma, keeps cytokinesis in check
94	d1lcda_	Alignment	not modelled	25.2	13	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
95	c3bhqB_	Alignment	not modelled	24.9	8	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator; **PDBTitle:** crystal structure of a putative tetr-family transcriptional regulator2 (mlr_4833) from mesorhizobium loti maff303099 at 1.54 a resolution
96	c2r0qF_	Alignment	not modelled	24.8	11	**PDB header:**recombination/dna **Chain:** F: **PDB Molecule:**putative transposon tn552 dna-invertase bin3; **PDBTitle:** crystal structure of a serine recombinase- dna regulatory2 complex
97	c2uxoB_	Alignment	not modelled	24.6	8	**PDB header:**transcription **Chain:** B: **PDB Molecule:**hth-type transcriptional regulator ttgr; **PDBTitle:** ttgr in complex with tetracycline
98	d1r1ta_	Alignment	not modelled	24.5	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ArsR-like transcriptional regulators
99	c3cwrA_	Alignment	not modelled	24.4	9	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, tetr family; **PDBTitle:** crystal structure of transcriptional regulator of tetr2 family (yp_425770.1) from rhodospirillum rubrum atcc 111703 at 1.50 a resolution
100	d1z0xa1	Alignment	not modelled	24.0	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
101	c3cdlA_	Alignment	not modelled	23.5	8	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator aefr; **PDBTitle:** crystal structure of a tetr family transcriptional regulator

						from2 pseudomonas syringae pv. tomato str. dc3000
102	c3e7lD_	Alignment	not modelled	23.5	13	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** crystal structure of sigma54 activator ntrc4's dna binding2 domain
103	c2iaiA_	Alignment	not modelled	23.3	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative transcriptional regulator sco3833; **PDBTitle:** crystal structure of sco3833, a member of the tetr transcriptional2 regulator family from streptomyces coelicolor a3
104	c2rekA_	Alignment	not modelled	23.2	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative tetr-family transcriptional regulator; **PDBTitle:** crystal structure of tetr-family transcriptional regulator
105	c3e7qB_	Alignment	not modelled	23.2	16	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator; **PDBTitle:** the crystal structure of the putative transcriptional regulator from2 pseudomonas aeruginosa pao1
106	c3colB_	Alignment	not modelled	23.2	18	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**putative transcription regulator; **PDBTitle:** crystal structure of putative transcription regulator from2 lactobacillus plantarum
107	d2g3ba1	Alignment	not modelled	23.1	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
108	d1ui5a1	Alignment	not modelled	22.9	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
109	c1pb6D_	Alignment	not modelled	22.7	11	**PDB header:**transcription **Chain:** D: **PDB Molecule:**hypothetical transcriptional regulator ycdc; **PDBTitle:** crystal structure of hypothetical transcriptional regulator ycdc
110	c3eupA_	Alignment	not modelled	22.6	16	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, tetr family; **PDBTitle:** the crystal structure of the transcriptional regulator, tetr family2 from cytophaga hutchinsonii
111	d1nvma1	Alignment	not modelled	22.3	17	**Fold:**RuvA C-terminal domain-like **Superfamily:**post-HMGL domain-like **Family:**DmpG/LeuA communication domain-like
112	c2oerA_	Alignment	not modelled	22.2	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**probable transcriptional regulator; **PDBTitle:** probable transcriptional regulator from pseudomonas2 aeruginosa
113	c2jscB_	Alignment	not modelled	22.2	9	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator rv1994c/mt2050; **PDBTitle:** nmr structure of the cadmium metal-sensor cmtr from mycobacterium2 tuberculosis
114	c1rktA_	Alignment	not modelled	21.7	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**protein yfir; **PDBTitle:** crystal structure of yfir, a putative transcriptional regulator from2 bacillus subtilis
115	c2rn7A_	Alignment	not modelled	21.7	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
116	c2oqgA_	Alignment	not modelled	21.6	9	**PDB header:**transcription **Chain:** A: **PDB Molecule:**possible transcriptional regulator, arsr family protein; **PDBTitle:** arsr-like transcriptional regulator from rhodococcus sp. rha1
117	c3iwfA_	Alignment	not modelled	21.6	9	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcription regulator rpir family; **PDBTitle:** the crystal structure of the n-terminal domain of a rpir2 transcriptional regulator from staphylococcus epidermidis to 1.4a
118	c2yvhA_	Alignment	not modelled	21.5	18	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**transcriptional regulator; **PDBTitle:** crystal structure of the operator-binding form of the multi-drug2 binding transcriptional repressor cgmr
119	c2iu5A_	Alignment	not modelled	21.5	3	**PDB header:**transcription **Chain:** A: **PDB Molecule:**hth-type dhaklm operon transcriptional activator dhas; **PDBTitle:** dihydroxyacetone kinase operon activator dhas
120	c2l8nA_	Alignment	not modelled	21.4	7	**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