
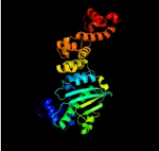




















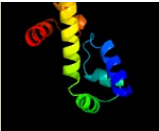










Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1395_(-)_1571053_1572087
Date	Wed Jul 31 22:05:50 BST 2019
Unique Job ID	ad4a797e350825be

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5chhA_	 Alignment		100.0	23	PDB header: transcription Chain: A: PDB Molecule: arac family transcriptional regulator; PDBTitle: crystal structure of transcriptional regulator cdpr from pseudomonas2 aeruginosa
2	c3gbgA_	 Alignment		99.9	26	PDB header: transcription regulator Chain: A: PDB Molecule: tcp pilus virulence regulatory protein; PDBTitle: crystal structure of toxt from vibrio cholerae o395
3	c1d5yD_	 Alignment		99.9	19	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	c3mkhB_	 Alignment		99.9	30	PDB header: transcription regulator Chain: B: PDB Molecule: hth-type transcriptional regulator gadx; PDBTitle: crystal structure of dna-binding transcriptional dual regulator from2 escherichia coli k-12
5	c3w6vA_	 Alignment		99.9	23	PDB header: transcription activator/dna Chain: A: PDB Molecule: adpa; PDBTitle: crystal structure of the dna-binding domain of adpa, the global2 transcriptional factor, in complex with a target dna
6	c3oioA_	 Alignment		99.9	19	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
7	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
8	c2k9sA_	 Alignment		99.9	19	PDB header: transcription Chain: A: PDB Molecule: arabinose operon regulatory protein; PDBTitle: solution structure of dna binding domain of e. coli arac
9	c1b10A_	 Alignment		99.9	16	PDB header: transcription/dna Chain: A: PDB Molecule: protein (multiple antibiotic resistance protein); PDBTitle: multiple antibiotic resistance protein (mara)/dna complex
10	c3mn2B_	 Alignment		99.9	19	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
11	c4fe4C_	 Alignment		99.9	20	PDB header: transcription Chain: C: PDB Molecule: xylose operon regulatory protein; PDBTitle: crystal structure of apo e. coli xylr

12	c3lsgD	Alignment		99.7	21	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
13	d1bl0a2	Alignment		99.5	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: AraC type transcriptional activator
14	d1d5ya2	Alignment		99.5	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: AraC type transcriptional activator
15	c5nlaA	Alignment		98.9	13	PDB header: transcription Chain: A: PDB Molecule: putative transcriptional regulator transcription regulator PDBTitle: crystal structure of the arac-like transcriptional activator cuxr
16	d1d5ya1	Alignment		98.2	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: AraC type transcriptional activator
17	d1bl0a1	Alignment		98.2	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: AraC type transcriptional activator
18	c1zgwA	Alignment		98.2	19	PDB header: transcription regulator/dna Chain: A: PDB Molecule: ada polyprotein; PDBTitle: nmr structure of e. coli ada protein in complex with dna
19	c1u78A	Alignment		95.3	15	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
20	d2hsga1	Alignment		94.7	22	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
21	c2m8gX	Alignment	not modelled	94.7	19	PDB header: transcription Chain: X: PDB Molecule: transcriptional regulator; PDBTitle: structure, function, and tethering of dna-binding domains in 542 transcriptional activators
22	d1fipa	Alignment	not modelled	94.6	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
23	d1qpza1	Alignment	not modelled	94.4	17	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
24	c5yszA	Alignment	not modelled	94.4	22	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, lacI family; PDBTitle: transcriptional regulator celr-cellobiose complex
25	c1bdhA	Alignment	not modelled	94.4	15	PDB header: transcription/dna Chain: A: PDB Molecule: protein (purine repressor); PDBTitle: purine repressor mutant-hypoxanthine-palindromic operator2 complex
26	d1efaa1	Alignment	not modelled	94.2	20	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
27	c5fglA	Alignment	not modelled	94.1	10	PDB header: apoptosis Chain: A: PDB Molecule: nicr; PDBTitle: co-crystal structure of nicr2_hsp
28	c1zvva	Alignment	not modelled	94.1	25	PDB header: transcription/dna Chain: A: PDB Molecule: glucose-resistance amylase regulator; PDBTitle: crystal structure of a ccpa-crh-dna complex
29	c3iwfA	Alignment	not modelled	94.0	9	PDB header: transcription regulator Chain: A: PDB Molecule: transcription regulator rpir family; PDBTitle: the crystal structure of the n-terminal domain of a rpir2 transcriptional regulator from staphylococcus epidermidis to 1.4a

30	d1etxa	Alignment	not modelled	94.0	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
31	d2bjca1	Alignment	not modelled	94.0	14	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
32	c1g2hA	Alignment	not modelled	93.9	16	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulatory protein tyrr homolog; PDBTitle: solution structure of the dna-binding domain of the tyrr2 protein of haemophilus influenzae
33	d1g2ha	Alignment	not modelled	93.9	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
34	d1etob	Alignment	not modelled	93.8	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
35	c4fcyA	Alignment	not modelled	93.8	16	PDB header: dna binding protein/dna Chain: A: PDB Molecule: transposase; PDBTitle: crystal structure of the bacteriophage mu transpososome
36	c4I5eA	Alignment	not modelled	93.7	20	PDB header: protein binding Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of a. aeolicus ntrc1 dna binding domain
37	c1efaA	Alignment	not modelled	93.6	14	PDB header: transcription/dna Chain: A: PDB Molecule: lac repressor; PDBTitle: crystal structure of the lac repressor dimer bound to operator and the2 anti-inducer onpf
38	c1umqA	Alignment	not modelled	93.6	26	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
39	d1umqa	Alignment	not modelled	93.6	26	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
40	c5xqlA	Alignment	not modelled	93.6	17	PDB header: transcription Chain: A: PDB Molecule: multidrug-efflux transporter 1 regulator; PDBTitle: crystal structure of a pseudomonas aeruginosa transcriptional2 regulator
41	c1lbgB	Alignment	not modelled	93.5	20	PDB header: PDB COMPND:
42	c3e7ID	Alignment	not modelled	93.3	11	PDB header: transcription regulator Chain: D: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigma54 activator ntrc4's dna binding2 domain
43	c5m7nA	Alignment	not modelled	93.2	22	PDB header: signaling protein Chain: A: PDB Molecule: nitrogen assimilation regulatory protein; PDBTitle: crystal structure of ntrx from brucella abortus in complex with atp2 processed with the crystaldirect automated mounting and cryo-cooling3 technology
44	d1ntca	Alignment	not modelled	93.1	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
45	c4ivnB	Alignment	not modelled	93.1	14	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator; PDBTitle: the vibrio vulnificus nanr protein complexed with mannac-6p
46	c3kxD	Alignment	not modelled	93.0	27	PDB header: transcription regulator Chain: D: PDB Molecule: transcriptional regulator, lacI family; PDBTitle: crystal structure of a transcriptional regulator, lacI2 family protein from silicibacter pomeroyi
47	c5wayB	Alignment	not modelled	92.8	13	PDB header: transcription Chain: B: PDB Molecule: transcriptional activator; PDBTitle: mgaspn protein, mga regulator from streptococcus pneumoniae
48	c3onqB	Alignment	not modelled	92.4	21	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: regulator of polyketide synthase expression; PDBTitle: crystal structure of regulator of polyketide synthase expression2 bad_0249 from bifidobacterium adolescentis
49	c2eh3A	Alignment	not modelled	92.4	5	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
50	c3gziA	Alignment	not modelled	92.2	10	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
51	c3h5tA	Alignment	not modelled	92.2	22	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, lacI family; PDBTitle: crystal structure of a transcriptional regulator, lacI2 family protein from corynebacterium glutamicum
52	d1t56a1	Alignment	not modelled	91.9	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
53	c2f07A	Alignment	not modelled	91.7	7	PDB header: transcription Chain: A: PDB Molecule: yvdt; PDBTitle: crystal structure of yvdt from bacillus subtilis
54	d1jt6a1	Alignment	not modelled	91.6	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain

55	d2d6ya1	Alignment	not modelled	91.5	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
56	c1bjzA	Alignment	not modelled	91.3	16	PDB header: transcription regulation Chain: A: PDB Molecule: tetracycline repressor; PDBTitle: tetracycline chelated mg2+-ion initiates helix unwinding for tet2 repressor induction
57	d1j5ya1	Alignment	not modelled	91.3	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Biotin repressor-like
58	c5d1rA	Alignment	not modelled	91.2	21	PDB header: transcription Chain: A: PDB Molecule: rv1816 transcriptional regulator; PDBTitle: crystal structure of mycobacterium tuberculosis rv1816 transcriptional2 regulator.
59	c2r0qF	Alignment	not modelled	91.2	13	PDB header: recombination/dna Chain: F: PDB Molecule: putative transposon tn552 dna-invertase bin3; PDBTitle: crystal structure of a serine recombinase- dna regulatory2 complex
60	d1vi0a1	Alignment	not modelled	91.0	8	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
61	d2g7sa1	Alignment	not modelled	90.9	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
62	d1rp3a1	Alignment	not modelled	90.8	29	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma3 domain
63	c5ydpC	Alignment	not modelled	90.8	15	PDB header: gene regulation Chain: C: PDB Molecule: tetr transcriptional regulatory protein; PDBTitle: crystal structure of tetr family repressor alkx from dietzia sp.2 strain dq12-45-1b implicated in biodegradation of n-alkanes
64	c3colB	Alignment	not modelled	90.8	10	PDB header: transcription regulator Chain: B: PDB Molecule: putative transcription regulator; PDBTitle: crystal structure of putative transcription regulator from2 lactobacillus plantarum
65	d2o7ta1	Alignment	not modelled	90.8	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
66	c1ojjD	Alignment	not modelled	90.7	13	PDB header: response regulator Chain: D: PDB Molecule: transcriptional regulatory protein zrar; PDBTitle: crystal structure of a sigma54-activator suggests the mechanism for2 the conformational switch necessary for sigma54 binding
67	d1lcda	Alignment	not modelled	90.7	25	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
68	c3bniA	Alignment	not modelled	90.7	15	PDB header: transcription regulator Chain: A: PDB Molecule: putative tetr-family transcriptional regulator; PDBTitle: crystal structure of tetr-family transcriptional regulator from2 streptomyces coelicolor
69	d1pb6a1	Alignment	not modelled	90.6	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
70	d1ui5a1	Alignment	not modelled	90.6	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
71	d2np5a1	Alignment	not modelled	90.6	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
72	d1v7ba1	Alignment	not modelled	90.6	8	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
73	c2g3bB	Alignment	not modelled	90.3	14	PDB header: transcription Chain: B: PDB Molecule: putative tetr-family transcriptional regulator; PDBTitle: crystal structure of putative tetr-family transcriptional regulator2 from rhodococcus sp.
74	c1jumB	Alignment	not modelled	90.3	10	PDB header: transcription Chain: B: PDB Molecule: hypothetical transcriptional regulator in qaca 5'region; PDBTitle: crystal structure of the multidrug binding transcriptional repressor2 qacr bound to the natural drug berberine
75	c2nx4A	Alignment	not modelled	90.2	15	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.
76	c2qtqB	Alignment	not modelled	90.2	5	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
77	d2fq4a1	Alignment	not modelled	90.1	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
78	c1vi0B	Alignment	not modelled	90.1	8	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of a transcriptional regulator
79	c1ui6B	Alignment	not modelled	90.0	17	PDB header: antibiotic Chain: B: PDB Molecule: a-factor receptor homolog; PDBTitle: crystal structure of gamma-butyrolactone receptor (arpa-like protein)

80	d2id3a1	Alignment	not modelled	90.0	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
81	d2gena1	Alignment	not modelled	89.9	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
82	d2hya1	Alignment	not modelled	89.9	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
83	c2hytA	Alignment	not modelled	89.8	10	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
84	c3g56A	Alignment	not modelled	89.8	17	PDB header: dna binding protein Chain: A: PDB Molecule: regulator of macrolide 2'-phosphotransferase i; PDBTitle: structure of the macrolide biosensor protein, mphr(a)
85	c6mj1A	Alignment	not modelled	89.8	12	PDB header: dna binding protein Chain: A: PDB Molecule: probable hth-type transcriptional regulator yttp; PDBTitle: crystal structure of refz (regulator of ftsz) from bacillus subtilis
86	d2g3ba1	Alignment	not modelled	89.7	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
87	c2gfnA	Alignment	not modelled	89.7	15	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
88	c3bhqB	Alignment	not modelled	89.6	12	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
89	d3c07a1	Alignment	not modelled	89.6	8	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
90	d1biaa1	Alignment	not modelled	89.5	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Biotin repressor-like
91	c2genA	Alignment	not modelled	89.5	10	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
92	d2fbqa1	Alignment	not modelled	89.5	5	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
93	c3anpD	Alignment	not modelled	89.5	8	PDB header: transcription Chain: D: PDB Molecule: transcriptional repressor, tetr family; PDBTitle: crystal structure of thermus thermophilus fadr, a tetr family2 transcriptional repressor, in complex with lauroyl-coa.
94	c3ppbB	Alignment	not modelled	89.4	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
95	c3iuvA	Alignment	not modelled	89.4	20	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
96	d1jhfa1	Alignment	not modelled	89.4	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: LexA repressor, N-terminal DNA-binding domain
97	c2yvha	Alignment	not modelled	89.3	8	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
98	c2o3fC	Alignment	not modelled	89.3	13	PDB header: transcription Chain: C: PDB Molecule: putative hth-type transcriptional regulator ybbh; PDBTitle: structural genomics, the crystal structure of the n-2 terminal domain of the putative transcriptional regulator3 ybbh from bacillus subtilis subsp. subtilis str. 168.
99	d2o3fa1	Alignment	not modelled	89.3	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: RpiR-like
100	c5d19A	Alignment	not modelled	89.3	7	PDB header: transcription Chain: A: PDB Molecule: tetr family transcriptional regulator; PDBTitle: crystal structure of mycobacterium tuberculosis rv0302, form ii
101	d2oi8a1	Alignment	not modelled	89.1	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
102	c3sqnA	Alignment	not modelled	89.0	16	PDB header: transcription regulator Chain: A: PDB Molecule: conserved domain protein; PDBTitle: putative mga family transcriptional regulator from enterococcus2 faecalis
103	c3dcfB	Alignment	not modelled	89.0	7	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator of the tetr/acrr family; PDBTitle: crystal structure of transcriptional regulator of the tetr/acrr family2 (yp_290855.1) from thermobifida fusca yx-er1 at 2.50 a resolution
104	d2cg4a1	Alianment	not modelled	89.0	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain

						Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
105	c1rktA_	Alignment	not modelled	88.9	15	PDB header: transcription Chain: A: PDB Molecule: protein yfir; PDBTitle: crystal structure of yfir, a putative transcriptional regulator from2 bacillus subtilis
106	c3geuC_	Alignment	not modelled	88.9	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
107	c3vprA_	Alignment	not modelled	88.9	10	PDB header: dna binding protein Chain: A: PDB Molecule: transcriptional regulator, tetr family; PDBTitle: crystal structure of a tetr family transcriptional regulator pfmr from2 thermus thermophilus hb8
108	c3qkxB_	Alignment	not modelled	88.9	12	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
109	c3b6aC_	Alignment	not modelled	88.7	12	PDB header: transcription Chain: C: PDB Molecule: actr protein; PDBTitle: crystal structure of the streptomyces coelicolor tetr family protein2 actr in complex with actinorhodin
110	c3rd3B_	Alignment	not modelled	88.7	7	PDB header: transcription Chain: B: PDB Molecule: probable transcriptional regulator; PDBTitle: structure of pseudomonas aeruginosa transcriptional regulator pa2196
111	c5k7fA_	Alignment	not modelled	88.7	8	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, tetr family; PDBTitle: crystal structure of apo aibr
112	c3lwjA_	Alignment	not modelled	88.7	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
113	c3f1bA_	Alignment	not modelled	88.7	8	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.
114	d2i10a1	Alignment	not modelled	88.6	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
115	c4cgrA_	Alignment	not modelled	88.4	15	PDB header: transcription Chain: A: PDB Molecule: putative tetr-family transcriptional regulator; PDBTitle: structure of regulator protein sco3201 from streptomyces coelicolor
116	c6j05B_	Alignment	not modelled	88.4	12	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator arsr; PDBTitle: structures of two arsr as(iii)-responsive repressors: implications for2 the mechanism of derepression
117	c4me9B_	Alignment	not modelled	88.4	10	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, tetr family; PDBTitle: crystal structure of a transcriptional regulator, tetr family2 (bce_2991) from bacillus cereus atcc 10987 at 2.50 a resolution
118	c2vbzA_	Alignment	not modelled	88.3	11	PDB header: dna-binding protein Chain: A: PDB Molecule: transcriptional regulatory protein; PDBTitle: feast or famine regulatory protein (rv3291c)from m.2 tuberculosis complexed with l-tryptophan
119	d2vkea1	Alignment	not modelled	88.3	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
120	c2o7tA_	Alignment	not modelled	88.2	15	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