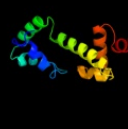


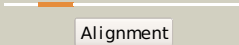
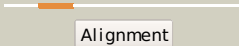
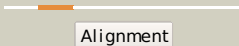
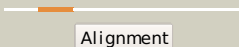
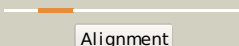
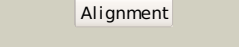
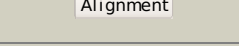
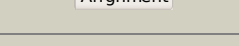
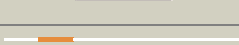
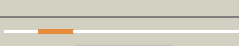
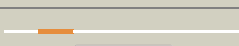
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1d5yD_	 Alignment		100.0	100	PDB header: transcription/dna Chain: D: PDB Molecule: rob transcription factor; PDBTitle: crystal structure of the e. coli rob transcription factor2 in complex with dna
2	d1d5ya3	 Alignment		100.0	100	Fold: Probable bacterial effector-binding domain Superfamily: Probable bacterial effector-binding domain Family: Rob transcription factor, C-terminal domain
3	c3gbgA_	 Alignment		99.9	17	PDB header: transcription regulator Chain: A: PDB Molecule: tcp pilus virulence regulatory protein; PDBTitle: crystal structure of toxT from vibrio cholerae o395
4	c3lurB_	 Alignment		99.9	18	PDB header: transcription activator Chain: B: PDB Molecule: putative bacterial transcription regulation protein; PDBTitle: crystal structure of putative bacterial transcription regulation2 protein (np_372959.1) from staphylococcus aureus mu50 at 1.81 a3 resolution
5	c1bl0A_	 Alignment		99.9	46	PDB header: transcription/dna Chain: A: PDB Molecule: protein (multiple antibiotic resistance protein); PDBTitle: multiple antibiotic resistance protein (mara)/dna complex
6	c3oouA_	 Alignment		99.9	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lin2118 protein; PDBTitle: the structure of a protein with unkown function from listeria innocua
7	c2k9sA_	 Alignment		99.9	27	PDB header: transcription Chain: A: PDB Molecule: arabinose operon regulatory protein; PDBTitle: solution structure of dna binding domain of e. coli arac
8	c3oioA_	 Alignment		99.9	27	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator (arac-type dna-binding domain- PDBTitle: crystal structure of transcriptional regulator (arac-type dna-binding domain-containing proteins) from chromobacterium violaceum
9	d1jyha_	 Alignment		99.9	7	Fold: Probable bacterial effector-binding domain Superfamily: Probable bacterial effector-binding domain Family: Gyrase inhibitory protein Gyrl (SbmC, YeeB)
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	c3mklB_	 Alignment		99.9	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

12	c3gk6A_	Alignment		99.9	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: integron cassette protein vch_cass2; PDBTitle: crystal structure from the mobile metagenome of vibrio cholerae.2 integron cassette protein vch_cass2.
13	c3lsgD_	Alignment		99.8	23	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
14	c2kcuA_	Alignment		99.8	10	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: protein ctr107; PDBTitle: nmr solution structure of the c-terminal domain of the two-2 chlorobium tepidum. northeast structural genomics target3 ctr107
15	c3b49A_	Alignment		99.6	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lin2189 protein; PDBTitle: crystal structure of an uncharacterized conserved protein from2 listeria innocua
16	d1d5ya2	Alignment		99.5	100	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: AraC type transcriptional activator
17	d1bl0a2	Alignment		99.4	37	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: AraC type transcriptional activator
18	c3d6zA_	Alignment		99.4	12	PDB header: transcription regulator/dna Chain: A: PDB Molecule: multi drug-efflux transporter 1 regulator; PDBTitle: crystal structure of r275e mutant of bmrR bound to dna and rhodamine
19	d1r8ea2	Alignment		99.4	14	Fold: Probable bacterial effector-binding domain Superfamily: Probable bacterial effector-binding domain Family: Multi drug-binding domain of transcription activator BmrR
20	d1d5ya1	Alignment		99.1	100	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: AraC type transcriptional activator
21	d1bl0a1	Alignment	not modelled	99.1	58	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: AraC type transcriptional activator
22	c1zgwA_	Alignment	not modelled	99.0	30	PDB header: transcription regulator/dna Chain: A: PDB Molecule: ada polypeptide; PDBTitle: nmr structure of e. coli ada protein in complex with dna
23	c3iwfA_	Alignment	not modelled	94.2	12	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
24	d2hsga1	Alignment	not modelled	94.0	15	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
25	d1sgma1	Alignment	not modelled	93.6	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
26	d1lefaa1	Alignment	not modelled	93.6	23	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
27	d2bjca1	Alignment	not modelled	93.4	21	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
28	d1qpza1	Alignment	not modelled	93.4	17	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
29	d1biaa1	Alignment	not modelled	92.9	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain

					Family: Biotin repressor-like
30	d1jt6a1	Alignment	not modelled	92.9	13 Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
31	d2i10a1	Alignment	not modelled	92.9	12 Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
32	c2o3fC_	Alignment	not modelled	92.9	20 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.
33	d2o3fa1	Alignment	not modelled	92.8	20 Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: RpiR-like
34	d2vkea1	Alignment	not modelled	92.8	19 Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
35	d2fq4a1	Alignment	not modelled	92.6	20 Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
36	d2fbqa1	Alignment	not modelled	92.4	18 Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
37	d2g3ba1	Alignment	not modelled	92.2	17 Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
38	d2id3a1	Alignment	not modelled	92.0	20 Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
39	c1vi0B_	Alignment	not modelled	92.0	17 PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of a transcriptional regulator
40	d1pb6a1	Alignment	not modelled	92.0	25 Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
41	d2gena1	Alignment	not modelled	91.9	16 Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
42	d2np5a1	Alignment	not modelled	91.9	19 Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
43	d1j5ya1	Alignment	not modelled	91.9	14 Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Biotin repressor-like
44	c2f07A_	Alignment	not modelled	91.5	15 PDB header: transcription Chain: A: PDB Molecule: yvdt; PDBTitle: crystal structure of yvdt from bacillus subtilis
45	c3kxD_	Alignment	not modelled	91.5	21 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
46	c1bdhA_	Alignment	not modelled	91.4	15 PDB header: transcription/dna Chain: A: PDB Molecule: protein (purine repressor); PDBTitle: purine repressor mutant-hypoxanthine-palindromic operator2 complex
47	c3h5tA_	Alignment	not modelled	91.3	34 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
48	d2fx0a1	Alignment	not modelled	91.3	12 Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
49	c3bniA_	Alignment	not modelled	91.3	22 PDB header: transcription regulator Chain: A: PDB Molecule: putative tetr-family transcriptional regulator; PDBTitle: crystal structure of tetr-family transcriptional regulator from2 streptomyces coelicolor
50	d1ui5a1	Alignment	not modelled	91.2	25 Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
51	c1sgmA_	Alignment	not modelled	91.2	14 PDB header: transcription Chain: A: PDB Molecule: putative hth-type transcriptional regulator yxaf; PDBTitle: crystal structure of hypothetical protein yxaf
52	d2d6ya1	Alignment	not modelled	91.0	20 Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
53	c2g3bB_	Alignment	not modelled	91.0	23 PDB header: transcription Chain: B: PDB Molecule: putative tetr-family transcriptional regulator; PDBTitle: crystal structure of putative tetr-family transcriptional regulator2 from rhodococcus sp.
54	d3c07a1	Alignment	not modelled	91.0	18 Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
55	d2hya1	Alignment	not modelled	91.0	13 Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain

56	c2fq4A_	Alignment	not modelled	91.0	20	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
57	d1mkma1	Alignment	not modelled	90.9	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Transcriptional regulator ICLR, N-terminal domain
58	d2fd5a1	Alignment	not modelled	90.9	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
59	c2nx4A_	Alignment	not modelled	90.9	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: transcriptional regulator, tetr family protein; PDBTitle: the crystal structure of at the putative tetr-family transcriptional2 regulator rha06780 from rhodococcus sp. rha1.
60	d2gfnal	Alignment	not modelled	90.9	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
61	c1jumB_	Alignment	not modelled	90.9	15	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
62	c3bhqB_	Alignment	not modelled	90.9	24	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
63	d2g7sa1	Alignment	not modelled	90.8	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
64	c3lwjA_	Alignment	not modelled	90.8	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
65	c2eh3A_	Alignment	not modelled	90.8	20	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
66	d1v7ba1	Alignment	not modelled	90.7	28	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
67	c3o60A_	Alignment	not modelled	90.7	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
68	c2hytA_	Alignment	not modelled	90.6	17	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
69	d2id6a1	Alignment	not modelled	90.5	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
70	c3anpD_	Alignment	not modelled	90.5	15	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.
71	c2i10A_	Alignment	not modelled	90.5	12	PDB header: transcription Chain: A: PDB Molecule: putative tetr transcriptional regulator; PDBTitle: putative tetr transcriptional regulator from rhodococcus sp. rha1
72	c3b6aC_	Alignment	not modelled	90.4	19	PDB header: transcription Chain: C: PDB Molecule: actr protein; PDBTitle: crystal structure of the streptomyces coelicolor tetr2 family protein actr in complex with actinorhodin
73	d2vkva1	Alignment	not modelled	90.4	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
74	c3f1bA_	Alignment	not modelled	90.2	23	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.
75	c1zvva_	Alignment	not modelled	90.2	14	PDB header: transcription/dna Chain: A: PDB Molecule: glucose-resistance amylase regulator; PDBTitle: crystal structure of a ccpa-crh-dna complex
76	d1t56a1	Alignment	not modelled	90.2	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
77	c3ppbB_	Alignment	not modelled	90.1	20	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
78	c2genA_	Alignment	not modelled	90.1	18	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
79	c3b81A_	Alignment	not modelled	90.0	18	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
						PDB header: transcription

80	c2qtqB_	Alignment	not modelled	90.0	10	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	c3kkcB_	Alignment	not modelled	89.9	10	PDB header: transcription regulator Chain: B: PDB Molecule: tetr family transcriptional regulator; PDBTitle: the crystal structure of tetr transcriptional regulator from2 streptococcus agalactiae 2603v
82	c3dewA_	Alignment	not modelled	89.9	14	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, tetr family; PDBTitle: the structure of a putative tetr family transcriptional regulator from2 geobacter sulfurreducens pca.
83	c3bcgA_	Alignment	not modelled	89.9	20	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
84	d1lcda_	Alignment	not modelled	89.9	28	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
85	c2fbqA_	Alignment	not modelled	89.8	17	PDB header: transcription Chain: A: PDB Molecule: probable transcriptional regulator; PDBTitle: the crystal structure of transcriptional regulator pa3006
86	d1zk8a1	Alignment	not modelled	89.7	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
87	c2id3A_	Alignment	not modelled	89.7	20	PDB header: transcription Chain: A: PDB Molecule: putative transcriptional regulator; PDBTitle: crystal structure of transcriptional regulator sco5951 from2 streptomyces coelicolor a3(2)
88	c2dg7A_	Alignment	not modelled	89.6	20	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)
89	c3bruA_	Alignment	not modelled	89.6	15	PDB header: transcription Chain: A: PDB Molecule: regulatory protein, tetr family; PDBTitle: crystal structure of regulatory protein tetr from rhodobacter2 sphaeroides
90	d1vi0a1	Alignment	not modelled	89.5	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
91	c3dcfB_	Alignment	not modelled	89.5	23	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator of the tetr/acrr PDBTitle: crystal structure of transcriptional regulator of the 2 tetr/acrr family (yp_290855.1) from thermobifida fusca yx-3 er1 at 2.50 a resolution
92	c3c07B_	Alignment	not modelled	89.5	18	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)
93	c2wuiA_	Alignment	not modelled	89.4	17	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of mexz, a key repressor responsible for2 antibiotic resistance in pseudomonas aeruginosa.
94	c2of7A_	Alignment	not modelled	89.4	15	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
95	c2np5A_	Alignment	not modelled	89.3	23	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of a transcriptional regulator (rha1_ro04179) from2 rhodococcus sp. rha1.
96	c3f0cA_	Alignment	not modelled	89.3	17	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of transcriptional regulator from cytophaga2 hutchinsonii atcc 33406
97	c2gfnA_	Alignment	not modelled	89.3	12	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
98	c3he0A_	Alignment	not modelled	89.3	23	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.
99	c2yvha_	Alignment	not modelled	89.3	27	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
100	c2raeA_	Alignment	not modelled	89.2	25	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
101	d2g7la1	Alignment	not modelled	89.2	7	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
102	c3on4D_	Alignment	not modelled	89.2	9	PDB header: transcription Chain: D: PDB Molecule: transcriptional regulator, tetr family; PDBTitle: crystal structure of tetr transcriptional regulator from legionella2 pneumophila
103	d1rkta1	Alignment	not modelled	89.2	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
104	d2o7ta1	Alignment	not modelled	89.2	27	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain

105	c3iuvA	 Alignment	not modelled	89.1	23	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
106	c3cwrA	 Alignment	not modelled	89.1	22	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
107	c2pbxB	 Alignment	not modelled	89.1	13	PDB header: transcription Chain: B: PDB Molecule: hemagglutinin/protease regulatory protein; PDBTitle: vibrio cholerae hapr
108	c3fiwB	 Alignment	not modelled	89.0	19	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
109	c3npiB	 Alignment	not modelled	88.9	19	PDB header: gene regulation Chain: B: PDB Molecule: tetr family regulatory protein; PDBTitle: crystal structure of a tetr family regulatory protein (dip1788) from2 corynebacterium diphtheriae at 2.96 a resolution
110	c2ibdB	 Alignment	not modelled	88.9	13	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: possible transcriptional regulator; PDBTitle: crystal structure of probable transcriptional regulatory protein2 rha5900
111	d1rp3a1	 Alignment	not modelled	88.9	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma3 domain
112	c3mvpA	 Alignment	not modelled	88.7	17	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
113	c3c2bA	 Alignment	not modelled	88.7	25	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, tetr family; PDBTitle: crystal structure of tetr transcriptional regulator from agrobacterium2 tumefaciens
114	c2zb9A	 Alignment	not modelled	88.6	23	PDB header: transcription Chain: A: PDB Molecule: putative transcriptional regulator; PDBTitle: crystal structure of tetr family transcription regulator2 sco0332
115	c2jk3A	 Alignment	not modelled	88.5	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
116	c3colB	 Alignment	not modelled	88.4	18	PDB header: transcription regulator Chain: B: PDB Molecule: putative transcription regulator; PDBTitle: crystal structure of putative transcription regulator from2 lactobacillus plantarum
117	c3cdlA	 Alignment	not modelled	88.4	22	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
118	c2guhA	 Alignment	not modelled	88.4	18	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
119	c3ljlB	 Alignment	not modelled	88.4	15	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator luxT; PDBTitle: the crystal structure of the full-length transcriptional regulator2 luxT from vibrio parahaemolyticus rimd 2210633.
120	d1luxda	 Alignment	not modelled	88.4	16	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator