



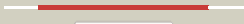









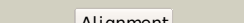

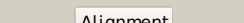

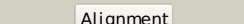

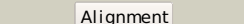








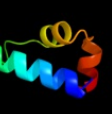

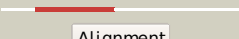
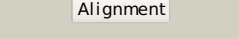


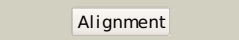

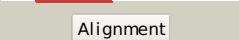
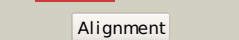



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3gbgA_</a>	 Alignment		99.9	18	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> tcp pilus virulence regulatory protein; <b>PDBTitle:</b> crystal structure of toxT from vibrio cholerae o395
2	<a href="#">c1d5yD_</a>	 Alignment		99.9	55	<b>PDB header:</b> transcription/dna <b>Chain:</b> D: <b>PDB Molecule:</b> rob transcription factor; <b>PDBTitle:</b> crystal structure of the e. coli rob transcription factor2 in complex with dna
3	<a href="#">c3oouA_</a>	 Alignment		99.9	27	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> lin2118 protein; <b>PDBTitle:</b> the structure of a protein with unkown function from listeria innocua
4	<a href="#">c3oi0A_</a>	 Alignment		99.9	27	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator (arac-type dna-binding domain- <b>PDBTitle:</b> crystal structure of transcriptional regulator (arac-type dna-binding2 domain-containing proteins) from chromobacterium violaceum
5	<a href="#">c1bl0A_</a>	 Alignment		99.9	39	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> protein (multiple antibiotic resistance protein); <b>PDBTitle:</b> multiple antibiotic resistance protein (mara)/dna complex
6	<a href="#">c2k9sA_</a>	 Alignment		99.9	26	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> arabinose operon regulatory protein; <b>PDBTitle:</b> solution structure of dna binding domain of e. coli arac
7	<a href="#">c3mklB_</a>	 Alignment		99.9	21	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> hth-type transcriptional regulator gadx; <b>PDBTitle:</b> crystal structure of dna-binding transcriptional dual regulator from2 escherichia coli k-12
8	<a href="#">c3mn2B_</a>	 Alignment		99.9	19	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> probable arac family transcriptional regulator; <b>PDBTitle:</b> the crystal structure of a probable arac family transcriptional2 regulator from rhodopseudomonas palustris cga009
9	<a href="#">c3lsgD_</a>	 Alignment		99.8	24	<b>PDB header:</b> transcription regulator <b>Chain:</b> D: <b>PDB Molecule:</b> two-component response regulator yesn; <b>PDBTitle:</b> the crystal structure of the c-terminal domain of the two-2 component response regulator yesn from fusobacterium3 nucleatum subsp. nucleatum atcc 25586
10	<a href="#">d1bl0a2</a>	 Alignment		99.3	34	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> AraC type transcriptional activator
11	<a href="#">d1d5ya2</a>	 Alignment		99.3	53	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> AraC type transcriptional activator

12	<a href="#">d1d5ya1</a>	Alignment		99.0	57	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> AraC type transcriptional activator
13	<a href="#">d1bl0a1</a>	Alignment		99.0	43	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> AraC type transcriptional activator
14	<a href="#">c1zgwA_</a>	Alignment		98.8	18	<b>PDB header:</b> transcription regulator/dna <b>Chain:</b> A: <b>PDB Molecule:</b> ada polypeptide; <b>PDBTitle:</b> nmr structure of e. coli ada protein in complex with dna
15	<a href="#">d2vkea1</a>	Alignment		95.4	17	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
16	<a href="#">c3iwfA_</a>	Alignment		95.3	12	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcription regulator rpir family; <b>PDBTitle:</b> the crystal structure of the n-terminal domain of a rpir2 transcriptional regulator from staphylococcus epidermidis to 1.4a
17	<a href="#">c3b6aC_</a>	Alignment		94.9	12	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> actr protein; <b>PDBTitle:</b> crystal structure of the streptomyces coelicolor tetr2 family protein actr in complex with actinorhodin
18	<a href="#">d1jt6a1</a>	Alignment		94.8	20	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
19	<a href="#">c2eh3A_</a>	Alignment		94.8	17	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> crystal structure of aq_1058, a transcriptional regulator (terr/acrr2 family) from aquifex aeolicus vf5
20	<a href="#">d2fq4a1</a>	Alignment		94.6	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
21	<a href="#">d2fbqa1</a>	Alignment	not modelled	94.5	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
22	<a href="#">c3npiB_</a>	Alignment	not modelled	94.5	24	<b>PDB header:</b> gene regulation <b>Chain:</b> B: <b>PDB Molecule:</b> tetr family regulatory protein; <b>PDBTitle:</b> crystal structure of a tetr family regulatory protein (dip1788) from2 corynebacterium diphtheriae at 2.96 a resolution
23	<a href="#">d3c07a1</a>	Alignment	not modelled	94.5	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
24	<a href="#">d2i10a1</a>	Alignment	not modelled	94.5	17	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
25	<a href="#">d2id3a1</a>	Alignment	not modelled	94.4	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
26	<a href="#">c1jumB_</a>	Alignment	not modelled	94.4	20	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical transcriptional regulator in qaca <b>PDBTitle:</b> crystal structure of the multidrug binding transcriptional2 repressor qacr bound to the natural drug berberine
27	<a href="#">d1pb6a1</a>	Alignment	not modelled	94.4	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
28	<a href="#">c2np5A_</a>	Alignment	not modelled	94.4	24	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> crystal structure of a transcriptional regulator (rha1_ro04179) from2 rhodococcus sp. rha1.

29	<a href="#">d2np5a1</a>	Alignment	not modelled	94.3	24	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
30	<a href="#">d2g7la1</a>	Alignment	not modelled	94.3	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
31	<a href="#">c2g3bB_</a>	Alignment	not modelled	94.3	22	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> putative tetr-family transcriptional regulator; <b>PDBTitle:</b> crystal structure of putative tetr-family transcriptional regulator2 from rhodococcus sp.
32	<a href="#">c2qtqB_</a>	Alignment	not modelled	94.2	12	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, tetr family; <b>PDBTitle:</b> crystal structure of a predicted dna-binding transcriptional regulator2 (saro_1072) from novosphingobium aromaticivorans dsm at 1.85 a3 resolution
33	<a href="#">c2f07A_</a>	Alignment	not modelled	94.2	27	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> yvdt; <b>PDBTitle:</b> crystal structure of yvdt from bacillus subtilis
34	<a href="#">c3kkcB_</a>	Alignment	not modelled	94.2	10	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> tetr family transcriptional regulator; <b>PDBTitle:</b> the crystal structure of tetr transcriptional regulator from2 streptococcus agalactiae 2603v
35	<a href="#">d1ui5a1</a>	Alignment	not modelled	94.2	17	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
36	<a href="#">d2g3ba1</a>	Alignment	not modelled	94.2	22	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
37	<a href="#">c2dg7A_</a>	Alignment	not modelled	94.2	17	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> crystal structure of the putative transcriptional regulator sco03372 from streptomyces coelicolor a3(2)
38	<a href="#">c3anpD_</a>	Alignment	not modelled	94.1	12	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> transcriptional repressor, tetr family; <b>PDBTitle:</b> crystal structure of thermus thermophilus fadr, a tetr family2 transcriptional repressor, in complex with lauroyl-coa.
39	<a href="#">d2d6ya1</a>	Alignment	not modelled	94.1	17	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
40	<a href="#">d2bjca1</a>	Alignment	not modelled	94.1	16	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> GalR/LacI-like bacterial regulator
41	<a href="#">c2fq4A_</a>	Alignment	not modelled	94.1	15	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, tetr family; <b>PDBTitle:</b> the crystal structure of the transcriptional regulator (tetr family)2 from bacillus cereus
42	<a href="#">d1sgma1</a>	Alignment	not modelled	94.0	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
43	<a href="#">d2gena1</a>	Alignment	not modelled	94.0	28	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
44	<a href="#">c1sgmA_</a>	Alignment	not modelled	93.9	16	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative hth-type transcriptional regulator yxaf; <b>PDBTitle:</b> crystal structure of hypothetical protein yxaf
45	<a href="#">d2hyja1</a>	Alignment	not modelled	93.9	17	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
46	<a href="#">c2of7A_</a>	Alignment	not modelled	93.9	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative tetr-family transcriptional regulator; <b>PDBTitle:</b> structural genomics, the crystal structure of a tetr-family2 transcriptional regulator from streptomyces coelicolor a3
47	<a href="#">c2nx4A_</a>	Alignment	not modelled	93.9	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, tetr family protein; <b>PDBTitle:</b> the crystal structure of a putative tetr-family transcriptional2 regulator rha06780 from rhodococcus sp. rha1.
48	<a href="#">c2o3fC_</a>	Alignment	not modelled	93.9	13	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> putative hth-type transcriptional regulator ybbh; <b>PDBTitle:</b> structural genomics, the crystal structure of the n-2 terminal domain of the putative transcriptional regulator3 ybbh from bacillus subtilis subsp. subtilis str. 168.
49	<a href="#">c1vi0B_</a>	Alignment	not modelled	93.8	20	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> crystal structure of a transcriptional regulator
50	<a href="#">d2g7sa1</a>	Alignment	not modelled	93.8	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
51	<a href="#">c3bniA_</a>	Alignment	not modelled	93.8	20	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> putative tetr-family transcriptional regulator; <b>PDBTitle:</b> crystal structure of tetr-family transcriptional regulator from2 streptomyces coelicolor
52	<a href="#">c3bhqB_</a>	Alignment	not modelled	93.8	24	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> crystal structure of a putative tetr-family transcriptional regulator2 (mlr_4833) from mesorhizobium loti maff303099 at 1.54 a resolution
53	<a href="#">d2o3fa1</a>	Alignment	not modelled	93.8	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> RpiR-like

54	<a href="#">c3ppbB</a>	 Alignment	not modelled	93.8	15	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> putative tetr family transcription regulator; <b>PDBTitle:</b> crystal structure of a putative tetr family transcription regulator2 (shew_3104) from shewanella sp. pv-4 at 2.10 a resolution
55	<a href="#">d1v7ba1</a>	 Alignment	not modelled	93.8	29	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
56	<a href="#">d1zk8a1</a>	 Alignment	not modelled	93.7	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
57	<a href="#">c3f1bA</a>	 Alignment	not modelled	93.7	18	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> tetr-like transcriptional regulator; <b>PDBTitle:</b> the crystal structure of a tetr-like transcriptional regulator from2 rhodococcus sp. rha1.
58	<a href="#">c2fbgA</a>	 Alignment	not modelled	93.7	12	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> probable transcriptional regulator; <b>PDBTitle:</b> the crystal structure of transcriptional regulator pa3006
59	<a href="#">c2guhA</a>	 Alignment	not modelled	93.7	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative tetr-family transcriptional regulator; <b>PDBTitle:</b> crystal structure of the putative tetr-family transcriptional2 regulator from rhodococcus sp. rha1
60	<a href="#">c3nnrA</a>	 Alignment	not modelled	93.7	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, tetr family; <b>PDBTitle:</b> crystal structure of a tetr-family transcriptional regulator2 (maqu_3571) from marinobacter aquaeolei vt8 at 2.49 a resolution
61	<a href="#">c1bjzA</a>	 Alignment	not modelled	93.7	17	<b>PDB header:</b> transcription regulation <b>Chain:</b> A: <b>PDB Molecule:</b> tetracycline repressor; <b>PDBTitle:</b> tetracycline chelated mg2+-ion initiates helix unwinding for tet2 repressor induction
62	<a href="#">c3g56A</a>	 Alignment	not modelled	93.7	20	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> regulator of macrolide 2'-phosphotransferase i; <b>PDBTitle:</b> structure of the macrolide biosensor protein, mphr(a)
63	<a href="#">c2raeA</a>	 Alignment	not modelled	93.7	27	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, acrr family protein; <b>PDBTitle:</b> crystal structure of a tetr/acrr family transcriptional regulator from2 rhodococcus sp. rha1
64	<a href="#">d1j5ya1</a>	 Alignment	not modelled	93.6	10	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Biotin repressor-like
65	<a href="#">d2fx0a1</a>	 Alignment	not modelled	93.6	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
66	<a href="#">c3dcfB</a>	 Alignment	not modelled	93.6	20	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator of the tetr/acrr <b>PDBTitle:</b> crystal structure of transcriptional regulator of the2 tetr/acrr family (yp_290855.1) from thermobifida fusca yx-3 er1 at 2.50 a resolution
67	<a href="#">c3dewA</a>	 Alignment	not modelled	93.6	12	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, tetr family; <b>PDBTitle:</b> the structure of a putative tetr family transcriptional regulator from2 geobacter sulfurreducens pca.
68	<a href="#">c3gziA</a>	 Alignment	not modelled	93.6	17	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, tetr family; <b>PDBTitle:</b> crystal structure of a transcriptional regulator of the tetr family2 (shew_3567) from shewanella loihica pv-4 at 2.05 a resolution
69	<a href="#">d1t56a1</a>	 Alignment	not modelled	93.6	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
70	<a href="#">c2id3A</a>	 Alignment	not modelled	93.6	12	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> crystal structure of transcriptional regulator sco5951 from2 streptomyces coelicolor a3(2)
71	<a href="#">c2wuiA</a>	 Alignment	not modelled	93.6	12	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> crystal structure of mexz, a key repressor responsible for2 antibiotic resistance in pseudomonas aeruginosa.
72	<a href="#">c3o60A</a>	 Alignment	not modelled	93.5	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> lin0861 protein; <b>PDBTitle:</b> the crystal structure of lin0861 from listeria innocua to 2.8a
73	<a href="#">c3bcgA</a>	 Alignment	not modelled	93.5	15	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional regulator acrr; <b>PDBTitle:</b> conformational changes of the acrr regulator reveal a2 mechanism of induction
74	<a href="#">c2g7lA</a>	 Alignment	not modelled	93.5	12	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> tetr-family transcriptional regulator; <b>PDBTitle:</b> crystal structure of putative transcription regulator sco7704 from2 streptomyces coelicor
75	<a href="#">c3lwjA</a>	 Alignment	not modelled	93.5	17	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> putative tetr-family transcriptional regulator; <b>PDBTitle:</b> crystal structure of putative tetr-family transcriptional regulator2 (yp_752756.1) from syntrophomonas wolfei str. goettingen at 2.07 a3 resolution
76	<a href="#">d2gfna1</a>	Alignment	not modelled	93.5	23	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
77	<a href="#">c3c07B</a>	Alignment	not modelled	93.5	15	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> putative tetr-family transcriptional regulator; <b>PDBTitle:</b> crystal structure of a tetr family transcriptional regulator

						from2 streptomyces coelicolor a3(2)
78	<a href="#">c3on4D_</a>	Alignment	not modelled	93.5	12	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> transcriptional regulator, tetr family; <b>PDBTitle:</b> crystal structure of tetr transcriptional regulator from legionella2 pneumophila
79	<a href="#">d1vi0a1</a>	Alignment	not modelled	93.5	20	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
80	<a href="#">c3he0A_</a>	Alignment	not modelled	93.4	22	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, tetr family; <b>PDBTitle:</b> the structure of a putative transcriptional regulator tetr family2 protein from vibrio parahaemolyticus.
81	<a href="#">c1ui6B_</a>	Alignment	not modelled	93.4	17	<b>PDB header:</b> antibiotic <b>Chain:</b> B: <b>PDB Molecule:</b> a-factor receptor homolog; <b>PDBTitle:</b> crystal structure of gamma-butyrolactone receptor (arpa-like protein)
82	<a href="#">c2d6yA_</a>	Alignment	not modelled	93.4	17	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> putative tetr family regulatory protein; <b>PDBTitle:</b> crystal structure of transcriptional factor sco4008 from streptomyces2 coelicolor a3(2)
83	<a href="#">c3bjbE_</a>	Alignment	not modelled	93.4	24	<b>PDB header:</b> transcription regulator <b>Chain:</b> E: <b>PDB Molecule:</b> probable transcriptional regulator, tetr family protein; <b>PDBTitle:</b> crystal structure of a tetr transcriptional regulator from rhodococcus2 sp. rha1
84	<a href="#">c1zk8A_</a>	Alignment	not modelled	93.4	19	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, tetr family; <b>PDBTitle:</b> crystal structure of transcriptional regulator from bacillus cereus2 atcc 14579
85	<a href="#">c2zb9A_</a>	Alignment	not modelled	93.4	20	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> crystal structure of tetr family transcription regulator2 sco0332
86	<a href="#">c2genA_</a>	Alignment	not modelled	93.3	28	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> probable transcriptional regulator; <b>PDBTitle:</b> structural genomics, the crystal structure of a probable2 transcriptional regulator from pseudomonas aeruginosa pao1
87	<a href="#">d2hkua1</a>	Alignment	not modelled	93.3	10	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
88	<a href="#">d2g7ga1</a>	Alignment	not modelled	93.3	7	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
89	<a href="#">d2o7ta1</a>	Alignment	not modelled	93.3	22	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
90	<a href="#">d1qpza1</a>	Alignment	not modelled	93.3	20	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> GalR/LacI-like bacterial regulator
91	<a href="#">c2hytA_</a>	Alignment	not modelled	93.3	10	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> tetr-family transcriptional regulator; <b>PDBTitle:</b> crystal structure of a tetr-family transcriptional regulator (eca1819)2 from pectobacterium atrosepticum at 1.64 a resolution
92	<a href="#">c3g7rB_</a>	Alignment	not modelled	93.2	12	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> crystal structure of sco4454, a tetr-family transcriptional2 regulator from streptomyces coelicolor
93	<a href="#">c2gfnA_</a>	Alignment	not modelled	93.2	23	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional regulator pksa related protein; <b>PDBTitle:</b> crystal structure of hth-type transcriptional regulator pksa related2 protein from rhodococcus sp. rha1
94	<a href="#">c2pbxB_</a>	Alignment	not modelled	93.1	7	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> hemagglutinin/protease regulatory protein; <b>PDBTitle:</b> vibrio cholerae hapr
95	<a href="#">c2yvha_</a>	Alignment	not modelled	93.1	29	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> crystal structure of the operator-binding form of the multi-drug2 binding transcriptional repressor cgmnr
96	<a href="#">c3b81A_</a>	Alignment	not modelled	93.1	15	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, acrr family; <b>PDBTitle:</b> crystal structure of predicted dna-binding transcriptional regulator2 of tetr/acrr family (np_350189.1) from clostridium acetobutylicum at3 2.10 a resolution
97	<a href="#">c2i10A_</a>	Alignment	not modelled	93.0	18	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative tetr transcriptional regulator; <b>PDBTitle:</b> putative tetr transcriptional regulator from rhodococcus sp. rha1
98	<a href="#">c2ibdB_</a>	Alignment	not modelled	93.0	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> possible transcriptional regulator; <b>PDBTitle:</b> crystal structure of probable transcriptional regulatory protein2 rha5900
99	<a href="#">c2vprA_</a>	Alignment	not modelled	93.0	17	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> tetracycline resistance repressor protein; <b>PDBTitle:</b> tet repressor class h in complex with 5a,6-2 anhydrotetracycline-mg
100	<a href="#">d2id6a1</a>	Alignment	not modelled	92.9	17	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
101	<a href="#">c2o7ta_</a>	Alignment	not modelled	92.9	22	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> crystal structure of a tetr family transcriptional regulator2 (ncgl1578, cgl1640) from corynebacterium glutamicum at 2.10 a3 resolution
102	<a href="#">c3mvpA_</a>	Alignment	not modelled	92.8	22	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> tetr/acrr transcriptional regulator; <b>PDBTitle:</b> the crystal structure of a tetr/acrr transcriptional regulator from2 streptococcus mutans to 1.85a



103	<a href="#">d2vkva1</a>	Alignment	not modelled	92.8	20	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
104	<a href="#">c3iuvA</a>	Alignment	not modelled	92.8	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized tetr family protein; <b>PDBTitle:</b> the structure of a member of tetr family (sco1917) from2 streptomyces coelicolor a3
105	<a href="#">c3bruA</a>	Alignment	not modelled	92.8	20	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> regulatory protein, tetr family; <b>PDBTitle:</b> crystal structure of regulatory protein tetr from rhodobacter2 sphaeroides
106	<a href="#">c2rasB</a>	Alignment	not modelled	92.8	22	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, tetr family; <b>PDBTitle:</b> crystal structure of a putative tetr/acrr family transcriptional2 regulator (saro_0558) from novosphingobium aromaticivorans dsm at3 1.80 a resolution
107	<a href="#">d2fd5a1</a>	Alignment	not modelled	92.8	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
108	<a href="#">c2g7gA</a>	Alignment	not modelled	92.8	8	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> rha04620, putative transcriptional regulator; <b>PDBTitle:</b> the crystal structure of the putative transcriptional regulator2 rha04620 from rhodococcus sp. rha1
109	<a href="#">c3c2bA</a>	Alignment	not modelled	92.8	18	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, tetr family; <b>PDBTitle:</b> crystal structure of tetr transcriptional regulator from agrobacterium2 tumefaciens
110	<a href="#">c3qkxB</a>	Alignment	not modelled	92.7	13	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized hth-type transcriptional regulator hi_0893; <b>PDBTitle:</b> crystal structure of a tetr-family transcriptional regulator (hi0893)2 from haemophilus influenzae rd at 2.35 a resolution
111	<a href="#">c3f0cA</a>	Alignment	not modelled	92.7	17	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> crystal structure of transcriptional regulator from cytophaga2 hutchinsonii atcc 33406
112	<a href="#">c3fiwB</a>	Alignment	not modelled	92.6	19	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> putative tetr-family transcriptional regulator; <b>PDBTitle:</b> structure of sco0253, a tetr-family transcriptional regulator from2 streptomyces coelicolor
113	<a href="#">c3dpjB</a>	Alignment	not modelled	92.6	10	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> transcription regulator, tetr family; <b>PDBTitle:</b> the crystal structure of a tetr transcription regulator2 from silicibacter pomeroyi dss
114	<a href="#">c3rh2A</a>	Alignment	not modelled	92.6	24	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical tetr-like transcriptional regulator; <b>PDBTitle:</b> crystal structure of a hypothetical tetr-like transcriptional2 regulator (sama_0099) from shewanella amazonensis sb2b at 2.42 a3 resolution
115	<a href="#">d1z0xa1</a>	Alignment	not modelled	92.6	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
116	<a href="#">c2uxoB</a>	Alignment	not modelled	92.6	12	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> hth-type transcriptional regulator ttgr; <b>PDBTitle:</b> ttgr in complex with tetracycline
117	<a href="#">c3s5rA</a>	Alignment	not modelled	92.6	10	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator tetr family; <b>PDBTitle:</b> crystal structure of a putative transcriptional regulator of the tetr2 family (syn_02108) from syntrophus aciditrophicus at 2.60 a3 resolution
118	<a href="#">c2q24A</a>	Alignment	not modelled	92.6	20	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative tetr family transcriptional regulator; <b>PDBTitle:</b> crystal structure of tetr transcriptional regulator sco0520 from2 streptomyces coelicolor
119	<a href="#">d1biaa1</a>	Alignment	not modelled	92.5	17	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Biotin repressor-like
120	<a href="#">c2iu5A</a>	Alignment	not modelled	92.5	5	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type dhaklm operon transcriptional activator dhas; <b>PDBTitle:</b> dihydroxyacetone kinase operon activator dhas