Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P0ACH5
Date	Thu Jan 5 11:18:11 GMT 2012
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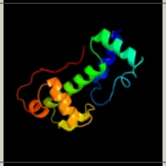
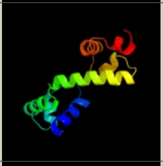
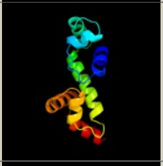
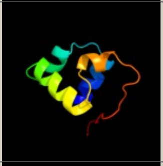
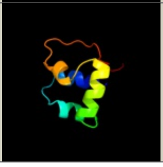
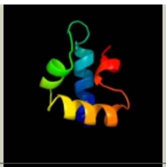
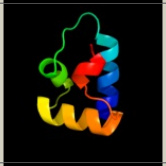
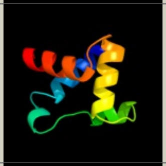
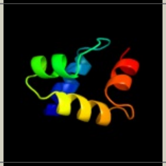
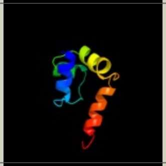
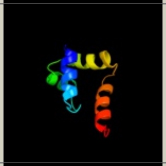
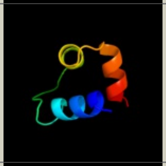
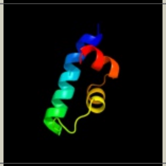
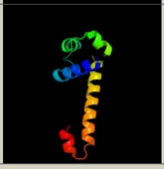
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1bl0A_	Alignment		100.0	100	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**protein (multiple antibiotic resistance protein); **PDBTitle:** multiple antibiotic resistance protein (mara)/dna complex
2	c3gbgA_	Alignment		100.0	16	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**tcp pilus virulence regulatory protein; **PDBTitle:** crystal structure of toxt from vibrio cholerae o395
3	c1d5yD_	Alignment		99.9	45	**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
4	c3oouA_	Alignment		99.9	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lin2118 protein; **PDBTitle:** the structure of a protein with unkown function from listeria innocua
5	c3oioA_	Alignment		99.9	25	**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	c2k9sA_	Alignment		99.9	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**arabinose operon regulatory protein; **PDBTitle:** solution structure of dna binding domain of e. coli arac
7	c3mklB_	Alignment		99.9	18	**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
8	c3mn2B_	Alignment		99.9	17	**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	c3lsgD_	Alignment		99.8	25	**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
10	d1bl0a2	Alignment		99.5	100	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**AraC type transcriptional activator
11	d1d5ya2	Alignment		99.5	37	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**AraC type transcriptional activator

12	d1bl0a1	Alignment		99.1	100	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**AraC type transcriptional activator
13	d1d5ya1	Alignment		99.0	58	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**AraC type transcriptional activator
14	c1zgwA_	Alignment		98.8	24	**PDB header:**transcription regulator/dna **Chain:** A: **PDB Molecule:**ada polyprotein; **PDBTitle:** nmr structure of e. coli ada protein in complex with dna
15	c3iwfA_	Alignment		95.8	13	**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
16	c2o3fC_	Alignment		94.3	12	**PDB header:**transcription **Chain:** C: **PDB Molecule:**putative hth-type transcriptional regulator ybbh; **PDBTitle:** structural genomics, the crystal structure of the n-2 terminal domain of the putative transcriptional regulator3 ybbh from bacillus subtilis subsp. subtilis str. 168.
17	d2o3fa1	Alignment		94.3	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**RpiR-like
18	d1j5ya1	Alignment		94.1	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Biotin repressor-like
19	d1ui5a1	Alignment		93.6	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
20	c3on4D_	Alignment		93.6	10	**PDB header:**transcription **Chain:** D: **PDB Molecule:**transcriptional regulator, tetr family; **PDBTitle:** crystal structure of tetr transcriptional regulator from legionella2 pneumophila
21	d1jt6a1	Alignment	not modelled	93.4	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
22	d2gfna1	Alignment	not modelled	93.3	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
23	d2fbqa1	Alignment	not modelled	93.3	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
24	d1v7ba1	Alignment	not modelled	93.2	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
25	c3f1bA_	Alignment	not modelled	93.2	15	**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.
26	c2gfnA_	Alignment	not modelled	93.2	16	**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
27	c2f07A_	Alignment	not modelled	92.8	9	**PDB header:**transcription **Chain:** A: **PDB Molecule:**yvdt; **PDBTitle:** crystal structure of yvdt from bacillus subtilis
28	d2fx0a1	Alignment	not modelled	92.6	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
						PDB header:transcription/dna

29	c1bdhA_	Alignment	not modelled	92.6	12	**Chain:** A: **PDB Molecule:**protein (purine repressor); **PDBTitle:** purine repressor mutant-hypoxanthine-palindromic operator2 complex
30	c3s5rA_	Alignment	not modelled	92.2	9	**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
31	c1jumB_	Alignment	not modelled	92.1	17	**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
32	c3ppbB_	Alignment	not modelled	92.0	14	**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
33	c3h5tA_	Alignment	not modelled	92.0	23	**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
34	c3dpjB_	Alignment	not modelled	91.8	14	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**transcription regulator, tetr family; **PDBTitle:** the crystal structure of a tetr transcription regulator2 from silicibacter pomeroyi dss
35	d1sgma1	Alignment	not modelled	91.8	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
36	c2raeA_	Alignment	not modelled	91.8	20	**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
37	c2dg7A_	Alignment	not modelled	91.6	14	**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)
38	d2fq4a1	Alignment	not modelled	91.5	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
39	d2hsga1	Alignment	not modelled	91.4	9	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
40	d3c07a1	Alignment	not modelled	91.3	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
41	c3gziA_	Alignment	not modelled	91.3	13	**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
42	d2i10a1	Alignment	not modelled	91.2	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
43	d1t56a1	Alignment	not modelled	91.1	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
44	d2vkea1	Alignment	not modelled	91.1	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
45	c2nx4A_	Alignment	not modelled	91.0	11	**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.
46	d2jn6a1	Alignment	not modelled	91.0	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Cgl2762-like
47	c2yvhA_	Alignment	not modelled	90.9	16	**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
48	d2np5a1	Alignment	not modelled	90.9	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
49	c2fbqA_	Alignment	not modelled	90.9	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**probable transcriptional regulator; **PDBTitle:** the crystal structure of transcriptional regulator pa3006
50	c2g7sA_	Alignment	not modelled	90.8	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, tetr family; **PDBTitle:** the crystal structure of transcriptional regulator, tetr family, from2 agrobacterium tumefaciens
51	c3geuC_	Alignment	not modelled	90.7	15	**PDB header:**cell adhesion **Chain:** C: **PDB Molecule:**intercellular adhesion protein r; **PDBTitle:** crystal structure of icar from staphylococcus aureus, a member of the2 tetracycline repressor protein family
52	d2g7sa1	Alignment	not modelled	90.7	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
53	c3lwjA_	Alignment	not modelled	90.7	11	**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
54	d1mkma1	Alignment	not modelled	90.6	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Transcriptional regulator IclR, N-terminal domain
55	c2g3bB_	Alignment	not modelled	90.6	20	**PDB header:**transcription **Chain:** B: **PDB Molecule:**putative tetr-family transcriptional regulator; **PDBTitle:** crystal structure of putative tetr-family transcriptional regulator2 from rhodococcus sp.
56	c2eh3A_	Alignment	not modelled	90.5	17	**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
57	c2jk3A_	Alignment	not modelled	90.5	11	**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
58	d1biaa1	Alignment	not modelled	90.5	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Biotin repressor-like
59	c1u78A_	Alignment	not modelled	90.5	13	**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
60	c3iuvA_	Alignment	not modelled	90.4	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized tetr family protein; **PDBTitle:** the structure of a member of tetr family (sco1917) from2 streptomyces coelicolor a3
61	d2d6ya1	Alignment	not modelled	90.3	7	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
62	d2g3ba1	Alignment	not modelled	90.3	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
63	d1qpza1	Alignment	not modelled	90.3	10	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
64	d2gena1	Alignment	not modelled	90.2	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
65	c3cwrA_	Alignment	not modelled	90.2	13	**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
66	d2id3a1	Alignment	not modelled	90.2	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
67	d1pb6a1	Alignment	not modelled	90.0	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
68	c3b6aC_	Alignment	not modelled	89.8	13	**PDB header:**transcription **Chain:** C: **PDB Molecule:**actr protein; **PDBTitle:** crystal structure of the streptomyces coelicolor tetr2 family protein actr in complex with actinorhodin
69	c2d6yA_	Alignment	not modelled	89.8	7	**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)
70	c3bruA_	Alignment	not modelled	89.8	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**regulatory protein, tetr family; **PDBTitle:** crystal structure of regulatory protein tetr from rhodobacter2 sphaeroides
71	c2fq4A_	Alignment	not modelled	89.7	15	**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
72	c2qtqB_	Alignment	not modelled	89.7	14	**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
73	c2pbxB_	Alignment	not modelled	89.6	11	**PDB header:**transcription **Chain:** B: **PDB Molecule:**hemagglutinin/protease regulatory protein; **PDBTitle:** vibrio cholerae hapr
74	c3bjbE_	Alignment	not modelled	89.6	16	**PDB header:**transcription regulator **Chain:** E: **PDB Molecule:**probable transcriptional regulator, tetr family protein; **PDBTitle:** crystal structure of a tetr transcriptional regulator from rhodococcus2 sp. rha1
75	c3qbmA_	Alignment	not modelled	89.5	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
76	c2of7A_	Alignment	not modelled	89.5	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative tetr-family transcriptional regulator; **PDBTitle:** structural genomics, the crystal structure of a tetr-family2 transcriptional regulator from streptomyces coelicolor a3
77	c2np5A_	Alignment	not modelled	89.4	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator; **PDBTitle:** crystal structure of a transcriptional regulator (rha1_ro04179) from2 rhodococcus sp. rha1.
						PDB header:transcription

78	c2hytA_	Alignment	not modelled	89.3	11	**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
79	c3e7qB_	Alignment	not modelled	89.3	12	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator; **PDBTitle:** the crystal structure of the putative transcriptional regulator from2 pseudomonas aeruginosa pao1
80	c2ibdB_	Alignment	not modelled	89.3	6	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**possible transcriptional regulator; **PDBTitle:** crystal structure of probable transcriptional regulatory protein2 rha5900
81	d1lcda_	Alignment	not modelled	89.3	19	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
82	c3dewA_	Alignment	not modelled	89.3	9	**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.
83	d2bjca1	Alignment	not modelled	89.3	19	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
84	c2zcxA_	Alignment	not modelled	89.3	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**tetr-family transcriptional regulator; **PDBTitle:** crystal structure of tetr family transcriptional regulator2 sco7815
85	c1vi0B_	Alignment	not modelled	89.2	16	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator; **PDBTitle:** crystal structure of a transcriptional regulator
86	c3dcfB_	Alignment	not modelled	89.2	17	**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
87	c3kkcB_	Alignment	not modelled	89.2	10	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**tetr family transcriptional regulator; **PDBTitle:** the crystal structure of tetr transcriptional regulator from2 streptococcus agalactiae 2603v
88	d1efaa1	Alignment	not modelled	89.1	19	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
89	c2wuiA_	Alignment	not modelled	89.1	7	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator; **PDBTitle:** crystal structure of mexz, a key repressor responsible for2 antibiotic resistance in pseudomonas aeruginosa.
90	c1sgmA_	Alignment	not modelled	89.1	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative hth-type transcriptional regulator yxaf; **PDBTitle:** crystal structure of hypothetical protein yxaf
91	c3c07B_	Alignment	not modelled	89.1	11	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**putative tetr-family transcriptional regulator; **PDBTitle:** crystal structure of a tetr family transcriptional regulator from2 streptomyces coelicolor a3(2)
92	c3anpD_	Alignment	not modelled	89.0	2	**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.
93	c3he0A_	Alignment	not modelled	89.0	17	**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.
94	c3kjxD_	Alignment	not modelled	89.0	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
95	d2hyja1	Alignment	not modelled	88.9	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
96	d2id6a1	Alignment	not modelled	88.8	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
97	c2id3A_	Alignment	not modelled	88.8	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** crystal structure of transcriptional regulator sco5951 from2 streptomyces coelicolor a3(2)
98	d2cg4a1	Alignment	not modelled	88.7	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
99	c3bniA_	Alignment	not modelled	88.6	17	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**putative tetr-family transcriptional regulator; **PDBTitle:** crystal structure of tetr-family transcriptional regulator from2 streptomyces coelicolor
100	d1jhfa1	Alignment	not modelled	88.6	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**LexA repressor, N-terminal DNA-binding domain
101	c3bhqB_	Alignment	not modelled	88.6	20	**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
102	d1rp3a1	Alignment	not modelled	88.6	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma3 domain
103	d1vi0a1	Alignment	not modelled	88.4	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like

						Family: Tetracyclin repressor-like, N-terminal domain
104	c2kpjA_	Alignment	not modelled	88.2	14	**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
105	c3eusB_	Alignment	not modelled	88.2	10	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**dna-binding protein; **PDBTitle:** the crystal structure of the dna binding protein from silicibacter2 pomeroyi
106	c2guhA_	Alignment	not modelled	88.2	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative tetr-family transcriptional regulator; **PDBTitle:** crystal structure of the putative tetr-family transcriptional2 regulator from rhodococcus sp. rha1
107	c2hxiA_	Alignment	not modelled	88.1	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** structural genomics, the crystal structure of a putative2 transcriptional regulator from streptomyces coelicolor a3(2)
108	c3r0aB_	Alignment	not modelled	88.1	14	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** possible transcriptional regulator from methanosarcina mazei go1 (gi2 21227196)
109	c3bcgA_	Alignment	not modelled	88.1	17	**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
110	c3g7rB_	Alignment	not modelled	88.1	7	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** crystal structure of sco4454, a tetr-family transcriptional2 regulator from streptomyces coelicolor
111	d2hkua1	Alignment	not modelled	88.0	5	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
112	c1j5yA_	Alignment	not modelled	88.0	18	**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
113	d2o7ta1	Alignment	not modelled	88.0	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
114	d2oi8a1	Alignment	not modelled	87.9	30	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
115	c2genA_	Alignment	not modelled	87.8	20	**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
116	c2hyjA_	Alignment	not modelled	87.8	10	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative tetr-family transcriptional regulator; **PDBTitle:** the crystal structure of a tetr-family transcriptional regulator from2 streptomyces coelicolor
117	c3jsjC_	Alignment	not modelled	87.7	12	**PDB header:**transcription **Chain:** C: **PDB Molecule:**putative tetr-family transcriptional regulator; **PDBTitle:** crystal structure of a putative tetr-transcriptional regulator2 (sav143) from streptomyces avermitilis ma-4680 at 2.10 a resolution
118	c3nnrA_	Alignment	not modelled	87.7	19	**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
119	d2vkva1	Alignment	not modelled	87.7	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
120	c2zb9A_	Alignment	not modelled	87.5	24	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** crystal structure of tetr family transcription regulator2 sco0332