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Description	RVBD3750c_(-)_4198383_4198775
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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4j2nA_	 Alignment		99.4	24	PDB header: viral protein Chain: A: PDB Molecule: gp37; PDBTitle: crystal structure of mycobacteriophage pukovnik xis
2	c4j2nB_	 Alignment		99.3	24	PDB header: viral protein Chain: B: PDB Molecule: gp37; PDBTitle: crystal structure of mycobacteriophage pukovnik xis
3	c6amaO_	 Alignment		98.9	22	PDB header: dna binding protein/dna Chain: O: PDB Molecule: putative dna-binding protein; PDBTitle: structure of s. coelicolor/s. venezuelae bidc-smea-ssfa complex to2 3.09 angstrom
4	c1z4hA_	 Alignment		98.9	9	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
5	c1y6uA_	 Alignment		98.4	19	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
6	c5i44E_	 Alignment		97.8	16	PDB header: dna binding protein/dna Chain: E: PDB Molecule: chromosome-anchoring protein raca; PDBTitle: structure of raca-dna complex; p21 form
7	c2kfsA_	 Alignment		97.8	16	PDB header: dna-binding protein Chain: A: PDB Molecule: conserved hypothetical regulatory protein; PDBTitle: nmr structure of rv2175c
8	c2zhhA_	 Alignment		97.8	25	PDB header: transcription Chain: A: PDB Molecule: redox-sensitive transcriptional activator soxT; PDBTitle: crystal structure of soxT
9	c4r24B_	 Alignment		97.7	8	PDB header: transcription/dna Chain: B: PDB Molecule: hth-type transcriptional regulator tnra; PDBTitle: complete dissection of b. subtilis nitrogen homeostatic circuitry
10	c4r4eA_	 Alignment		97.5	17	PDB header: transcription regulator/dna Chain: A: PDB Molecule: hth-type transcriptional regulator glnr; PDBTitle: structure of glnr-dna complex
11	c5c8eC_	 Alignment		97.5	19	PDB header: transcription regulator/dna Chain: C: PDB Molecule: light-dependent transcriptional regulator carh; PDBTitle: crystal structure of thermus thermophilus carh bound to2 adenosylcobalamin and a 26-bp dna segment

12	d1j9ia_	Alignment		97.4	17	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: Terminase gpNU1 subunit domain
13	d1q06a_	Alignment		97.3	13	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: DNA-binding N-terminal domain of transcription activators
14	c2vz4A_	Alignment		97.2	22	PDB header: transcription Chain: A: PDB Molecule: hth-type transcriptional activator tipa; PDBTitle: the n-terminal domain of merr-like protein tipal bound to promoter dna
15	c5af3A_	Alignment		97.2	26	PDB header: dna binding Chain: A: PDB Molecule: vapbc49; PDBTitle: x-ray crystal structure of rv2018 from mycobacterium tuberculosis
16	c3gp4B_	Alignment		97.1	22	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, merr family; PDBTitle: crystal structure of putative merr family transcriptional regulator2 from listeria monocytogenes
17	d1r8da_	Alignment		96.9	17	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: DNA-binding N-terminal domain of transcription activators
18	c3gpvA_	Alignment		96.9	13	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, merr family; PDBTitle: crystal structure of a transcriptional regulator, merr2 family from bacillus thuringiensis
19	c3qaoA_	Alignment		96.8	22	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
20	c2jmlA_	Alignment		96.6	20	PDB header: transcription Chain: A: PDB Molecule: dna binding domain/transcriptional regulator; PDBTitle: solution structure of the n-terminal domain of cara repressor
21	c3hh0C_	Alignment	not modelled	96.5	22	PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulator, merr family; PDBTitle: crystal structure of a transcriptional regulator, merr family from2 bacillus cereus
22	c3ucsB_	Alignment	not modelled	96.5	17	PDB header: chaperone Chain: B: PDB Molecule: chaperone-modulator protein cbpm; PDBTitle: crystal structure of the complex between cbpa j-domain and cbpm
23	d1r8ea1	Alignment	not modelled	96.4	18	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: DNA-binding N-terminal domain of transcription activators
24	c5gpeB_	Alignment	not modelled	96.4	20	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator, merr-family; PDBTitle: crystal structure of the transcription regulator pbrr691 from2 ralstonia metallidurans ch34 in complex with lead(ii)
25	c5cr1A_	Alignment	not modelled	95.1	17	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)
26	c2oqgA_	Alignment	not modelled	94.9	18	PDB header: transcription Chain: A: PDB Molecule: possible transcriptional regulator, arsr family protein; PDBTitle: arsr-like transcriptional regulator from rhodococcus sp. rha1
27	c1g2hA_	Alignment	not modelled	94.9	24	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
						Fold: DNA/RNA-binding 3-helical bundle

28	dlg2ha_	Alignment	not modelled	94.9	24	Superfamily: Homeodomain-like Family: FIS-like
29	dl1fipa_	Alignment	not modelled	94.8	28	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
30	clr22B_	Alignment	not modelled	94.6	19	PDB header: transcription repressor Chain: B: PDB Molecule: transcriptional repressor smtb; PDBTitle: crystal structure of the cyanobacterial metallothionein2 repressor smtb (c14s/c61s/c121s mutant) in the zn2alpha5-3 form
31	clumqA_	Alignment	not modelled	94.6	36	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
32	dlumqa_	Alignment	not modelled	94.6	36	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
33	dl1etxa_	Alignment	not modelled	94.6	28	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
34	c2m8gX_	Alignment	not modelled	94.2	24	PDB header: transcription Chain: X: PDB Molecule: transcriptional regulator; PDBTitle: structure, function, and tethering of dna-binding domains in 542 transcriptional activators
35	dlr1ta_	Alignment	not modelled	94.2	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ArsR-like transcriptional regulators
36	c5m7nA_	Alignment	not modelled	94.0	20	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
37	dlntca_	Alignment	not modelled	93.6	36	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
38	c4l5eA_	Alignment	not modelled	93.6	28	PDB header: protein binding Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of a. aeolicus ntrc1 dna binding domain
39	dl1etob_	Alignment	not modelled	93.5	28	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
40	c5xqlA_	Alignment	not modelled	93.4	19	PDB header: transcription Chain: A: PDB Molecule: multidrug-efflux transporter 1 regulator; PDBTitle: crystal structure of a pseudomonas aeruginosa transcriptional2 regulator
41	clu78A_	Alignment	not modelled	93.4	14	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
42	c3d6zA_	Alignment	not modelled	93.2	16	PDB header: transcription regulator/dna Chain: A: PDB Molecule: multidrug-efflux transporter 1 regulator; PDBTitle: crystal structure of r275e mutant of bmrr bound to dna and rhodamine
43	dlj5ya1	Alignment	not modelled	93.2	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Biotin repressor-like
44	c3e7lD_	Alignment	not modelled	93.1	19	PDB header: transcription regulator Chain: D: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigma54 activator ntrc4's dna binding2 domain
45	c6j05B_	Alignment	not modelled	93.0	16	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
46	c3gn5B_	Alignment	not modelled	92.6	19	PDB header: dna binding protein Chain: B: PDB Molecule: hth-type transcriptional regulator mqsa (ygit/b3021); PDBTitle: structure of the e. coli protein mqsa (ygit/b3021)
47	c6fkqC_	Alignment	not modelled	92.5	26	PDB header: toxin Chain: C: PDB Molecule: rv1990c (mbca); PDBTitle: crystal structure of the m.tuberculosis mbct-mbca toxin-antitoxin2 complex.
48	cl0jID_	Alignment	not modelled	92.4	41	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
49	dlbiaa1	Alignment	not modelled	91.7	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Biotin repressor-like
50	dlmkma1	Alignment	not modelled	91.5	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Transcriptional regulator lclR, N-terminal domain
51	d2d1ha1	Alignment	not modelled	91.2	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: TrmB-like
52	c3jthA_	Alignment	not modelled	91.2	22	PDB header: transcription Chain: A: PDB Molecule: transcription activator hlyu; PDBTitle: crystal structure of a transcriptional regulator hlyu from2 vibrio vulnificus cmcp6
53	c2r0qF_	Alignment	not modelled	91.0	29	PDB header: recombination/dna Chain: F: PDB Molecule: putative transposon tn552 dna-invertase bin3; PDBTitle: crystal structure of a serine recombinase- dna

						regulatory2 complex
54	d2gaua1	Alignment	not modelled	90.7	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: CAP C-terminal domain-like
55	c3f6vA	Alignment	not modelled	90.7	24	PDB header: transcription regulator Chain: A: PDB Molecule: possible transcriptional regulator, arsr family protein; PDBTitle: crystal structure of possible transcriptional regulator for arsenical2 resistance
56	c4lhfa	Alignment	not modelled	90.5	23	PDB header: viral protein Chain: A: PDB Molecule: regulatory protein cox; PDBTitle: crystal structure of a dna binding protein from phage p2
57	c3ezfA	Alignment	not modelled	90.5	13	PDB header: biosynthetic protein Chain: A: PDB Molecule: para; PDBTitle: partition protein
58	c1mkmA	Alignment	not modelled	90.1	14	PDB header: transcription Chain: A: PDB Molecule: iclr transcriptional regulator; PDBTitle: crystal structure of the thermotoga maritima iclr
59	c6paxA	Alignment	not modelled	90.0	15	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
60	d2isya1	Alignment	not modelled	90.0	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Iron-dependent repressor protein
61	c2g7uB	Alignment	not modelled	89.9	26	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
62	c3eqxB	Alignment	not modelled	89.7	14	PDB header: dna binding protein Chain: B: PDB Molecule: fic domain containing transcriptional regulator; PDBTitle: crystal structure of a fic family protein (so_4266) from shewanella2 oneidensis at 1.6 a resolution
63	c4omzG	Alignment	not modelled	89.7	14	PDB header: transcription Chain: G: PDB Molecule: nlr; PDBTitle: crystal structure of nlr from sinorhizobium fredii
64	d2jn6a1	Alignment	not modelled	89.6	30	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Cg12762-like
65	c1f5tA	Alignment	not modelled	89.6	20	PDB header: transcription/dna Chain: A: PDB Molecule: diphtheria toxin repressor; PDBTitle: diphtheria tox repressor (c102d mutant) complexed with2 nickel and dtxr consensus binding sequence
66	c6hn7A	Alignment	not modelled	89.5	28	PDB header: dna binding protein Chain: A: PDB Molecule: redirecting phage packaging protein c (rppc); PDBTitle: hijacking the hijackers: escherichia coli pathogenicity islands2 redirect helper phage packaging for their own benefit.
67	c4go1A	Alignment	not modelled	89.4	43	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator lsrr; PDBTitle: crystal structure of full length transcription repressor lsrr from e.2 coli.
68	c2jscB	Alignment	not modelled	89.4	20	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator rv1994c/mt2050; PDBTitle: nmr structure of the cadmium metal-sensor cmtr from mycobacterium2 tuberculosis
69	c3f6oB	Alignment	not modelled	89.4	27	PDB header: transcription regulator Chain: B: PDB Molecule: probable transcriptional regulator, arsr family PDBTitle: crystal structure of arsr family transcriptional regulator,2 rha00566
70	c3bd1B	Alignment	not modelled	89.4	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
71	d2ao9a1	Alignment	not modelled	89.3	38	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Nanomeric phage protein-like
72	d1g3wa1	Alignment	not modelled	89.2	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Iron-dependent repressor protein
73	c2gm4B	Alignment	not modelled	89.1	22	PDB header: recombination, dna Chain: B: PDB Molecule: transposon gamma-delta resolvase; PDBTitle: an activated, tetrameric gamma-delta resolvase: hin chimaera bound to2 cleaved dna
74	d1pm6a	Alignment	not modelled	89.1	34	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: Excisionase-like
75	c2zkzC	Alignment	not modelled	88.8	13	PDB header: transcription Chain: C: PDB Molecule: transcriptional repressor pagr; PDBTitle: crystal structure of the transcriptional repressor pagr of bacillus2 anthracis
76	c2w48D	Alignment	not modelled	88.7	39	PDB header: transcription Chain: D: PDB Molecule: sorbitol operon regulator; PDBTitle: crystal structure of the full-length sorbitol operon2 regulator sorc from klebsiella pneumoniae
77	c2xroE	Alignment	not modelled	88.6	26	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	d3e5ua1	Alignment	not modelled	88.3	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: CAP C-terminal domain-like
						PDB header: transcription regulation

79	c3e6dA	Alignment	not modelled	88.2	17	Chain: A: PDB Molecule: cyclic nucleotide-binding protein; PDBTitle: crystal structure of cprk c200s
80	d1r69a	Alignment	not modelled	88.1	27	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
81	d1rh6a	Alignment	not modelled	87.9	35	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: Excisionase-like
82	c6j0eB	Alignment	not modelled	87.8	25	PDB header: transcription Chain: B: PDB Molecule: arsenic responsive repressor arsr; PDBTitle: structures of two arsr as(iii)-responsive repressors: implications for2 the mechanism of derepression
83	c2kkoB	Alignment	not modelled	87.3	15	PDB header: dna binding protein Chain: B: PDB Molecule: possible transcriptional regulatory protein PDBTitle: solution nmr structure of the homodimeric winged helix-turn-2 helix dna-binding domain (fragment 1-100) mb0332 from3 mycobacterium bovis, a possible arsr-family transcriptional4 regulator. northeast structural genomics consortium target5 mbr242e.
84	c2lkpB	Alignment	not modelled	87.2	17	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, arsr family; PDBTitle: solution structure of apo-nmtr
85	c2q0oA	Alignment	not modelled	87.0	27	PDB header: transcription Chain: A: PDB Molecule: probable transcriptional activator protein trar; PDBTitle: crystal structure of an anti-activation complex in bacterial quorum2 sensing
86	c2it0A	Alignment	not modelled	87.0	20	PDB header: transcription/dna Chain: A: PDB Molecule: iron-dependent repressor ider; PDBTitle: crystal structure of a two-domain ider-dna complex crystal2 form ii
87	c2rn7A	Alignment	not modelled	87.0	18	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
88	d1r1ua	Alignment	not modelled	86.9	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ArsR-like transcriptional regulators
89	c5y6iB	Alignment	not modelled	86.8	15	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator kdgr; PDBTitle: crystal structure of pseudomonas aeruginosa hmgr
90	c2h09A	Alignment	not modelled	86.8	18	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator mntr; PDBTitle: crystal structure of diphtheria toxin repressor like protein2 from e. coli
91	c5dukA	Alignment	not modelled	86.7	25	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
92	c3sztB	Alignment	not modelled	86.7	21	PDB header: transcription Chain: B: PDB Molecule: quorum-sensing control repressor; PDBTitle: quorum sensing control repressor, qscr, bound to n-3-oxo-dodecanoyl-l-2 homoserine lactone
93	c2ia2D	Alignment	not modelled	86.0	24	PDB header: transcription Chain: D: PDB Molecule: putative transcriptional regulator; PDBTitle: the crystal structure of a putative transcriptional regulator rha061952 from rhodococcus sp. rha1
94	d1i5za1	Alignment	not modelled	85.9	27	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: CAP C-terminal domain-like
95	c2fjrB	Alignment	not modelled	85.8	19	PDB header: transcription regulator Chain: B: PDB Molecule: repressor protein ci; PDBTitle: crystal structure of bacteriophage 186
96	c5whmB	Alignment	not modelled	85.8	29	PDB header: transcription Chain: B: PDB Molecule: iclr family transcriptional regulator; PDBTitle: crystal structure of iclr family transcriptional regulator from2 brucella abortus
97	d1rzsA	Alignment	not modelled	85.6	29	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
98	c3omtA	Alignment	not modelled	85.4	15	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.
99	c2kpiA	Alignment	not modelled	85.4	26	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
100	c4ifuA	Alignment	not modelled	85.3	27	PDB header: dna binding protein Chain: A: PDB Molecule: regulatory protein sdia; PDBTitle: crystal structure of escherichia coli sdia in the space group c2
101	d2h6ca1	Alignment	not modelled	85.2	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: CAP C-terminal domain-like
102	c3cuoB	Alignment	not modelled	85.1	14	PDB header: transcription regulator Chain: B: PDB Molecule: uncharacterized hth-type transcriptional regulator ygav; PDBTitle: crystal structure of the predicted dna-binding transcriptional2 regulator from e. coli
103	c1h0mD	Alignment	not modelled	84.9	21	PDB header: transcription/dna Chain: D: PDB Molecule: transcriptional activator protein trar; PDBTitle: three-dimensional structure of the quorum sensing protein trar bound2 to its autoinducer and to its target dna

104	d2ofya1	Alignment	not modelled	84.8	24	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
105	c3hefB_	Alignment	not modelled	84.7	15	PDB header: viral protein Chain: B: PDB Molecule: gene 1 protein; PDBTitle: crystal structure of the bacteriophage sf6 terminase small subunit
106	c2ebyA_	Alignment	not modelled	84.7	29	PDB header: transcription Chain: A: PDB Molecule: putative hth-type transcriptional regulator ybaq; PDBTitle: crystal structure of a hypothetical protein from e. coli
107	c3i4pA_	Alignment	not modelled	84.7	17	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, asnc family; PDBTitle: crystal structure of asnc family transcriptional regulator from2 agrobacterium tumefaciens
108	d2oz6a1	Alignment	not modelled	84.6	27	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: CAP C-terminal domain-like
109	d2ev0a1	Alignment	not modelled	84.5	7	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Iron-dependent repressor protein
110	c1g3wA_	Alignment	not modelled	84.5	20	PDB header: gene regulation Chain: A: PDB Molecule: diphtheria toxin repressor; PDBTitle: cd-cys102ser dtxr
111	d2bgca1	Alignment	not modelled	84.1	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: CAP C-terminal domain-like
112	c3pgkD_	Alignment	not modelled	84.1	20	PDB header: transcription Chain: D: PDB Molecule: biofilm growth-associated repressor; PDBTitle: crystal structure of the transcriptional repressor bigr from xylella2 fastidiosa
113	d1pdnc_	Alignment	not modelled	83.7	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
114	c5h1aC_	Alignment	not modelled	83.4	10	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
115	d1a04a1	Alignment	not modelled	83.3	27	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators)
116	c3lmmB_	Alignment	not modelled	83.1	27	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the dip2311 protein from corynebacterium2 diphtheriae, northeast structural genomics consortium target cdr35
117	d1ft9a1	Alignment	not modelled	83.1	35	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: CAP C-terminal domain-like
118	d2cg4a1	Alignment	not modelled	83.0	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
119	c3voxD_	Alignment	not modelled	82.8	19	PDB header: transcription Chain: D: PDB Molecule: transcriptional regulator; PDBTitle: x-ray crystal structure of wild type hrtr in the apo form
120	c3qp5C_	Alignment	not modelled	82.8	33	PDB header: transcription Chain: C: PDB Molecule: cvir transcriptional regulator; PDBTitle: crystal structure of cvir bound to antagonist chlorolactone (cl)