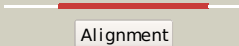

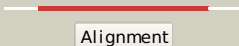

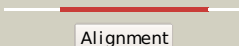
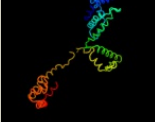
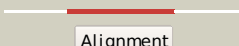



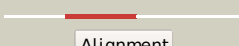

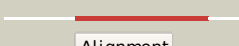





















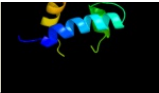
Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P0A0J0
Date	Tue Jul 17 17:05:06 BST 2012
Unique Job ID	b7b043ad490b71c4

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2a6eF_	 Alignment		100.0	67	PDB header: transferase Chain: F: PDB Molecule: rna polymerase sigma factor rpod; PDBTitle: crystal structure of the t. thermophilus rna polymerase2 holoenzyme
2	c3iydF_	 Alignment		100.0	52	PDB header: transcription/dna Chain: F: PDB Molecule: rna polymerase sigma factor rpod; PDBTitle: three-dimensional em structure of an intact activator-dependent2 transcription initiation complex
3	c1l9uH_	 Alignment		100.0	64	PDB header: transcription Chain: H: PDB Molecule: sigma factor siga; PDBTitle: thermus aquaticus rna polymerase holoenzyme at 4 a2 resolution
4	c1ku2A_	 Alignment		100.0	74	PDB header: transcription Chain: A: PDB Molecule: sigma factor siga; PDBTitle: crystal structure of thermus aquaticus rna polymerase sigma2 subunit fragment containing regions 1.2 to 3.1
5	d1ku2a2	 Alignment		100.0	75	Fold: Sigma2 domain of RNA polymerase sigma factors Superfamily: Sigma2 domain of RNA polymerase sigma factors Family: Sigma2 domain of RNA polymerase sigma factors
6	d1smyf3	 Alignment		100.0	74	Fold: Sigma2 domain of RNA polymerase sigma factors Superfamily: Sigma2 domain of RNA polymerase sigma factors Family: Sigma2 domain of RNA polymerase sigma factors
7	c1rp3G_	 Alignment		100.0	26	PDB header: transcription Chain: G: PDB Molecule: rna polymerase sigma factor sigma-28 (fliA); PDBTitle: cocrystal structure of the flagellar sigma/anti-sigma2 complex, sigma-28/flgm
8	d1siga_	 Alignment		100.0	34	Fold: Sigma2 domain of RNA polymerase sigma factors Superfamily: Sigma2 domain of RNA polymerase sigma factors Family: Sigma2 domain of RNA polymerase sigma factors
9	c3t72o_	 Alignment		99.8	63	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
10	c1or7A_	 Alignment		99.8	20	PDB header: transcription Chain: A: PDB Molecule: rna polymerase sigma-e factor; PDBTitle: crystal structure of escherichia coli sigmae with the cytoplasmic2 domain of its anti-sigma rsea
11	d1rp3a3	 Alignment		99.8	26	Fold: Sigma2 domain of RNA polymerase sigma factors Superfamily: Sigma2 domain of RNA polymerase sigma factors Family: Sigma2 domain of RNA polymerase sigma factors

12	d1smyf2	Alignment		99.8	59	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
13	c2q1zA	Alignment		99.7	17	PDB header: transcription Chain: A: PDB Molecule: rpoe, ecf sige; PDBTitle: crystal structure of rhodobacter sphaeroides sige in complex with the2 anti-sigma chr
14	d1ku7a	Alignment		99.7	63	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
15	d2p7vb1	Alignment		99.7	72	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
16	c3mzyA	Alignment		99.6	26	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
17	d1ttya	Alignment		99.6	69	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
18	d1ku3a	Alignment		99.6	66	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
19	c3t0yA	Alignment		99.4	16	PDB header: transcription regulator/protein binding Chain: A: PDB Molecule: response regulator; PDBTitle: structure of the phyr anti-anti-sigma domain bound to the anti-sigma2 factor, nepr
20	c2lfwA	Alignment		99.2	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
21	d1rp3a2	Alignment	not modelled	99.2	27	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
22	c3hugA	Alignment	not modelled	99.1	18	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 sigl
23	d1ku2a1	Alignment	not modelled	99.0	71	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma3 domain
24	c1l0oC	Alignment	not modelled	98.9	22	PDB header: protein binding Chain: C: PDB Molecule: sigma factor; PDBTitle: crystal structure of the bacillus stearothermophilus anti-2 sigma factor spoiab with the sporulation sigma factor3 sigmaf
25	d1l0oc	Alignment	not modelled	98.9	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
26	d1or7a2	Alignment	not modelled	98.9	24	Fold: Sigma2 domain of RNA polymerase sigma factors Superfamily: Sigma2 domain of RNA polymerase sigma factors Family: Sigma2 domain of RNA polymerase sigma factors
27	d1or7b2	Alignment	not modelled	98.8	24	Fold: Sigma2 domain of RNA polymerase sigma factors Superfamily: Sigma2 domain of RNA polymerase sigma factors Family: Sigma2 domain of RNA polymerase sigma factors
						PDB header: transcription Chain: A: PDB Molecule: rna polymerase sigma factor rpod;

28	c2k6xA	Alignment		98.8	22	PDBTitle: autoregulation of a group 1 bacterial sigma factor involves2 the formation of a region 1.1- induced compacted structure
29	d1or7a1	Alignment	not modelled	98.8	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
30	d1xsva	Alignment	not modelled	98.7	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: YlxM/p13-like
31	c2o8xA	Alignment	not modelled	98.6	19	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
32	d1s7oa	Alignment	not modelled	98.6	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: YlxM/p13-like
33	d1rp3a1	Alignment	not modelled	98.5	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma3 domain
34	c2o7gA	Alignment	not modelled	98.4	19	PDB header: transcription Chain: A: PDB Molecule: probable rna polymerase sigma-c factor; PDBTitle: crystal structure of the pribnow box recognition region of sigc from2 mycobacterium tuberculosis
35	d1yioa1	Alignment	not modelled	98.0	23	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)
36	c3qp5C	Alignment	not modelled	97.6	19	PDB header: transcription Chain: C: PDB Molecule: cvir transcriptional regulator; PDBTitle: crystal structure of cvir bound to antagonist chlorolactone (cl)
37	c1x3uA	Alignment	not modelled	97.6	17	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulatory protein fixj; PDBTitle: solution structure of the c-terminal transcriptional2 activator domain of fixj from sinorhizobium melilot
38	c2q0aA	Alignment	not modelled	97.6	22	PDB header: transcription Chain: A: PDB Molecule: probable transcriptional activator protein trar; PDBTitle: crystal structure of an anti-activation complex in bacterial quorum2 sensing
39	c3sztB	Alignment	not modelled	97.6	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
40	c1zljE	Alignment	not modelled	97.5	26	PDB header: transcription Chain: E: PDB Molecule: dormancy survival regulator; PDBTitle: crystal structure of the mycobacterium tuberculosis hypoxic2 response regulator dosr c-terminal domain
41	d1h3la	Alignment	not modelled	97.5	15	Fold: Sigma2 domain of RNA polymerase sigma factors Superfamily: Sigma2 domain of RNA polymerase sigma factors Family: Sigma2 domain of RNA polymerase sigma factors
42	c1h0mD	Alignment	not modelled	97.4	25	PDB header: transcription/dna Chain: D: PDB Molecule: transcriptional activator protein trar; PDBTitle: three-dimensional structure of the quorum sensing protein2 trar bound to its autoinducer and to its target dna
43	d1a04a1	Alignment	not modelled	97.4	20	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)
44	c2krfB	Alignment	not modelled	97.3	24	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulatory protein coma; PDBTitle: nmr solution structure of the dna binding domain of competence protein2 a
45	c2rnjA	Alignment	not modelled	97.3	23	PDB header: transcription Chain: A: PDB Molecule: response regulator protein vvar; PDBTitle: nmr structure of the s. aureus vvar dna binding domain
46	d1l3la1	Alignment	not modelled	97.3	28	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)
47	d1fsea	Alignment	not modelled	97.2	30	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)
48	d1p4wa	Alignment	not modelled	97.2	30	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)
49	c3cloC	Alignment	not modelled	97.1	17	PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of putative transcriptional regulator containing a2 luxr dna binding domain (np_811094.1) from bacteroides3 thetaiotomicron vpi-5482 at 2.04 a resolution
50	c2w48D	Alignment	not modelled	96.9	14	PDB header: transcription Chain: D: PDB Molecule: sorbitol operon regulator; PDBTitle: crystal structure of the full-length sorbitol operon2 regulator sorc from klebsiella pneumoniae
51	c3c3wB	Alignment	not modelled	96.9	24	PDB header: transcription Chain: B: PDB Molecule: two component transcriptional regulatory protein devr; PDBTitle: crystal structure of the mycobacterium tuberculosis hypoxic response2 regulator dosr
52	c3n0rA	Alignment	not modelled	96.7	16	PDB header: signaling protein Chain: A: PDB Molecule: response regulator; PDBTitle: structure of the phyr stress response regulator at 1.25 angstrom2 resolution

53	c3klnC_	Alignment	not modelled	96.5	21	PDB header: transcription Chain: C: PDB Molecule: transcriptional regulator, luxr family; PDBTitle: vibrio cholerae vpst
54	c1zn2A_	Alignment	not modelled	96.2	21	PDB header: transcription regulator Chain: A: PDB Molecule: response regulatory protein; PDBTitle: low resolution structure of response regulator styr
55	c2jpcA_	Alignment	not modelled	96.1	19	PDB header: dna binding protein Chain: A: PDB Molecule: ssrb; PDBTitle: ssrb dna binding protein
56	c1rnlA_	Alignment	not modelled	96.0	17	PDB header: signal transduction protein Chain: A: PDB Molecule: nitrate/nitrite response regulator protein narl; PDBTitle: the nitrate/nitrite response regulator protein narl from narl
57	c1u78A_	Alignment	not modelled	95.3	23	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
58	c2w7nA_	Alignment	not modelled	94.1	13	PDB header: transcription/dna Chain: A: PDB Molecule: trfb transcriptional repressor protein; PDBTitle: crystal structure of kora bound to operator dna: insight2 into repressor cooperation in rp4 gene regulation
59	d2d1ha1	Alignment	not modelled	94.0	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: TrmB-like
60	d1jhfa1	Alignment	not modelled	93.3	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: LexA repressor, N-terminal DNA-binding domain
61	d1biaa1	Alignment	not modelled	92.9	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Biotin repressor-like
62	c3r0aB_	Alignment	not modelled	92.7	16	PDB header: transcription regulator Chain: B: PDB Molecule: putative transcriptional regulator; PDBTitle: possible transcriptional regulator from methanosarcina mazei go1 (gi2 21227196)
63	d1nr3a_	Alignment	not modelled	92.5	21	Fold: DNA-binding protein Tfx Superfamily: DNA-binding protein Tfx Family: DNA-binding protein Tfx
64	d2o38a1	Alignment	not modelled	92.3	17	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE1354
65	c2o38A_	Alignment	not modelled	92.3	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: putative xre family transcriptional regulator
66	d2cfxa1	Alignment	not modelled	92.2	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
67	c2x4hA_	Alignment	not modelled	92.2	17	PDB header: transcription Chain: A: PDB Molecule: hypothetical protein sso2273; PDBTitle: crystal structure of the hypothetical protein sso2273 from2 sulfobolus solfataricus
68	c2elhA_	Alignment	not modelled	91.9	27	PDB header: dna binding protein Chain: A: PDB Molecule: cg11849-pa; PDBTitle: solution structure of the cenp-b n-terminal dna-binding2 domain of fruit fly distal antenna cg11849-pa
69	d1pdnc_	Alignment	not modelled	91.1	8	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
70	c2l4aA_	Alignment	not modelled	91.1	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
71	c2dbbA_	Alignment	not modelled	90.9	22	PDB header: transcriptional regulator Chain: A: PDB Molecule: putative hth-type transcriptional regulator ph0061; PDBTitle: crystal structure of ph0061
72	d2a6ca1	Alignment	not modelled	90.9	15	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE1354
73	c6paxA_	Alignment	not modelled	90.7	10	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
74	c2it0A_	Alignment	not modelled	90.3	21	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
75	d1stza1	Alignment	not modelled	90.1	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Heat-inducible transcription repressor HrcA, N-terminal domain
76	d2cg4a1	Alignment	not modelled	90.1	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
77	d1l1ga1	Alignment	not modelled	89.9	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
78	c2p6tH_	Alignment	not modelled	89.8	13	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 Fold: DNA/RNA-binding 3-helical bundle

79	dli5za1	Alignment	not modelled	89.5	30	Superfamily: "Winged helix" DNA-binding domain Family: CAP C-terminal domain-like
80	dlvz0a1	Alignment	not modelled	89.5	26	Fold: DNA/RNA-binding 3-helical bundle Superfamily: KorB DNA-binding domain-like Family: KorB DNA-binding domain-like
81	d1ft9a1	Alignment	not modelled	89.3	30	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: CAP C-terminal domain-like
82	c2cfxD_	Alignment	not modelled	89.2	11	PDB header: transcription Chain: D: PDB Molecule: hth-type transcriptional regulator lrpc; PDBTitle: structure of b.subtilis lrpc
83	c2vbzA_	Alignment	not modelled	89.1	19	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
84	c3fmyA_	Alignment	not modelled	89.0	18	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 (ygitb3021)
85	d2oz6a1	Alignment	not modelled	88.8	30	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: CAP C-terminal domain-like
86	d2cyya1	Alignment	not modelled	88.5	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
87	d2ao9a1	Alignment	not modelled	88.5	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Nanomeric phage protein-like
88	d2h6ca1	Alignment	not modelled	88.4	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: CAP C-terminal domain-like
89	c2wteB_	Alignment	not modelled	88.4	9	PDB header: antiviral protein Chain: B: PDB Molecule: csa3; PDBTitle: the structure of the crispr-associated protein, csa3, from2 sulfolobus solfataricus at 1.8 angstrom resolution.
90	c3nqoB_	Alignment	not modelled	88.2	15	PDB header: transcription Chain: B: PDB Molecule: marr-family transcriptional regulator; PDBTitle: crystal structure of a marr family transcriptional regulator (cd1569)2 from clostridium difficile 630 at 2.20 a resolution
91	d1trra_	Alignment	not modelled	87.9	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: TrpR-like Family: Trp repressor, TrpR
92	c3mfc_	Alignment	not modelled	87.9	29	PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulator; PDBTitle: putative transcriptional regulator from staphylococcus aureus.
93	c2gm4B_	Alignment	not modelled	87.8	12	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
94	c1y9qA_	Alignment	not modelled	87.8	27	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
95	d1rioa_	Alignment	not modelled	87.8	9	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
96	c2bnoA_	Alignment	not modelled	87.7	18	PDB header: oxidoreductase Chain: A: PDB Molecule: epoxidase; PDBTitle: the structure of hydroxypropylphosphonic acid epoxidase2 from s. wedmorenis.
97	d3e5ua1	Alignment	not modelled	87.6	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: CAP C-terminal domain-like
98	d2coha1	Alignment	not modelled	87.5	26	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: CAP C-terminal domain-like
99	d1k78a1	Alignment	not modelled	87.5	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
100	c3mkyP_	Alignment	not modelled	87.4	10	PDB header: dna binding protein/dna Chain: P: PDB Molecule: protein sobp; PDBTitle: structure of sobp(155-323)-18mer dna complex, i23 form
101	c2cg4B_	Alignment	not modelled	87.4	23	PDB header: transcription Chain: B: PDB Molecule: regulatory protein asnc; PDBTitle: structure of e.coli asnc
102	d1hlva1	Alignment	not modelled	87.3	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Centromere-binding
103	c2r0qF_	Alignment	not modelled	87.3	10	PDB header: recombination/dna Chain: F: PDB Molecule: putative transposon tn552 dna-invertase bin3; PDBTitle: crystal structure of a serine recombinase- dna regulatory2 complex
104	c3tgnA_	Alignment	not modelled	87.1	19	PDB header: transcription Chain: A: PDB Molecule: adc operon repressor adcr; PDBTitle: crystal structure of the zinc-dependent marr family transcriptional2 regulator adcr in the zn(ii)-bound state
105	c3trbA_	Alignment	not modelled	87.1	18	PDB header: dna binding protein Chain: A: PDB Molecule: virulence-associated protein i; PDBTitle: structure of an addiction module antidote protein of a

						higa (higa)2 family from coxiella burnetii PDB header: transcription regulator Chain: A: PDB Molecule: 150aa long hypothetical transcriptional regulator; PDBTitle: structure of the Irp/asnc like transcriptional regulator from <i>Sulfolobus tokodaii</i> 7 complexed with its cognate ligand
106	c2e7xA	Alignment	not modelled	87.1	11	PDB header: transcription Chain: A: PDB Molecule: gntr-family protein transcriptional regulator; PDBTitle: crystal structure of phnf from <i>Mycobacterium smegmatis</i>
107	c3f8mA	Alignment	not modelled	87.0	33	PDB header: transcription/dna Chain: A: PDB Molecule: diphtheria toxin repressor; PDBTitle: diphtheria tox repressor (c102d mutant) complexed with 2 nickel and dtxr consensus binding sequence
108	c1f5tA	Alignment	not modelled	87.0	22	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, crp/fnr family; PDBTitle: crystal structure of transcriptional regulator, crp/fnr family from <i>Porphyromonas gingivalis</i> (apc80792), structural genomics, mcsG
109	c2gauA	Alignment	not modelled	86.9	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ArsR-like transcriptional regulators
110	d1r1ua	Alignment	not modelled	86.9	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative hth-type transcriptional regulator pf0864; PDBTitle: transcriptional regulatory protein pf0864 from <i>Pyrococcus furiosus</i> a2 member of the asnc family (pf0864)
111	c2ia0A	Alignment	not modelled	86.7	27	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Cody HTH domain
112	d2b0la1	Alignment	not modelled	86.7	26	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: CAP C-terminal domain-like
113	d2gaua1	Alignment	not modelled	86.6	15	PDB header: transcription regulator Chain: A: PDB Molecule: putative hth-type transcription factor; PDBTitle: crystal structure of c.ecot38is
114	c2ef8A	Alignment	not modelled	86.6	21	PDB header: transcriptional regulation Chain: A: PDB Molecule: fatty acid metabolism regulator protein; PDBTitle: fadr, fatty acid responsive transcription factor from <i>E. coli</i>
115	c1e2xA	Alignment	not modelled	86.2	26	PDB header: hydrolase Chain: A: PDB Molecule: lexa repressor; PDBTitle: crystal structure of a lexa protein from <i>Thermotoga maritima</i>
116	c3k2zA	Alignment	not modelled	86.0	16	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
117	d1y7ya1	Alignment	not modelled	85.9	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: TrpR-like Family: Trp repressor, TrpR
118	d1jhga	Alignment	not modelled	85.8	18	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
119	d2ofya1	Alignment	not modelled	85.8	25	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
120	c2e1cA	Alignment	not modelled	85.7	18	