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Description	P36547
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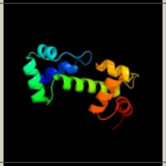
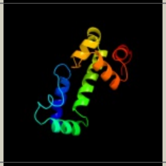
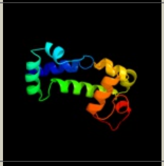
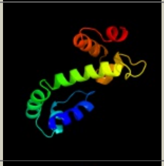
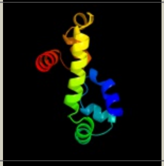
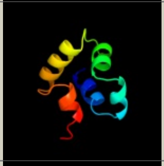
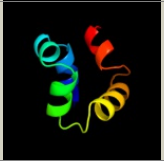
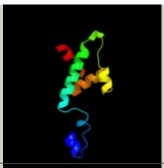
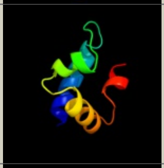
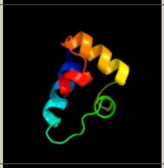
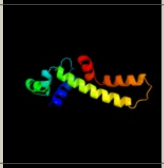
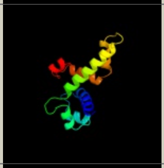
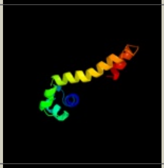
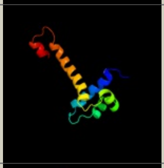
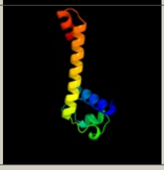
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3gbgA_	Alignment		99.9	16	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**tcp pilus virulence regulatory protein; **PDBTitle:** crystal structure of toxt from vibrio cholerae o395
2	c3oioA_	Alignment		99.9	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
3	c1d5yD_	Alignment		99.9	17	**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	20	**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	c3mn2B_	Alignment		99.9	35	**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
6	c1bl0A_	Alignment		99.8	13	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**protein (multiple antibiotic resistance protein); **PDBTitle:** multiple antibiotic resistance protein (mara)/dna complex
7	c3mklB_	Alignment		99.8	13	**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	c2k9sA_	Alignment		99.8	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**arabinose operon regulatory protein; **PDBTitle:** solution structure of dna binding domain of e. coli arac
9	c3lsgD_	Alignment		99.7	20	**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		99.0	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**AraC type transcriptional activator
11	d1d5ya2	Alignment		99.0	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**AraC type transcriptional activator

12	c1zgwA_	Alignment		98.9	22	**PDB header:**transcription regulator/dna **Chain:** A: **PDB Molecule:**ada polyprotein; **PDBTitle:** nmr structure of e. coli ada protein in complex with dna
13	d1d5ya1	Alignment		98.8	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**AraC type transcriptional activator
14	d1bl0a1	Alignment		98.8	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**AraC type transcriptional activator
15	c2zcxA_	Alignment		96.1	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**tetr-family transcriptional regulator; **PDBTitle:** crystal structure of tetr family transcriptional regulator2 sco7815
16	c3ppbB_	Alignment		95.9	12	**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
17	c1vi0B_	Alignment		95.8	13	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator; **PDBTitle:** crystal structure of a transcriptional regulator
18	c3f1bA_	Alignment		95.8	7	**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.
19	c2f07A_	Alignment		95.8	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**yvdt; **PDBTitle:** crystal structure of yvdt from bacillus subtilis
20	c3g7rB_	Alignment		95.7	19	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** crystal structure of sco4454, a tetr-family transcriptional2 regulator from streptomyces coelicolor
21	c2gfnA_	Alignment	not modelled	95.7	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
22	c3iuvA_	Alignment	not modelled	95.7	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
23	d1sgma1	Alignment	not modelled	95.7	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
24	d2fbqa1	Alignment	not modelled	95.7	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
25	c3bhqB_	Alignment	not modelled	95.6	7	**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
26	c3dcfB_	Alignment	not modelled	95.6	10	**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
27	c2genA_	Alignment	not modelled	95.6	12	**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
						PDB header:transcription **Chain:** B: **PDB Molecule:**putative tetr-family transcriptional

28	c2g3bB_	Alignment	not modelled	95.5	12	regulator; **PDBTitle:** crystal structure of putative tetr-family transcriptional regulator2 from rhodococcus sp.
29	c2nx4A_	Alignment	not modelled	95.5	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.
30	c2dg8D_	Alignment	not modelled	95.5	11	**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)
31	c3gziA_	Alignment	not modelled	95.4	15	**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
32	c2g7sA_	Alignment	not modelled	95.4	8	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, tetr family; **PDBTitle:** the crystal structure of transcriptional regulator, tetr family, from2 agrobacterium tumefaciens
33	c2ibdB_	Alignment	not modelled	95.4	15	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**possible transcriptional regulator; **PDBTitle:** crystal structure of probable transcriptional regulatory protein2 rha5900
34	c3nnrA_	Alignment	not modelled	95.4	16	**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
35	c3f0cA_	Alignment	not modelled	95.3	7	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator; **PDBTitle:** crystal structure of transcriptional regulator from cytophaga2 hutchinsonii atcc 33406
36	d2gfna1	Alignment	not modelled	95.3	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
37	c2hytA_	Alignment	not modelled	95.3	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
38	c3bruA_	Alignment	not modelled	95.3	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**regulatory protein, tetr family; **PDBTitle:** crystal structure of regulatory protein tetr from rhodobacter2 sphaeroides
39	d1t56a1	Alignment	not modelled	95.3	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
40	c2dg7A_	Alignment	not modelled	95.2	26	**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)
41	d1vi0a1	Alignment	not modelled	95.2	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
42	d1v7ba1	Alignment	not modelled	95.2	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
43	c3rh2A_	Alignment	not modelled	95.2	11	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**hypothetical tetr-like transcriptional regulator; **PDBTitle:** crystal structure of a hypothetical tetr-like transcriptional2 regulator (sama_0099) from shewanella amazonensis sb2b at 2.42 a3 resolution
44	c2fbqA_	Alignment	not modelled	95.2	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**probable transcriptional regulator; **PDBTitle:** the crystal structure of transcriptional regulator pa3006
45	c1sgmA_	Alignment	not modelled	95.2	10	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative hth-type transcriptional regulator yxaf; **PDBTitle:** crystal structure of hypothetical protein yxaf
46	c3anpD_	Alignment	not modelled	95.2	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.
47	c3geuC_	Alignment	not modelled	95.1	11	**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
48	c2yvhA_	Alignment	not modelled	95.1	14	**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
49	c3ni7A_	Alignment	not modelled	95.1	15	**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
50	c2np5A_	Alignment	not modelled	95.1	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator; **PDBTitle:** crystal structure of a transcriptional regulator (rha1_ro04179) from2 rhodococcus sp. rha1.
51	c3dpjB_	Alignment	not modelled	95.1	9	**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
52	d2o7ta1	Alignment	not modelled	95.1	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain

53	c2hkuB_	Alignment	not modelled	95.1	11	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**a putative transcriptional regulator; **PDBTitle:** structural genomics, the crystal structure of a putative2 transcriptional regulator from rhodococcus sp. rha1
54	d1jt6a1	Alignment	not modelled	95.1	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
55	c2eh3A_	Alignment	not modelled	95.0	10	**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
56	c3he0A_	Alignment	not modelled	95.0	11	**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.
57	c2pz9A_	Alignment	not modelled	95.0	9	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative regulatory protein; **PDBTitle:** crystal structure of putative transcriptional regulator sco4942 from2 streptomyces coelicolor
58	c3qkxB_	Alignment	not modelled	95.0	9	**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
59	c3cjdB_	Alignment	not modelled	95.0	6	**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
60	c1ui6B_	Alignment	not modelled	95.0	16	**PDB header:**antibiotic **Chain:** B: **PDB Molecule:**a-factor receptor homolog; **PDBTitle:** crystal structure of gamma-butyrolactone receptor (arpa-like protein)
61	c2oi8A_	Alignment	not modelled	95.0	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative regulatory protein sco4313; **PDBTitle:** crystal structure of putative regulatory protein sco4313
62	c2fq4A_	Alignment	not modelled	95.0	25	**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
63	c3lwjA_	Alignment	not modelled	95.0	12	**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
64	c2hyjA_	Alignment	not modelled	95.0	17	**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
65	d2fq4a1	Alignment	not modelled	95.0	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
66	c2rasB_	Alignment	not modelled	94.9	16	**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
67	d1ui5a1	Alignment	not modelled	94.9	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
68	c2raeA_	Alignment	not modelled	94.9	16	**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
69	c2of7A_	Alignment	not modelled	94.9	16	**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
70	d2g3ba1	Alignment	not modelled	94.9	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
71	c3bniA_	Alignment	not modelled	94.9	11	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**putative tetr-family transcriptional regulator; **PDBTitle:** crystal structure of tetr-family transcriptional regulator from2 streptomyces coelicolor
72	d1pb6a1	Alignment	not modelled	94.9	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
73	c1jumB_	Alignment	not modelled	94.9	13	**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
74	c2d6yA_	Alignment	not modelled	94.9	5	**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)
75	c3b81A_	Alignment	not modelled	94.9	15	**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
76	c2id3A_	Alignment	not modelled	94.9	10	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative transcriptional regulator;

76	c2id3A_	Alignment	not modelled	94.9	10	**PDBTitle:** crystal structure of transcriptional regulator sco5951 from2 streptomyces coelicolor a3(2)
77	c3b6aC_	Alignment	not modelled	94.8	12	**PDB header:**transcription **Chain:** C: **PDB Molecule:**actr protein; **PDBTitle:** crystal structure of the streptomyces coelicolor tetr2 family protein actr in complex with actinorhodin
78	c3knwB_	Alignment	not modelled	94.8	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)
79	d2np5a1	Alignment	not modelled	94.8	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
80	c2qtqB_	Alignment	not modelled	94.8	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
81	d3c07a1	Alignment	not modelled	94.8	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
82	d2d6ya1	Alignment	not modelled	94.8	5	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
83	c3on4D_	Alignment	not modelled	94.8	11	**PDB header:**transcription **Chain:** D: **PDB Molecule:**transcriptional regulator, tetr family; **PDBTitle:** crystal structure of tetr transcriptional regulator from legionella2 pneumophila
84	c1rktA_	Alignment	not modelled	94.8	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**protein yfir; **PDBTitle:** crystal structure of yfir, a putative transcriptional regulator from2 bacillus subtilis
85	d2gena1	Alignment	not modelled	94.7	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
86	c3jsjC_	Alignment	not modelled	94.7	19	**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
87	c3qbmA_	Alignment	not modelled	94.7	9	**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
88	c2guhA_	Alignment	not modelled	94.7	19	**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
89	c3c2bA_	Alignment	not modelled	94.7	19	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, tetr family; **PDBTitle:** crystal structure of tetr transcriptional regulator from agrobacterium2 tumefaciens
90	d2i10a1	Alignment	not modelled	94.7	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
91	c2rekA_	Alignment	not modelled	94.6	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative tetr-family transcriptional regulator; **PDBTitle:** crystal structure of tetr-family transcriptional regulator
92	c3cdlA_	Alignment	not modelled	94.6	20	**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
93	d2oi8a1	Alignment	not modelled	94.6	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
94	c2wuiA_	Alignment	not modelled	94.6	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.
95	c3c07B_	Alignment	not modelled	94.6	19	**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)
96	c3himA_	Alignment	not modelled	94.5	11	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**probable transcriptional regulator; **PDBTitle:** the crystal structure of a bacterial regulatory protein in the tetr2 family from rhodococcus rha1 to 2.2a
97	c3bcgA_	Alignment	not modelled	94.5	12	**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
98	d2fx0a1	Alignment	not modelled	94.4	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
99	d1t33a1	Alignment	not modelled	94.4	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
100	c2pbxB_	Alignment	not modelled	94.4	12	**PDB header:**transcription **Chain:** B: **PDB Molecule:**hemagglutinin/protease regulatory protein;

						PDBTitle: vibrio cholerae hapr
101	c3bjbE_	Alignment	not modelled	94.4	23	**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
102	c3mnlA_	Alignment	not modelled	94.4	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
103	d2vkea1	Alignment	not modelled	94.4	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
104	c1zkgB_	Alignment	not modelled	94.4	11	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator, tetr family; **PDBTitle:** crystal structure of transcriptional regulator, tetr family (tm1030)2 from thermotoga maritima at 2.30 a resolution
105	d2fd5a1	Alignment	not modelled	94.4	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
106	c3dewA_	Alignment	not modelled	94.4	19	**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.
107	c3o60A_	Alignment	not modelled	94.4	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lin0861 protein; **PDBTitle:** the crystal structure of lin0861 from listeria innocua to 2.8a
108	d2hkua1	Alignment	not modelled	94.3	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
109	c2q24A_	Alignment	not modelled	94.3	10	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative tetr family transcriptional regulator; **PDBTitle:** crystal structure of tetr transcriptional regulator sco0520 from2 streptomyces coelicolor
110	d2id3a1	Alignment	not modelled	94.3	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
111	d2id6a1	Alignment	not modelled	94.2	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
112	c2i10A_	Alignment	not modelled	94.2	24	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative tetr transcriptional regulator; **PDBTitle:** putative tetr transcriptional regulator from rhodococcus sp. rha1
113	d2g7sa1	Alignment	not modelled	94.1	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
114	c2zb9A_	Alignment	not modelled	94.1	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** crystal structure of tetr family transcription regulator2 sco0332
115	c3mvpA_	Alignment	not modelled	94.1	19	**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
116	c2qkoA_	Alignment	not modelled	94.1	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**possible transcriptional regulator, tetr family protein; **PDBTitle:** crystal structure of transcriptional regulator rha06399 from2 rhodococcus sp. rha1
117	c2g7lA_	Alignment	not modelled	94.1	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**tetr-family transcriptional regulator; **PDBTitle:** crystal structure of putative transcription regulator sco7704 from2 streptomyces coelicor
118	c2uxoB_	Alignment	not modelled	94.0	13	**PDB header:**transcription **Chain:** B: **PDB Molecule:**hth-type transcriptional regulator ttgr; **PDBTitle:** ttgr in complex with tetracycline
119	c3s5rA_	Alignment	not modelled	94.0	12	**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
120	d2hyja1	Alignment	not modelled	94.0	26	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain