






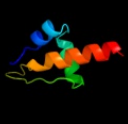




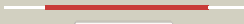



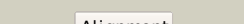

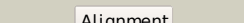

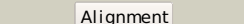

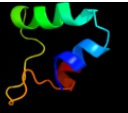










Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	Q2EES9
Date	Thu Jan 5 12:33:50 GMT 2012
Unique Job ID	33ad1e6c1a47ab58

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1z4hA_	 Alignment		100.0	100	PDB header: protein binding, dna binding protein Chain: A: PDB Molecule: tor inhibition protein; PDBTitle: the response regulator tori belongs to a new family of2 atypical excisionase
2	c1y6uA_	 Alignment		97.7	4	PDB header: dna binding protein Chain: A: PDB Molecule: excisionase from transposon tn916; PDBTitle: the structure of the excisionase (xis) protein from2 conjugative transposon tn916 provides insights into the3 regulation of heterobivalent tyrosine recombinases
3	c3qaoA_	 Alignment		96.8	16	PDB header: transcription regulator Chain: A: PDB Molecule: merr-like transcriptional regulator; PDBTitle: the crystal structure of the n-terminal domain of a merr-like2 transcriptional regulator from listeria monocytogenes egd-e
4	c2zhhA_	 Alignment		96.8	9	PDB header: transcription Chain: A: PDB Molecule: redox-sensitive transcriptional activator soxR; PDBTitle: crystal structure of soxR
5	c2vz4A_	 Alignment		96.4	18	PDB header: transcription Chain: A: PDB Molecule: hth-type transcriptional activator tipa; PDBTitle: the n-terminal domain of merr-like protein tipal bound to2 promoter dna
6	d1q06a_	 Alignment		96.2	13	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: DNA-binding N-terminal domain of transcription activators
7	d1r8da_	 Alignment		96.2	13	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: DNA-binding N-terminal domain of transcription activators
8	c3gp4B_	 Alignment		96.0	16	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, merr family; PDBTitle: crystal structure of putative merr family transcriptional regulator2 from listeria monocytogenes
9	c3gpvA_	 Alignment		95.6	12	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, merr family; PDBTitle: crystal structure of a transcriptional regulator, merr2 family from bacillus thuringiensis
10	c3hh0C_	 Alignment		95.0	11	PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulator, merr family; PDBTitle: crystal strucure of a transcriptional regulator, merr family2 from bacillus cereus
11	d1r8ea1	 Alignment		94.9	8	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: DNA-binding N-terminal domain of transcription activators

12	c2jmlA_	Alignment		94.0	9	PDB header: transcription Chain: A: PDB Molecule: dna binding domain/transcriptional regulator; PDBTitle: solution structure of the n-terminal domain of cara repressor
13	c2kfsA_	Alignment		93.9	18	PDB header: dna-binding protein Chain: A: PDB Molecule: conserved hypothetical regulatory protein; PDBTitle: nmr structure of rv2175c
14	d1j9ia_	Alignment		92.9	11	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: Terminase gpNU1 subunit domain
15	c1umqA_	Alignment		92.5	0	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
16	d1umqa_	Alignment		92.5	0	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
17	d1fipa_	Alignment		91.2	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
18	d1biaa1	Alignment		91.1	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Biotin repressor-like
19	d1etxa_	Alignment		90.5	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
20	d1g2ha_	Alignment		90.4	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
21	d1ntca_	Alignment	not modelled	89.6	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
22	d2icta1	Alignment	not modelled	89.3	6	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
23	d2ao9a1	Alignment	not modelled	89.1	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Nanomeric phage protein-like
24	d1j5ya1	Alignment	not modelled	88.5	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Biotin repressor-like
25	d1etob_	Alignment	not modelled	88.4	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
26	c2kpiA_	Alignment	not modelled	88.3	13	PDB header: transcription regulator Chain: A: PDB Molecule: sos-response transcriptional repressor, lexa; PDBTitle: solution structure of protein sos-response transcriptional2 repressor, lexa from eubacterium rectale. northeast3 structural genomics consortium target err9a
27	c3clcC_	Alignment	not modelled	88.1	11	PDB header: transcription regulator/dna Chain: C: PDB Molecule: regulatory protein; PDBTitle: crystal structure of the restriction-modification controller protein2 c.esp1396i tetramer in complex with its natural 35 base-pair operator
28	c3e7ID_	Alignment	not modelled	88.0	36	PDB header: transcription regulator Chain: D: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigma54 activator ntrc4's dna binding2 domain

29	c3omtA	Alignment	not modelled	87.6	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: putative antitoxin component, chu_2935 protein, from xre family from2 prevotella buccae.
30	d1y9qa1	Alignment	not modelled	87.3	17	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Probable transcriptional regulator VC1968, N-terminal domain
31	c3bs3A	Alignment	not modelled	87.2	11	PDB header: dna binding protein Chain: A: PDB Molecule: putative dna-binding protein; PDBTitle: crystal structure of a putative dna-binding protein from bacteroides2 fragilis
32	c2ebyA	Alignment	not modelled	86.9	7	PDB header: transcription Chain: A: PDB Molecule: putative hth-type transcriptional regulator ybaq; PDBTitle: crystal structure of a hypothetical protein from e. coli
33	d2jn6a1	Alignment	not modelled	86.8	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Cgl2762-like
34	c1u78A	Alignment	not modelled	86.8	13	PDB header: dna binding protein/dna Chain: A: PDB Molecule: transposable element tc3 transposase; PDBTitle: structure of the bipartite dna-binding domain of tc32 transposase bound to transposon dna
35	c1hlvA	Alignment	not modelled	86.0	7	PDB header: dna binding protein/dna Chain: A: PDB Molecule: major centromere autoantigen b; PDBTitle: crystal structure of cenp-b(1-129) complexed with the cenp-2 b box dna
36	d1sq8a	Alignment	not modelled	86.0	11	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
37	c2dg6A	Alignment	not modelled	85.9	19	PDB header: gene regulation Chain: A: PDB Molecule: putative transcriptional regulator; PDBTitle: crystal structure of the putative transcriptional regulator sco55502 from streptomyces coelicolor a3(2)
38	c3t76A	Alignment	not modelled	85.4	11	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator vanug; PDBTitle: crystal structure of transcriptional regulator vanug, form ii
39	d1adra	Alignment	not modelled	85.3	14	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
40	d2ppxa1	Alignment	not modelled	85.3	10	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
41	c2ppxA	Alignment	not modelled	85.3	10	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein atu1735; PDBTitle: crystal structure of a hth xre-family like protein from agrobacterium2 tumefaciens
42	c2xcjB	Alignment	not modelled	85.0	11	PDB header: viral protein Chain: B: PDB Molecule: c protein; PDBTitle: crystal structure of p2 c, the immunity repressor of2 temperate e. coli phage p2
43	d1rh6a	Alignment	not modelled	84.8	4	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: Excisionase-like
44	d1pm6a	Alignment	not modelled	84.7	8	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: Excisionase-like
45	c1b0nA	Alignment	not modelled	84.6	10	PDB header: transcription regulator Chain: A: PDB Molecule: protein (sinr protein); PDBTitle: sinr protein/sini protein complex
46	c2gm4B	Alignment	not modelled	84.2	13	PDB header: recombination, dna Chain: B: PDB Molecule: transposon gamma-delta resolvase; PDBTitle: an activated, tetrameric gamma-delta resolvase: hin chimera bound to2 cleaved dna
47	c3op9A	Alignment	not modelled	84.2	9	PDB header: transcription regulator Chain: A: PDB Molecule: pli0006 protein; PDBTitle: crystal structure of transcriptional regulator from listeria innocua
48	d1utxa	Alignment	not modelled	84.0	14	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
49	d1y7ya1	Alignment	not modelled	83.8	4	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
50	d1mkma1	Alignment	not modelled	83.4	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Transcriptional regulator IclR, N-terminal domain
51	d1r69a	Alignment	not modelled	83.3	7	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
52	c6paxA	Alignment	not modelled	83.3	6	PDB header: gene regulation/dna Chain: A: PDB Molecule: homeobox protein pax-6; PDBTitle: crystal structure of the human pax-6 paired domain-dna2 complex reveals a general model for pax protein-dna3 interactions
53	c1y9qA	Alignment	not modelled	83.2	19	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, hth_3 family; PDBTitle: crystal structure of hth_3 family transcriptional regulator2 from vibrio cholerae
54	c3cecA	Alignment	not modelled	83.1	10	PDB header: transcription Chain: A: PDB Molecule: putative antidote protein of plasmid maintenance system; PDBTitle: crystal structure of a putative antidote protein of plasmid2 maintenance system (npun_f2943) from nostoc punctiforme pcc 73102 at3 1.60 a resolution

55	c3b7hA_	Alignment	not modelled	82.7	7	PDB header: structural protein Chain: A: PDB Molecule: prophage lp1 protein 11; PDBTitle: crystal structure of the prophage lp1 protein 11
56	c2g7uB_	Alignment	not modelled	82.6	9	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: transcriptional regulator; PDBTitle: 2.3 a structure of putative catechol degradative operon regulator from2 rhodococcus sp. rha1
57	d1b0na2	Alignment	not modelled	82.1	10	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
58	c3trbA_	Alignment	not modelled	81.9	3	PDB header: dna binding protein Chain: A: PDB Molecule: virulence-associated protein i; PDBTitle: structure of an addition module antidote protein of a higa (higa)2 family from coxiella burnetii
59	d2fq4a1	Alignment	not modelled	81.9	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
60	d2croa_	Alignment	not modelled	81.6	11	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
61	c3mlfC_	Alignment	not modelled	81.2	14	PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulator; PDBTitle: putative transcriptional regulator from staphylococcus aureus.
62	c3bd1B_	Alignment	not modelled	81.0	19	PDB header: transcription Chain: B: PDB Molecule: cro protein; PDBTitle: structure of the cro protein from putative prophage element xfaso 1 in2 xylella fastidiosa strain ann-1
63	c3hefB_	Alignment	not modelled	80.7	13	PDB header: viral protein Chain: B: PDB Molecule: gene 1 protein; PDBTitle: crystal structure of the bacteriophage sf6 terminase small2 subunit
64	c2rn7A_	Alignment	not modelled	80.4	9	PDB header: unknown function Chain: A: PDB Molecule: is629 orfa; PDBTitle: nmr solution structure of tnpe protein from shigella2 flexneri. northeast structural genomics target sfr125
65	c2ao9H_	Alignment	not modelled	80.4	16	PDB header: structural genomics, unknown function Chain: H: PDB Molecule: phage protein; PDBTitle: structural genomics, the crystal structure of a phage protein2 (phbc6a51) from bacillus cereus atcc 14579
66	d1jt6a1	Alignment	not modelled	80.3	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
67	d2fbqa1	Alignment	not modelled	80.2	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
68	c3fmyA_	Alignment	not modelled	80.1	13	PDB header: dna binding protein Chain: A: PDB Molecule: hth-type transcriptional regulator mqsa PDBTitle: structure of the c-terminal domain of the e. coli protein2 mqsa (ygit/b3021)
69	c3d6zA_	Alignment	not modelled	79.8	7	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
70	d1x57a1	Alignment	not modelled	79.4	15	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: EDF1-like
71	c3ivpD_	Alignment	not modelled	79.4	11	PDB header: dna binding protein Chain: D: PDB Molecule: putative transposon-related dna-binding protein; PDBTitle: the structure of a possible transposon-related dna-binding protein2 from clostridium difficile 630.
72	c1mkmA_	Alignment	not modelled	79.4	14	PDB header: transcription Chain: A: PDB Molecule: iclr transcriptional regulator; PDBTitle: crystal structure of the thermotoga maritima iclr
73	c3f52A_	Alignment	not modelled	79.2	7	PDB header: transcription activator Chain: A: PDB Molecule: clp gene regulator (clgr); PDBTitle: crystal structure of the clp gene regulator clgr from c. glutamicum
74	d1t56a1	Alignment	not modelled	79.1	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
75	c2r0qF_	Alignment	not modelled	79.0	9	PDB header: recombination/dna Chain: F: PDB Molecule: putative transposon tn552 dna-invertase bin3; PDBTitle: crystal structure of a serine recombinase- dna regulatory2 complex
76	c3f1bA_	Alignment	not modelled	78.7	20	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.
77	c2xroE_	Alignment	not modelled	78.5	18	PDB header: dna-binding protein/dna Chain: E: PDB Molecule: hth-type transcriptional regulator ttgv; PDBTitle: crystal structure of ttgv in complex with its dna operator
78	d1vi0a1	Alignment	not modelled	78.4	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
79	d2r1j11	Alignment	not modelled	78.4	14	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
80	c2ef8A_	Alignment	not modelled	78.4	7	PDB header: transcription regulator Chain: A: PDB Molecule: putative transcription factor; PDBTitle: crystal structure of c.ecot38is
						Fold: lambda repressor-like DNA-binding domains

81	d1l1ib_	Alignment	not modelled	77.9	11	Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
82	c3r4kD_	Alignment	not modelled	77.7	18	PDB header: dna binding protein Chain: D: PDB Molecule: transcriptional regulator, iclr family; PDBTitle: crystal structure of a putative iclr transcriptional regulator2 (tm1040_3717) from silicibacter sp. tm1040 at 2.46 a resolution
83	c2nx4A_	Alignment	not modelled	77.7	10	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.
84	d2vkva1	Alignment	not modelled	77.6	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
85	d2gena1	Alignment	not modelled	77.6	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
86	c3e7qB_	Alignment	not modelled	77.3	20	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator; PDBTitle: the crystal structure of the putative transcriptional regulator from2 pseudomonas aeruginosa pao1
87	c2ia2D_	Alignment	not modelled	77.3	9	PDB header: transcription Chain: D: PDB Molecule: putative transcriptional regulator; PDBTitle: the crystal structure of a putative transcriptional regulator rha061952 from rhodococcus sp. rha1
88	d1ui5a1	Alignment	not modelled	77.1	30	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
89	c2gfnA_	Alignment	not modelled	76.8	10	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
90	c3eusB_	Alignment	not modelled	76.7	4	PDB header: dna binding protein Chain: B: PDB Molecule: dna-binding protein; PDBTitle: the crystal structure of the dna binding protein from silicibacter2 pomeroyi
91	c3ppbB_	Alignment	not modelled	76.6	10	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
92	c2fjrB_	Alignment	not modelled	76.5	7	PDB header: transcription regulator Chain: B: PDB Molecule: repressor protein ci; PDBTitle: crystal structure of bacteriophage 186
93	d2o7ta1	Alignment	not modelled	76.4	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
94	c2dg7A_	Alignment	not modelled	76.3	12	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)
95	c2o0yB_	Alignment	not modelled	76.2	23	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of putative transcriptional regulator rha1_ro069532 (iclr-family) from rhodococcus sp.
96	d2g3ba1	Alignment	not modelled	76.2	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
97	c1vi0B_	Alignment	not modelled	76.1	20	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of a transcriptional regulator
98	c3o60A_	Alignment	not modelled	76.1	10	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lin0861 protein; PDBTitle: the crystal structure of lin0861 from listeria innocua to 2.8a
99	c3mkyP_	Alignment	not modelled	76.0	17	PDB header: dna binding protein/dna Chain: P: PDB Molecule: protein sobp; PDBTitle: structure of sobp(155-323)-18mer dna complex, i23 form
100	c3pasA_	Alignment	not modelled	76.0	15	PDB header: transcription regulator Chain: A: PDB Molecule: tetr family transcription regulator; PDBTitle: crystal structure of a tetr family transcription regulator (maqu_1417)2 from marinobacter aquaeolei vt8 at 1.90 a resolution
101	c3dcfB_	Alignment	not modelled	76.0	35	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
102	d2ofya1	Alignment	not modelled	75.8	11	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
103	c3b6aC_	Alignment	not modelled	75.5	10	PDB header: transcription Chain: C: PDB Molecule: actr protein; PDBTitle: crystal structure of the streptomyces coelicolor tetr2 family protein actr in complex with actinorhodin
104	c3iuvA_	Alignment	not modelled	75.4	5	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
105	d1i1ga1	Alignment	not modelled	75.4	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
						Fold: lambda repressor-like DNA-binding domains

106	d1rioA_	Alignment	not modelled	75.3	7	Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
107	c3iwfA_	Alignment	not modelled	75.2	17	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
108	c2guhA_	Alignment	not modelled	75.2	30	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
109	c1jumB_	Alignment	not modelled	75.0	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
110	c2f07A_	Alignment	not modelled	75.0	15	PDB header: transcription Chain: A: PDB Molecule: yvdt; PDBTitle: crystal structure of yvdt from bacillus subtilis
111	c2i10A_	Alignment	not modelled	74.8	10	PDB header: transcription Chain: A: PDB Molecule: putative tetr transcriptional regulator; PDBTitle: putative tetr transcriptional regulator from rhodococcus sp. rha1
112	c2zb9A_	Alignment	not modelled	74.8	20	PDB header: transcription Chain: A: PDB Molecule: putative transcriptional regulator; PDBTitle: crystal structure of tetr family transcription regulator2 sco0332
113	d2id3a1	Alignment	not modelled	74.8	45	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
114	d1lmb3_	Alignment	not modelled	74.7	7	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
115	c3ezfA_	Alignment	not modelled	74.6	7	PDB header: biosynthetic protein Chain: A: PDB Molecule: para; PDBTitle: partition protein
116	d1luxa_	Alignment	not modelled	74.6	17	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
117	c3cjdB_	Alignment	not modelled	74.6	10	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
118	d2d6ya1	Alignment	not modelled	74.6	26	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
119	d1pb6a1	Alignment	not modelled	74.5	26	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
120	d1vz0a1	Alignment	not modelled	74.3	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: KorB DNA-binding domain-like Family: KorB DNA-binding domain-like