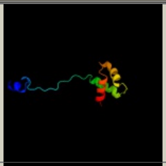
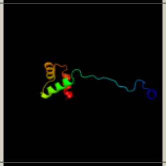
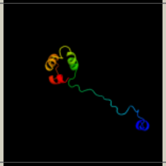
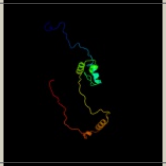
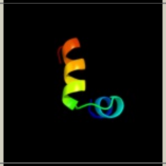
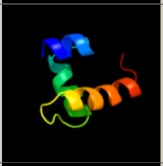
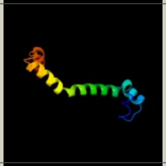
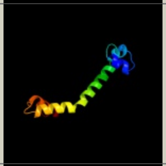
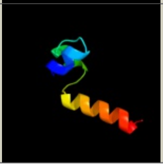
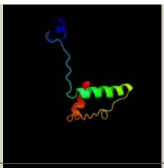
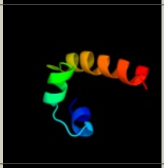
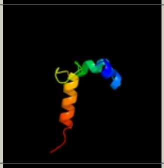
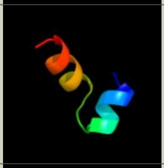
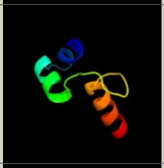
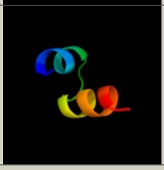
Phyre^{2}

Email	l.a.kelley@imperial.ac.uk
Description	P75680
Date	Thu Jan 5 12:12:59 GMT 2012
Unique Job ID	bf09233880d17cea

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1u78A_	Alignment		96.3	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
2	c6paxA_	Alignment		95.6	8	**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
3	d1pdnc_	Alignment		94.3	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
4	c3hosA_	Alignment		93.8	10	**PDB header:**transferase, dna binding protein/dna **Chain:** A: **PDB Molecule:**transposable element mariner, complete cds; **PDBTitle:** crystal structure of the mariner mos1 paired end complex with mg
5	c3hefB_	Alignment		91.5	23	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**gene 1 protein; **PDBTitle:** crystal structure of the bacteriophage sf6 terminase small2 subunit
6	c1umqA_	Alignment		88.6	8	**PDB header:**dna-binding protein **Chain:** A: **PDB Molecule:**photosynthetic apparatus regulatory protein; **PDBTitle:** solution structure and dna binding of the effector domain2 from the global regulator prra(rega) from r. sphaeroides:3 insights into dna binding specificity
7	d1umqa_	Alignment		88.6	8	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
8	c1z4hA_	Alignment		86.7	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
9	c2ao9H_	Alignment		86.6	14	**PDB header:**structural genomics, unknown function **Chain:** H: **PDB Molecule:**phage protein; **PDBTitle:** structural genomics, the crystal structure of a phage protein2 (phbc6a51) from bacillus cereus atcc 14579
10	d2ao9a1	Alignment		86.2	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Nanomeric phage protein-like
11	d1t56a1	Alignment		85.7	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain

12	c1hlvA_	Alignment		85.3	13	**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
13	d2fbqa1	Alignment		84.7	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
14	d2g3ba1	Alignment		84.4	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
15	d2id3a1	Alignment		84.1	8	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
16	d2jn6a1	Alignment		83.5	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Cgl2762-like
17	d1etxa_	Alignment		83.3	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
18	d1jt6a1	Alignment		82.7	3	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
19	d1vi0a1	Alignment		82.6	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
20	d1fipa_	Alignment		81.4	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
21	d1v7ba1	Alignment	not modelled	81.0	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
22	d2o7ta1	Alignment	not modelled	81.0	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
23	d1aoya_	Alignment	not modelled	80.6	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Arginine repressor (ArgR), N-terminal DNA-binding domain
24	d2np5a1	Alignment	not modelled	80.5	8	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
25	c3f1bA_	Alignment	not modelled	80.4	0	**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	d2vkva1	Alignment	not modelled	80.1	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
27	d3c07a1	Alignment	not modelled	79.8	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
28	c3ppbB_	Alignment	not modelled	79.6	17	**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

29	d2d6ya1	Alignment	not modelled	79.5	3	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
30	d1pb6a1	Alignment	not modelled	79.4	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
31	d2vkea1	Alignment	not modelled	79.3	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
32	c1vi0B_	Alignment	not modelled	79.0	17	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator; **PDBTitle:** crystal structure of a transcriptional regulator
33	c3g56A_	Alignment	not modelled	78.0	11	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**regulator of macrolide 2'-phosphotransferase i; **PDBTitle:** structure of the macrolide biosensor protein, mphr(a)
34	c2gfnA_	Alignment	not modelled	77.9	11	**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
35	c3o60A_	Alignment	not modelled	77.5	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lin0861 protein; **PDBTitle:** the crystal structure of lin0861 from listeria innocua to 2.8a
36	c3bniA_	Alignment	not modelled	77.3	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
37	d2hyja1	Alignment	not modelled	76.9	8	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
38	c3kkcB_	Alignment	not modelled	76.9	14	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**tetr family transcriptional regulator; **PDBTitle:** the crystal structure of tetr transcriptional regulator from2 streptococcus agalactiae 2603v
39	c2id3A_	Alignment	not modelled	76.9	6	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** crystal structure of transcriptional regulator sco5951 from2 streptomyces coelicolor a3(2)
40	c3b81A_	Alignment	not modelled	76.7	6	**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
41	c2hytA_	Alignment	not modelled	76.3	14	**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
42	d2id6a1	Alignment	not modelled	76.2	6	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
43	d1g2ha_	Alignment	not modelled	76.2	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
44	c3cjdB_	Alignment	not modelled	76.1	8	**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
45	d1z0xa1	Alignment	not modelled	76.0	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
46	c2nx4A_	Alignment	not modelled	75.8	14	**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.
47	d1rzsa_	Alignment	not modelled	75.7	12	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
48	d1rkta1	Alignment	not modelled	75.6	8	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
49	c3lwjA_	Alignment	not modelled	75.1	8	**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
50	c2eh3A_	Alignment	not modelled	75.1	3	**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
51	c3e7lD_	Alignment	not modelled	75.0	10	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** crystal structure of sigma54 activator ntrc4's dna binding2 domain
52	c2zb9A_	Alignment	not modelled	74.6	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** crystal structure of tetr family transcription regulator2 sco0332
53	d1stza1	Alignment	not modelled	74.6	7	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Heat-inducible transcription repressor HrcA, N-terminal

						domain
54	c3pasA_	Alignment	not modelled	74.5	8	**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
55	d2fq4a1	Alignment	not modelled	74.3	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
56	d2g7sa1	Alignment	not modelled	74.3	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
57	c2ibdB_	Alignment	not modelled	74.2	6	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**possible transcriptional regulator; **PDBTitle:** crystal structure of probable transcriptional regulatory protein2 rha5900
58	d2fd5a1	Alignment	not modelled	74.0	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
59	c3mnlA_	Alignment	not modelled	74.0	11	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulatory protein (probably tetr-family); **PDBTitle:** the crystal structure of kstr (rv3574) from mycobacterium tuberculosis2 h37rv
60	c3e7qB_	Alignment	not modelled	73.9	19	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator; **PDBTitle:** the crystal structure of the putative transcriptional regulator from2 pseudomonas aeruginosa pao1
61	c2o8kA_	Alignment	not modelled	73.9	16	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**rna polymerase sigma factor rpon; **PDBTitle:** nmr structure of the sigma-54 rpon domain bound to the-242 promoter element
62	c3cwrA_	Alignment	not modelled	73.8	11	**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
63	c3c2bA_	Alignment	not modelled	73.3	17	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, tetr family; **PDBTitle:** crystal structure of tetr transcriptional regulator from agrobacterium2 tumefaciens
64	c3ni7A_	Alignment	not modelled	73.3	6	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**bacterial regulatory proteins, tetr family; **PDBTitle:** crystal structure of the tetr transcriptional regulator from2 nitrosomonas europaea atcc 19718
65	c3bhqB_	Alignment	not modelled	73.1	11	**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
66	c2o7tA_	Alignment	not modelled	73.0	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator; **PDBTitle:** crystal structure of a tetr family transcriptional regulator2 (ncgl1578, cgl1640) from corynebacterium glutamicum at 2.10 a3 resolution
67	c1bjzA_	Alignment	not modelled	72.9	17	**PDB header:**transcription regulation **Chain:** A: **PDB Molecule:**tetracycline repressor; **PDBTitle:** tetracycline chelated mg2+-ion initiates helix unwinding for tet2 repressor induction
68	c2np5A_	Alignment	not modelled	72.9	8	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator; **PDBTitle:** crystal structure of a transcriptional regulator (rha1_ro04179) from2 rhodococcus sp. rha1.
69	c2rekA_	Alignment	not modelled	72.6	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative tetr-family transcriptional regulator; **PDBTitle:** crystal structure of tetr-family transcriptional regulator
70	d2gfna1	Alignment	not modelled	72.4	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
71	c3anpD_	Alignment	not modelled	72.3	17	**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.
72	c2iu5A_	Alignment	not modelled	72.1	6	**PDB header:**transcription **Chain:** A: **PDB Molecule:**hth-type dhaklm operon transcriptional activator dhas; **PDBTitle:** dihydroxyacetone kinase operon activator dhas
73	c3dcfB_	Alignment	not modelled	71.8	14	**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
74	c2genA_	Alignment	not modelled	71.6	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
75	d1ui5a1	Alignment	not modelled	71.5	6	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
76	d2i10a1	Alignment	not modelled	71.4	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
77	c3geuC_	Alignment	not modelled	71.4	8	**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
78	d2oi8a1	Alignment	not modelled	71.3	8	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like

						Family: Tetracyclin repressor-like, N-terminal domain
79	d2iu5a1	Alignment	not modelled	71.0	6	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
80	c3qkxB_	Alignment	not modelled	70.8	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
81	c2zcxA_	Alignment	not modelled	70.8	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**tetr-family transcriptional regulator; **PDBTitle:** crystal structure of tetr family transcriptional regulator2 sco7815
82	c2dg8D_	Alignment	not modelled	70.7	19	**PDB header:**gene regulation **Chain:** D: **PDB Molecule:**putative tetr-family transcriptional regulatory protein; **PDBTitle:** crystal structure of the putative trasncriptional regulator sco75182 from streptomyces coelicolor a3(2)
83	c2oerA_	Alignment	not modelled	70.4	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**probable transcriptional regulator; **PDBTitle:** probable transcriptional regulator from pseudomonas2 aeruginosa
84	c3mvpA_	Alignment	not modelled	70.2	6	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**tetr/acrr transcriptional regulator; **PDBTitle:** the crystal structure of a tetr/acrr transcriptional regulator from2 streptococcus mutans to 1.85a
85	c3omtA_	Alignment	not modelled	69.8	11	**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.
86	d2fx0a1	Alignment	not modelled	69.7	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
87	c3bruA_	Alignment	not modelled	69.7	6	**PDB header:**transcription **Chain:** A: **PDB Molecule:**regulatory protein, tetr family; **PDBTitle:** crystal structure of regulatory protein tetr from rhodobacter2 sphaeroides
88	c3he0A_	Alignment	not modelled	69.6	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.
89	c2yvhA_	Alignment	not modelled	69.1	22	**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
90	c1jumB_	Alignment	not modelled	69.1	3	**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
91	c3on4D_	Alignment	not modelled	69.0	6	**PDB header:**transcription **Chain:** D: **PDB Molecule:**transcriptional regulator, tetr family; **PDBTitle:** crystal structure of tetr transcriptional regulator from legionella2 pneumophila
92	c3fiwB_	Alignment	not modelled	68.7	17	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**putative tetr-family transcriptional regulator; **PDBTitle:** structure of sco0253, a tetr-family transcriptional regulator from2 streptomyces coelicolor
93	c2pbxB_	Alignment	not modelled	68.4	8	**PDB header:**transcription **Chain:** B: **PDB Molecule:**hemagglutinin/protease regulatory protein; **PDBTitle:** vibrio cholerae hapr
94	c3colB_	Alignment	not modelled	68.4	11	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**putative transcription regulator; **PDBTitle:** crystal structure of putative transcription regulator from2 lactobacillus plantarum
95	d2gena1	Alignment	not modelled	68.2	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
96	c3cdlA_	Alignment	not modelled	68.1	6	**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
97	d1sgma1	Alignment	not modelled	67.8	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
98	c3eupA_	Alignment	not modelled	67.2	14	**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
99	c2jk3A_	Alignment	not modelled	67.0	12	**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
100	c2wuiA_	Alignment	not modelled	66.8	22	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator; **PDBTitle:** crystal structure of mexz, a key repressor responsible for2 antibiotic resistance in pseudomonas aeruginosa.
101	c3iuvA_	Alignment	not modelled	66.8	11	**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
102	d1zk8a1	Alignment	not modelled	66.8	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
103	c1rktA_	Alignment	not modelled	66.6	8	**PDB header:**transcription **Chain:** A: **PDB Molecule:**protein yfir; **PDBTitle:** crystal structure of yfir, a putative transcriptional

						regulator from2 bacillus subtilis
104	c1u9nA_	Alignment	not modelled	66.5	17	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**transcriptional repressor ethr; **PDBTitle:** crystal structure of the transcriptional regulator ethr in2 a ligand bound conformation opens therapeutic perspectives3 against tuberculosis and leprosy
105	c2hyjA_	Alignment	not modelled	66.2	8	**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
106	c2g7sA_	Alignment	not modelled	66.2	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, tetr family; **PDBTitle:** the crystal structure of transcriptional regulator, tetr family, from2 agrobacterium tumefaciens
107	c1ui6B_	Alignment	not modelled	66.2	6	**PDB header:**antibiotic **Chain:** B: **PDB Molecule:**a-factor receptor homolog; **PDBTitle:** crystal structure of gamma-butyrolactone receptor (arpa-like protein)
108	c3mwmA_	Alignment	not modelled	66.1	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative metal uptake regulation protein; **PDBTitle:** graded expression of zinc-responsive genes through two regulatory2 zinc-binding sites in zur
109	c3f0cA_	Alignment	not modelled	66.0	11	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator; **PDBTitle:** crystal structure of transcriptional regulator from cytophaga2 hutchinsonii atcc 33406
110	c2g3bB_	Alignment	not modelled	65.9	19	**PDB header:**transcription **Chain:** B: **PDB Molecule:**putative tetr-family transcriptional regulator; **PDBTitle:** crystal structure of putative tetr-family transcriptional regulator2 from rhodococcus sp.
111	c2oi8A_	Alignment	not modelled	65.7	8	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative regulatory protein sco4313; **PDBTitle:** crystal structure of putative regulatory protein sco4313
112	c2iaiA_	Alignment	not modelled	65.6	22	**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
113	c3nxcA_	Alignment	not modelled	65.5	14	**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
114	c1zk8A_	Alignment	not modelled	64.9	19	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, tetr family; **PDBTitle:** crystal structure of transcriptional regulator from bacillus cereus2 atcc 14579
115	c2f07A_	Alignment	not modelled	64.7	8	**PDB header:**transcription **Chain:** A: **PDB Molecule:**yvdt; **PDBTitle:** crystal structure of yvdt from bacillus subtilis
116	c2g7gA_	Alignment	not modelled	64.5	25	**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
117	c2qwtA_	Alignment	not modelled	64.5	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, tetr family; **PDBTitle:** crystal structure of the tetr transcription regulatory2 protein from mycobacterium vanbaalenii
118	c3knwB_	Alignment	not modelled	64.0	11	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**putative transcriptional regulator (tetr/acrr family); **PDBTitle:** crystal structure of a putative transcriptional regulator (tetr/acrr2 family member) from putative transcriptional regulator (tetr/acrr3 family)
119	c3dpjB_	Alignment	not modelled	63.7	11	**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
120	c3gziA_	Alignment	not modelled	63.5	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