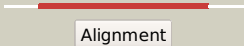



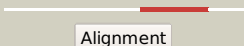



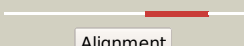



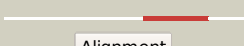




















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3736_(-)_4186812_4187873
Date	Fri Aug 9 18:20:43 BST 2019
Unique Job ID	651d215ddcec8ca1

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5chhA_	 Alignment		100.0	21	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	15	PDB header: transcription regulator Chain: A: PDB Molecule: tcp pilus virulence regulatory protein; PDBTitle: crystal structure of toxt from vibrio cholerae o395
3	c3mkIB_	 Alignment		99.9	21	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
4	c3w6vA_	 Alignment		99.9	19	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
5	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
6	c1d5yD_	 Alignment		99.9	21	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
7	c3oouA_	 Alignment		99.9	23	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	c1bl0A_	 Alignment		99.9	18	PDB header: transcription/dna Chain: A: PDB Molecule: protein (multiple antibiotic resistance protein); PDBTitle: multiple antibiotic resistance protein (mara)/dna complex
9	c3oioA_	 Alignment		99.9	12	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
10	c3mn2B_	 Alignment		99.9	17	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		99.8	17	PDB header: transcription Chain: C: PDB Molecule: xylose operon regulatory protein; PDBTitle: crystal structure of apo e. coli xylr

12	c3lsgD	Alignment		99.7	18	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	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: AraC type transcriptional activator
14	d1d5ya2	Alignment		99.5	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: AraC type transcriptional activator
15	c5nlaA	Alignment		98.7	16	PDB header: transcription Chain: A; PDB Molecule: putative transcriptional regulator transcription regulator PDBTitle: crystal structure of the arac-like transcriptional activator cuxr
16	c1zgwA	Alignment		98.0	20	PDB header: transcription regulator/dna Chain: A; PDB Molecule: ada polyprotein; PDBTitle: nmr structure of e. coli ada protein in complex with dna
17	d1d5ya1	Alignment		97.7	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: AraC type transcriptional activator
18	d1bl0a1	Alignment		97.7	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: AraC type transcriptional activator
19	c1u78A	Alignment		95.0	12	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	c2m8gX	Alignment		94.8	10	PDB header: transcription Chain: X; PDB Molecule: transcriptional regulator; PDBTitle: structure, function, and tethering of dna-binding domains in 542 transcriptional activators
21	d1fipa	Alignment	not modelled	94.7	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
22	c4l5eA	Alignment	not modelled	94.6	20	PDB header: protein binding Chain: A; PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of a. aeolicus ntrc1 dna binding domain
23	d1etob	Alignment	not modelled	94.5	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
24	d2hsga1	Alignment	not modelled	94.5	20	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
25	d1umqa	Alignment	not modelled	94.4	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
26	c1umqA	Alignment	not modelled	94.4	16	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
27	d1etxa	Alignment	not modelled	94.3	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
28	c3e7lD	Alignment	not modelled	94.3	18	PDB header: transcription regulator Chain: D; PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigma54 activator ntrc4's dna binding2 domain PDB header: transcription/dna Chain: A; PDB Molecule: putative transcriptional regulator

29	c1bdhA_	Alignment	not modelled	94.2	22	Chain: A: PDB Molecule: protein (purine repressor); PDBTitle: purine repressor mutant-hypoxanthine-palindromic operator2 complex
30	c5m7nA_	Alignment	not modelled	94.0	13	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
31	d1ntca_	Alignment	not modelled	94.0	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
32	d1qpza1	Alignment	not modelled	93.8	24	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
33	c5syszA_	Alignment	not modelled	93.7	27	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, lacI family; PDBTitle: transcriptional regulator celr-cellobiose complex
34	c1zvva_	Alignment	not modelled	93.7	22	PDB header: transcription/dna Chain: A: PDB Molecule: glucose-resistance amylase regulator; PDBTitle: crystal structure of a ccpa-crh-dna complex
35	c1lbgB_	Alignment	not modelled	93.6	20	PDB header: PDB COMPND:
36	d2bjca1	Alignment	not modelled	93.6	19	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
37	c1ojjD_	Alignment	not modelled	93.4	18	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
38	c5wayB_	Alignment	not modelled	93.3	15	PDB header: transcription Chain: B: PDB Molecule: transcriptional activator; PDBTitle: mgaspn protein, mga regulator from streptococcus pneumoniae
39	c1g2hA_	Alignment	not modelled	93.1	5	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
40	d1g2ha_	Alignment	not modelled	93.1	5	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
41	c3sqnA_	Alignment	not modelled	93.1	19	PDB header: transcription regulator Chain: A: PDB Molecule: conserved domain protein; PDBTitle: putative mga family transcriptional regulator from enterococcus2 faecalis
42	d1lefaa1	Alignment	not modelled	93.0	20	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
43	c1lefaA_	Alignment	not modelled	92.7	19	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
44	c5xqlA_	Alignment	not modelled	92.6	18	PDB header: transcription Chain: A: PDB Molecule: multidrug-efflux transporter 1 regulator; PDBTitle: crystal structure of a pseudomonas aeruginosa transcriptional2 regulator
45	c3h5tA_	Alignment	not modelled	92.5	24	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
46	d1biaa1	Alignment	not modelled	92.5	5	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Biotin repressor-like
47	d1j5ya1	Alignment	not modelled	92.1	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Biotin repressor-like
48	c3iwfA_	Alignment	not modelled	91.6	13	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
49	c2vbzA_	Alignment	not modelled	91.5	34	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
50	c2e7xA_	Alignment	not modelled	91.1	20	PDB header: transcription regulator Chain: A: PDB Molecule: 150aa long hypothetical transcriptional regulator; PDBTitle: structure of the lrp/asnc like transcriptional regulator from2 sulfobolus tokodaii 7 complexed with its cognate ligand
51	d2cg4a1	Alignment	not modelled	91.1	26	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
52	d1luxca_	Alignment	not modelled	90.9	15	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
53	c2cfxD_	Alignment	not modelled	90.9	14	PDB header: transcription Chain: D: PDB Molecule: hth-type transcriptional regulator lrpc; PDBTitle: structure of b.subtilis lrpc
54	c2cg4B_	Alignment	not modelled	90.9	26	PDB header: transcription Chain: B: PDB Molecule: regulatory protein asnc; PDBTitle: structure of e.coli asnc
						PDB header: viral protein

55	c3hefB	Alignment	not modelled	90.5	19	Chain: B: PDB Molecule: gene 1 protein; PDBTitle: crystal structure of the bacteriophage sf6 terminase small subunit
56	c2o3fC	Alignment	not modelled	90.3	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.
57	d2o3fa1	Alignment	not modelled	90.2	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: RpiR-like
58	c3kxD	Alignment	not modelled	90.1	29	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
59	c5fglA	Alignment	not modelled	90.1	15	PDB header: apoptosis Chain: A: PDB Molecule: nicr; PDBTitle: co-crystal structure of nicr2_hsp
60	d1lcda	Alignment	not modelled	90.1	24	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
61	c1i1gA	Alignment	not modelled	89.9	11	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator lrpa; PDBTitle: crystal structure of the lrp-like transcriptional regulator from the2 archaeon pyrococcus furiosus
62	c4ivnB	Alignment	not modelled	89.7	11	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator; PDBTitle: the vibrio vulnificus nanr protein complexed with mannan-6p
63	c3i4pA	Alignment	not modelled	89.6	23	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, asnc family; PDBTitle: crystal structure of asnc family transcriptional regulator from2 agrobacterium tumefaciens
64	c2e1cA	Alignment	not modelled	89.6	23	PDB header: transcription/dna Chain: A: PDB Molecule: putative hth-type transcriptional regulator ph1519; PDBTitle: structure of putative hth-type transcriptional regulator ph1519/dna2 complex
65	d2cfxa1	Alignment	not modelled	89.3	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
66	c2r0qF	Alignment	not modelled	89.2	15	PDB header: recombination/dna Chain: F: PDB Molecule: putative transposon tn552 dna-invertase bin3; PDBTitle: crystal structure of a serine recombinase- dna regulatory2 complex
67	d2cyya1	Alignment	not modelled	89.2	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
68	c2ia0A	Alignment	not modelled	89.1	26	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative hth-type transcriptional regulator pf0864; PDBTitle: transcriptional regulatory protein pf0864 from pyrococcus furiosus a2 member of the asnc family (pf0864)
69	c3colB	Alignment	not modelled	89.1	11	PDB header: transcription regulator Chain: B: PDB Molecule: putative transcription regulator; PDBTitle: crystal structure of putative transcription regulator from2 lactobacillus plantarum
70	c2dbbA	Alignment	not modelled	88.8	17	PDB header: transcriptional regulator Chain: A: PDB Molecule: putative hth-type transcriptional regulator ph0061; PDBTitle: crystal structure of ph0061
71	c2l4aA	Alignment	not modelled	88.8	20	PDB header: dna binding protein Chain: A: PDB Molecule: leucine responsive regulatory protein; PDBTitle: nmr structure of the dna-binding domain of e.coli lrp
72	c4pcqC	Alignment	not modelled	88.7	23	PDB header: transcription Chain: C: PDB Molecule: possible transcriptional regulatory protein (probably PDBTitle: crystal structure of mtbaldr (rv2779c)
73	c3gziA	Alignment	not modelled	88.7	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
74	c2jmlA	Alignment	not modelled	88.6	11	PDB header: transcription Chain: A: PDB Molecule: dna binding domain/transcriptional regulator; PDBTitle: solution structure of the n-terminal domain of cara repressor
75	d1i1ga1	Alignment	not modelled	88.3	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
76	c2p6tH	Alignment	not modelled	88.1	29	PDB header: transcription Chain: H: PDB Molecule: transcriptional regulator, lrp/asnc family; PDBTitle: crystal structure of transcriptional regulator nmb0573 and l-leucine2 complex from neisseria meningitidis
77	d1jt6a1	Alignment	not modelled	88.0	8	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
78	d1vi0a1	Alignment	not modelled	87.2	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
79	c3hosA	Alignment	not modelled	86.9	18	PDB header: transferase, dna binding protein/dna Chain: A: PDB Molecule: transposable element mariner, complete cds; PDBTitle: crystal structure of the mariner mos1 paired end complex

						with mg
80	d2d6ya1	Alignment	not modelled	86.8	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
81	c1bjzA	Alignment	not modelled	86.5	13	PDB header: transcription regulation Chain: A: PDB Molecule: tetracycline repressor; PDBTitle: tetracycline chelated mg2+-ion initiates helix unwinding for tet2 repressor induction
82	d2fq4a1	Alignment	not modelled	86.2	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
83	d1jhfa1	Alignment	not modelled	86.1	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: LexA repressor, N-terminal DNA-binding domain
84	c4go1A	Alignment	not modelled	86.0	13	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator lsrr; PDBTitle: crystal structure of full length transcription repressor lsrr from e.2 coli.
85	d2g7sa1	Alignment	not modelled	85.9	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
86	d2gena1	Alignment	not modelled	85.7	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
87	d1t56a1	Alignment	not modelled	85.6	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
88	c3bniA	Alignment	not modelled	85.5	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
89	d1rp3a1	Alignment	not modelled	85.5	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma3 domain PDB header: transcription
90	c2gqqB	Alignment	not modelled	85.4	20	Chain: B: PDB Molecule: leucine-responsive regulatory protein; PDBTitle: crystal structure of e. coli leucine-responsive regulatory protein2 (lrp)
91	c2g3bB	Alignment	not modelled	85.3	15	PDB header: transcription Chain: B: PDB Molecule: putative tetr-family transcriptional regulator; PDBTitle: crystal structure of putative tetr-family transcriptional regulator2 from rhodococcus sp.
92	d1ulya	Alignment	not modelled	85.3	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Hypothetical protein PH1932
93	c2eh3A	Alignment	not modelled	85.3	9	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
94	c5cr1A	Alignment	not modelled	85.3	12	PDB header: metal binding protein Chain: A: PDB Molecule: mercuric resistance operon regulatory protein; PDBTitle: crystal structure of the transcription activator tn501 merr in complex2 with mercury (ii)
95	c2zhha	Alignment	not modelled	85.3	18	PDB header: transcription Chain: A: PDB Molecule: redox-sensitive transcriptional activator soxr; PDBTitle: crystal structure of soxr
96	d2np5a1	Alignment	not modelled	85.2	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
97	d1pb6a1	Alignment	not modelled	85.2	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
98	c6j05B	Alignment	not modelled	85.2	8	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
99	d1ui5a1	Alignment	not modelled	85.2	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
100	c2mqkA	Alignment	not modelled	85.1	18	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent target dna activator b; PDBTitle: solution structure of n terminal domain of the mub aaa+ atpase
101	c2qtqB	Alignment	not modelled	84.9	11	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
102	d1r1ta	Alignment	not modelled	84.9	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ArsR-like transcriptional regulators
103	c1j5yA	Alignment	not modelled	84.8	14	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, biotin repressor family; PDBTitle: crystal structure of transcriptional regulator (tm1602) from2 thermotoga maritima at 2.3 a resolution
104	c1vi0B	Alignment	not modelled	84.8	11	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of a transcriptional regulator

105	c2f07A_	Alignment	not modelled	84.7	8	PDB header: transcription Chain: A: PDB Molecule: yvdt; PDBTitle: crystal structure of yvdt from bacillus subtilis
106	d2i10a1	Alignment	not modelled	84.6	5	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
107	c4r6iA_	Alignment	not modelled	84.6	10	PDB header: transcription Chain: A: PDB Molecule: anthrax toxin expression trans-acting positive regulator; PDBTitle: atxa protein, a virulence regulator from bacillus anthracis.
108	d2o7ta1	Alignment	not modelled	84.6	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
109	c2hytA_	Alignment	not modelled	84.5	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
110	c6fkgC_	Alignment	not modelled	84.5	21	PDB header: toxin Chain: C: PDB Molecule: rv1990c (mbca); PDBTitle: crystal structure of the m.tuberculosis mbct-mbca toxin-antitoxin2 complex.
111	d1v7ba1	Alignment	not modelled	84.5	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
112	c2genA_	Alignment	not modelled	84.4	9	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
113	c5ydpC_	Alignment	not modelled	84.4	13	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
114	c5dukA_	Alignment	not modelled	84.3	18	PDB header: transcription Chain: A: PDB Molecule: putative dna binding protein; PDBTitle: n-terminal structure of putative dna binding transcription factor from2 thermoplasmatales archaeon scgc ab-539-n05
115	d1r8da_	Alignment	not modelled	83.9	15	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: DNA-binding N-terminal domain of transcription activators
116	c1jumB_	Alignment	not modelled	83.9	8	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
117	c6mj1A_	Alignment	not modelled	83.8	11	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
118	c3rd3B_	Alignment	not modelled	83.6	6	PDB header: transcription Chain: B: PDB Molecule: probable transcriptional regulator; PDBTitle: structure of pseudomonas aeruginosa transcriptional regulator pa2196
119	c5h1aC_	Alignment	not modelled	83.6	17	PDB header: transcription regulator Chain: C: PDB Molecule: iclR transcription factor homolog; PDBTitle: crystal structure of an iclR homolog from microbacterium sp. strain2 hm58-2
120	c3r0aB_	Alignment	not modelled	83.5	17	PDB header: transcription regulator Chain: B: PDB Molecule: putative transcriptional regulator; PDBTitle: possible transcriptional regulator from methanosarcina mazei go1 (gi2 21227196)