

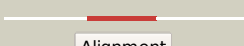
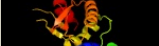

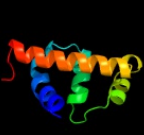

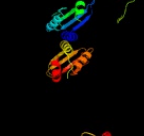

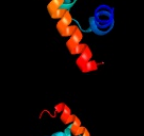



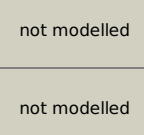


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1423_(whiA)_1597912_1598889
Date	Wed Jul 31 22:05:53 BST 2019
Unique Job ID	5f13fa60f8ff9368

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3hyiA_	 Alignment		100.0	22	PDB header: transcription regulator Chain: A: PDB Molecule: protein duf199/whia; PDBTitle: crystal structure of full-length duf199/whia from therratoga maritima
2	c3hyjD_	 Alignment		100.0	18	PDB header: transcription regulator Chain: D: PDB Molecule: protein duf199/whia; PDBTitle: crystal structure of the n-terminal laglidadg domain of duf199/whia
3	d1jvaa3	 Alignment		99.7	14	Fold: Homing endonuclease-like Superfamily: Homing endonucleases Family: Intein endonuclease
4	c1vdeA_	 Alignment		99.7	13	PDB header: endonuclease Chain: A: PDB Molecule: pi-scei; PDBTitle: pi-scei, a homing endonuclease with protein splicing2 activity
5	c1dq3A_	 Alignment		99.6	13	PDB header: hydrolase Chain: A: PDB Molecule: endonuclease; PDBTitle: crystal structure of an archaeal intein-encoded homing2 endonuclease pi-pfui
6	c1b24A_	 Alignment		99.6	12	PDB header: intron-encoded Chain: A: PDB Molecule: protein (i-dmoi); PDBTitle: i-dmoi, intron-encoded endonuclease
7	d1dq3a4	 Alignment		99.6	17	Fold: Homing endonuclease-like Superfamily: Homing endonucleases Family: Intein endonuclease
8	c2cw8A_	 Alignment		99.5	19	PDB header: hydrolase Chain: A: PDB Molecule: endonuclease pi-pkoi; PDBTitle: crystal structure of intein homing endonuclease ii
9	c1r7mA_	 Alignment		98.6	8	PDB header: hydrolase/dna Chain: A: PDB Molecule: intron-encoded endonuclease i-scei; PDBTitle: the homing endonuclease i-scei bound to its dna recognition2 region
10	c2dchX_	 Alignment		97.4	13	PDB header: hydrolase Chain: X: PDB Molecule: putative homing endonuclease; PDBTitle: crystal structure of archaeal intron-encoded homing endonuclease i-2 tsp061i
11	c2ab5B_	 Alignment		97.0	14	PDB header: protein binding Chain: B: PDB Molecule: mrna maturase; PDBTitle: bi3 laglidadg maturase

12	d1xsva_	Alignment		96.8	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: YlxM/p13-like
13	d1r7ma2	Alignment		96.7	13	Fold: Homing endonuclease-like Superfamily: Homing endonucleases Family: Group I mobile intron endonuclease
14	c3fd2A_	Alignment		96.4	15	PDB header: hydrolase/dna Chain: A: PDB Molecule: site-specific dna endonuclease i-msoi; PDBTitle: crystal structure of mmsoi/dna complex with calcium
15	c5espA_	Alignment		95.9	20	PDB header: hydrolase/dna Chain: A: PDB Molecule: i-panmi; PDBTitle: crystal structure of laglidadg meganuclease i-panmi with coordinated2 calcium ions
16	d1s7oa_	Alignment		95.8	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: YlxM/p13-like
17	c5ipmF_	Alignment		94.7	15	PDB header: transcription, transferase/dna/rna Chain: F: PDB Molecule: rna polymerase sigma factor rpos; PDBTitle: sigmas-transcription initiation complex with 4-nt nascent rna
18	c2qwwB_	Alignment		94.5	12	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator, marr family; PDBTitle: crystal structure of multiple antibiotic-resistance repressor (marr)2 (yp_013417.1) from listeria monocytogenes 4b f2365 at 2.07 a3 resolution
19	c3qqyA_	Alignment		94.4	13	PDB header: hydrolase/dna Chain: A: PDB Molecule: ribosomal protein 3/homing endonuclease-like protein PDBTitle: crystal structure of a novel laglidadg homing endonuclease, i-onui2 (from ophiostoma novo-ulmi subsp. americana)
20	c2qojZ_	Alignment		94.3	12	PDB header: hydrolase/dna Chain: Z: PDB Molecule: intron-encoded dna endonuclease i-anii; PDBTitle: coevolution of a homing endonuclease and its host target sequence
21	d1laf5a_	Alignment	not modelled	94.3	18	Fold: Homing endonuclease-like Superfamily: Homing endonucleases Family: Group I mobile intron endonuclease
22	d1ttya_	Alignment	not modelled	94.3	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
23	d2cg4a1	Alignment	not modelled	94.2	7	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
24	d1t9ia_	Alignment	not modelled	93.9	15	Fold: Homing endonuclease-like Superfamily: Homing endonucleases Family: Group I mobile intron endonuclease
25	c2p6tH_	Alignment	not modelled	93.7	14	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
26	d1i1ga1	Alignment	not modelled	93.7	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
27	c2l4aA_	Alignment	not modelled	93.7	16	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
28	d2cfxa1	Alignment	not modelled	93.6	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
29	d1ku3a_	Alignment	not modelled	93.3	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase

29	v1ku3a_	Alignment	not modelled	93.3	24	sigma factors Family: Sigma4 domain
30	c2dbbA_	Alignment	not modelled	93.3	20	PDB header: transcriptional regulator Chain: A: PDB Molecule: putative hth-type transcriptional regulator ph0061; PDBTitle: crystal structure of ph0061
31	c3r7pA_	Alignment	not modelled	93.2	17	PDB header: hydrolase/dna Chain: A: PDB Molecule: ribosomal protein 3/homing endonuclease-like fusion PDBTitle: the crystal structure of i-ltri
32	d2cyya1	Alignment	not modelled	93.1	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
33	d1rp3a2	Alignment	not modelled	93.1	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
34	c2vbzA_	Alignment	not modelled	93.0	28	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
35	d1b24a2	Alignment	not modelled	93.0	20	Fold: Homing endonuclease-like Superfamily: Homing endonucleases Family: Group I mobile intron endonuclease
36	c2ia0A_	Alignment	not modelled	92.9	14	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)
37	c2e7xA_	Alignment	not modelled	92.8	23	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
38	c3mxA_	Alignment	not modelled	92.7	16	PDB header: hydrolase/dna Chain: A: PDB Molecule: scv3v2(g19s); PDBTitle: molecular basis of engineered meganuclease targeting of the endogenous2 human rag1 locus
39	c1i1gA_	Alignment	not modelled	92.6	14	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator lrpa; PDBTitle: crystal structure of the lrp-like transcriptional regulator from the2 archaeon pyrococcus furiosus
40	c3hugA_	Alignment	not modelled	92.5	12	PDB header: transcription/membrane protein Chain: A: PDB Molecule: rna polymerase sigma factor; PDBTitle: crystal structure of mycobacterium tuberculosis anti-sigma factor rslA2 in complex with -35 promoter binding domain of sigI
41	c4efjA_	Alignment	not modelled	92.4	13	PDB header: hydrolase/dna Chain: A: PDB Molecule: laglidadg endonuclease; PDBTitle: crystal structure of i-gzeii laglidadg homing endonuclease in complex2 with dna target site
42	c2wteB_	Alignment	not modelled	92.2	13	PDB header: antiviral protein Chain: B: PDB Molecule: csa3; PDBTitle: the structure of the crispr-associated protein, csa3, from2 sulfobolus solfataricus at 1.8 angstrom resolution.
43	c1mowG_	Alignment	not modelled	92.2	10	PDB header: hydrolase/dna Chain: G: PDB Molecule: chimera of homing endonuclease i-dmoi and dna endonuclease PDBTitle: e-drei
44	c2cg4B_	Alignment	not modelled	92.2	7	PDB header: transcription Chain: B: PDB Molecule: regulatory protein asnc; PDBTitle: structure of e.coli asnc
45	d1ku7a_	Alignment	not modelled	92.2	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
46	c5gkka_	Alignment	not modelled	92.1	8	PDB header: hydrolase Chain: A: PDB Molecule: putative homing endonuclease; PDBTitle: crystal structure of a homing endonuclease, i-tnai
47	c2lfwA_	Alignment	not modelled	92.1	14	PDB header: signaling protein Chain: A: PDB Molecule: phyr sigma-like domain; PDBTitle: nmr structure of the phyrsl-nepr complex from sphingomonas sp. fr1
48	c6dvdF_	Alignment	not modelled	92.1	13	PDB header: transferase/dna Chain: F: PDB Molecule: ecf rna polymerase sigma factor sigI; PDBTitle: crystal structure of mycobacterium tuberculosis transcription2 initiation complex(ecf sigma factor I) with 6 nt spacer and bromine3 labelled in position "-11
49	c2e1cA_	Alignment	not modelled	92.1	21	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
50	d2p7vb1	Alignment	not modelled	91.8	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
51	d1m5xa_	Alignment	not modelled	91.8	15	Fold: Homing endonuclease-like Superfamily: Homing endonucleases Family: Group I mobile intron endonuclease
52	c3iwfA_	Alignment	not modelled	91.7	2	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
53	c3vepA_	Alignment	not modelled	91.4	22	PDB header: membrane protein/transcription Chain: A: PDB Molecule: probable rna polymerase sigma-d factor; PDBTitle: crystal structure of sigd4 in complex with its negative regulator rsda
						PDB header: hydrolase/dna

54	c4vitD_	Alignment	not modelled	91.4	11	Chain: D: PDB Molecule: meganuclease i-aabmi; PDBTitle: crystal structure of laglidadg meganuclease i-aabmi bound to uncleaved2 dna
55	c6c05F_	Alignment	not modelled	91.1	23	PDB header: transcription Chain: F: PDB Molecule: rna polymerase sigma factor siga; PDBTitle: mycobacterium tuberculosis rnap holo/rbpa in relaxed state
56	c4yisA_	Alignment	not modelled	91.0	14	PDB header: hydrolase/dna Chain: A: PDB Molecule: meganuclease i-cpami; PDBTitle: crystal structure of laglidadg meganuclease i-cpami bound to uncleaved2 dna
57	c4pcaC_	Alignment	not modelled	90.9	19	PDB header: transcription Chain: C: PDB Molecule: possible transcriptional regulatory protein (probably PDBTitle: crystal structure of mtbaldr (rv2779c)
58	c5dukA_	Alignment	not modelled	90.8	13	PDB header: transcription regulator 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
59	c2lkpB_	Alignment	not modelled	90.7	28	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, arsr family; PDBTitle: solution structure of apo-nmtr
60	c2gqqB_	Alignment	not modelled	90.3	16	PDB header: transcription Chain: B: PDB Molecule: leucine-responsive regulatory protein; PDBTitle: crystal structure of e. coli leucine-responsive regulatory protein2 (lrp)
61	d1mowa1	Alignment	not modelled	90.3	16	Fold: Homing endonuclease-like Superfamily: Homing endonucleases Family: Group I mobile intron endonuclease
62	d2d1ha1	Alignment	not modelled	90.3	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: TrmB-like
63	d1smyf2	Alignment	not modelled	90.2	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
64	c3mx9A_	Alignment	not modelled	90.1	13	PDB header: hydrolase/dna Chain: A: PDB Molecule: protein scv3v2(g19s); PDBTitle: molecular basis of engineered meganuclease targeting of the endogenous2 human rag1 locus
65	c3i4pA_	Alignment	not modelled	90.1	11	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, asnc family; PDBTitle: crystal structure of asnc family transcriptional regulator from2 agrobacterium tumefaciens
66	c3t72o_	Alignment	not modelled	90.0	17	PDB header: transcription/dna Chain: O: PDB Molecule: pho box dna (strand 1); PDBTitle: phob(e)-sigma70(4)-(rnap-beta-flap-tip-helix)-dna transcription2 activation sub-complex
67	c2cfxD_	Alignment	not modelled	89.7	23	PDB header: transcription Chain: D: PDB Molecule: hth-type transcriptional regulator lrpc; PDBTitle: structure of b.subtilis lrpc
68	c6cmvA_	Alignment	not modelled	89.7	14	PDB header: gene regulation Chain: A: PDB Molecule: transcriptional regulator lrs14-like protein; PDBTitle: crystal structure of archaeal biofilm regulator (abfr2) from2 sulfobolus acidocaldarius
69	d1r1ta_	Alignment	not modelled	89.5	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ArsR-like transcriptional regulators
70	c4nb5D_	Alignment	not modelled	89.4	18	PDB header: dna binding protein Chain: D: PDB Molecule: dna binding protein; PDBTitle: crystal structure of a transcriptional regulator
71	c3cuoB_	Alignment	not modelled	89.4	20	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
72	c4czdA_	Alignment	not modelled	89.3	18	PDB header: lyase Chain: A: PDB Molecule: putative transcriptional regulator, asnc family; PDBTitle: sirohaem decarboxylase ahba/b - an enzyme with structural homology2 to the lrp/asnc transcription factor family that is part of the3 alternative haem biosynthesis pathway.
73	c4omzG_	Alignment	not modelled	89.1	16	PDB header: transcription Chain: G: PDB Molecule: nolr; PDBTitle: crystal structure of nolr from sinorhizobium fredii
74	d1b24a1	Alignment	not modelled	88.9	18	Fold: Homing endonuclease-like Superfamily: Homing endonucleases Family: Group I mobile intron endonuclease
75	d1sfxa_	Alignment	not modelled	88.8	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: TrmB-like
76	c1r22B_	Alignment	not modelled	88.8	22	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
77	d2ev0a1	Alignment	not modelled	88.8	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Iron-dependent repressor protein
78	c5fgmA_	Alignment	not modelled	88.1	15	PDB header: hydrolase Chain: A: PDB Molecule: ecf rna polymerase sigma factor sigr; PDBTitle: streptomyces coelicolor sigr region 4
79	d1p8kz1	Alignment	not modelled	88.0	14	Fold: Homing endonuclease-like Superfamily: Homing endonucleases Family: Group I mobile intron endonuclease

80	d1g3wa1	Alignment	not modelled	87.9	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Iron-dependent repressor protein
81	c6paxA	Alignment	not modelled	87.8	18	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
82	d1r1ua	Alignment	not modelled	87.5	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ArsR-like transcriptional regulators
83	c3pgkD	Alignment	not modelled	86.9	18	PDB header: transcription Chain: D: PDB Molecule: biofilm growth-associated repressor; PDBTitle: crystal structure of the transcriptional repressor bigr from xylella2 fastidiosa
84	c3mzyA	Alignment	not modelled	86.9	10	PDB header: rna binding protein Chain: A: PDB Molecule: rna polymerase sigma-h factor; PDBTitle: the crystal structure of the rna polymerase sigma-h factor from2 fusobacterium nucleatum to 2.5a
85	c5zx3F	Alignment	not modelled	86.5	15	PDB header: transcription Chain: F: PDB Molecule: ecf rna polymerase sigma factor sigh; PDBTitle: mycobacterium tuberculosis rna polymerase holoenzyme with ecf sigma2 factor sigma h
86	c3r0aB	Alignment	not modelled	86.5	9	PDB header: transcription regulator Chain: B: PDB Molecule: putative transcriptional regulator; PDBTitle: possible transcriptional regulator from methanosarcina mazei go1 (gi2 21227196)
87	d2isyA1	Alignment	not modelled	86.4	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Iron-dependent repressor protein
88	c5tw1F	Alignment	not modelled	86.2	19	PDB header: transcription activator/transferase/dna Chain: F: PDB Molecule: rna polymerase sigma factor siga; PDBTitle: crystal structure of a mycobacterium smegmatis transcription2 initiation complex with rbpa
89	c4loxA	Alignment	not modelled	86.1	16	PDB header: hydrolase/dna Chain: A: PDB Molecule: laglidadg homing endonuclease i-smami; PDBTitle: crystal structure of the i-smami laglidadg homing endonuclease bound2 to cleaved dna
90	c5jbrA	Alignment	not modelled	86.0	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein bcav_2135; PDBTitle: crystal structure of uncharacterized protein bcav_2135 from2 beutenbergia cavernae
91	c3jthA	Alignment	not modelled	85.5	15	PDB header: transcription Chain: A: PDB Molecule: transcription activator hlyu; PDBTitle: crystal structure of a transcriptional regulator hlyu from2 vibrio vulnificus cmcp6
92	d1or7a1	Alignment	not modelled	85.3	33	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
93	d1p8kz2	Alignment	not modelled	85.3	10	Fold: Homing endonuclease-like Superfamily: Homing endonucleases Family: Group I mobile intron endonuclease
94	c5a72B	Alignment	not modelled	85.1	15	PDB header: hydrolase/dna Chain: B: PDB Molecule: dna endonuclease i-cvui; PDBTitle: crystal structure of the homing endonuclease i-cvui in complex2 with its target (sro1.3) in the presence of 2 mm ca
95	c6j05B	Alignment	not modelled	84.7	17	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
96	c4czdD	Alignment	not modelled	84.7	18	PDB header: lyase Chain: D: PDB Molecule: putative transcriptional regulator, asnc family; PDBTitle: sirohaem decarboxylase ahba/b - an enzyme with structural homology2 to the lrp/asnc transcription factor family that is part of the3 alternative haem biosynthesis pathway.
97	c2nnnB	Alignment	not modelled	84.3	19	PDB header: transcription Chain: B: PDB Molecule: probable transcriptional regulator; PDBTitle: crystal structure of probable transcriptional regulator from2 pseudomonas aeruginosa
98	c1fx7C	Alignment	not modelled	84.0	15	PDB header: signaling protein Chain: C: PDB Molecule: iron-dependent repressor ider; PDBTitle: crystal structure of the iron-dependent regulator (ider) from2 mycobacterium tuberculosis
99	d1utaa	Alignment	not modelled	83.9	24	Fold: Ferredoxin-like Superfamily: Sporulation related repeat Family: Sporulation related repeat
100	c2h09A	Alignment	not modelled	83.5	17	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator mntr; PDBTitle: crystal structure of diphtheria toxin repressor like protein2 from e. coli
101	c6c03A	Alignment	not modelled	83.4	16	PDB header: transcription Chain: A: PDB Molecule: putative rna polymerase ecf-subfamily sigma factor; PDBTitle: the crystal structure streptomyces venezuelae rsbn-bldn complex
102	c3e54A	Alignment	not modelled	83.4	14	PDB header: hydrolase/dna Chain: A: PDB Molecule: rrna intron-encoded endonuclease; PDBTitle: archaeal intron-encoded homing endonuclease i-vdi141i complexed with2 dna
103	d2etha1	Alignment	not modelled	83.2	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
104	c1g3wA	Alignment	not modelled	82.9	13	PDB header: gene regulation Chain: A: PDB Molecule: diphtheria toxin repressor; PDBTitle: cd-cys102ser dtxr
105	d1jhfa1	Alignment	not modelled	82.9	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain

						Family: LexA repressor, N-terminal DNA-binding domain
106	d1ulya_	Alignment	not modelled	82.9	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Hypothetical protein PH1932
107	c2oqgA_	Alignment	not modelled	82.6	16	PDB header: transcription Chain: A: PDB Molecule: possible transcriptional regulator, arsr family protein; PDBTitle: arsr-like transcriptional regulator from rhodococcus sp. rha1
108	c5cviB_	Alignment	not modelled	82.6	18	PDB header: transcription regulator Chain: B: PDB Molecule: slor; PDBTitle: structure of the manganese regulator slor
109	d2bv6a1	Alignment	not modelled	82.6	5	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
110	c2o8xA_	Alignment	not modelled	82.4	11	PDB header: transcription Chain: A: PDB Molecule: probable rna polymerase sigma-c factor; PDBTitle: crystal structure of the "-35 element" promoter recognition domain of2 mycobacterium tuberculosis sigc
111	d1biaa1	Alignment	not modelled	82.2	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Biotin repressor-like
112	c3ctaA_	Alignment	not modelled	82.1	8	PDB header: transferase Chain: A: PDB Molecule: riboflavin kinase; PDBTitle: crystal structure of riboflavin kinase from thermoplasma acidophilum
113	d1ub9a_	Alignment	not modelled	82.0	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
114	c3f6oB_	Alignment	not modelled	82.0	21	PDB header: transcription regulator Chain: B: PDB Molecule: probable transcriptional regulator, arsr family PDBTitle: crystal structure of arsr family transcriptional regulator,2 rha00566
115	c4cxfA_	Alignment	not modelled	82.0	17	PDB header: transcription Chain: A: PDB Molecule: rna polymerase sigma factor cnrh; PDBTitle: structure of cnrh in complex with the cytosolic domain of cnry
116	c2x4hA_	Alignment	not modelled	81.8	10	PDB header: transcription Chain: A: PDB Molecule: hypothetical protein sso2273; PDBTitle: crystal structure of the hypothetical protein sso2273 from2 sulfobolus solfataricus
117	c6j0eB_	Alignment	not modelled	81.7	18	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
118	c2it0A_	Alignment	not modelled	81.6	15	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
119	c4mnuA_	Alignment	not modelled	81.4	10	PDB header: transcription regulator Chain: A: PDB Molecule: slya-like transcription regulator; PDBTitle: crystal structure of uncharacterized slya-like transcription regulator2 from listeria monocytogenes
120	c3vdoA_	Alignment	not modelled	81.2	14	PDB header: dna binding protein/protein binding Chain: A: PDB Molecule: rna polymerase sigma factor sigk; PDBTitle: structure of extra-cytoplasmic function(ecf) sigma factor sigk in2 complex with its negative regulator rska from mycobacterium3 tuberculosis