Phyre^2

Email	l.a.kelley@imperial.ac.uk
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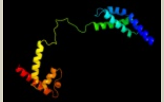
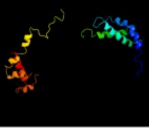
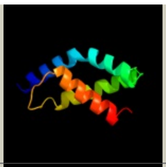
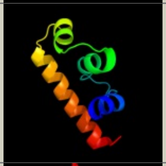
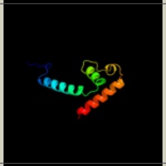
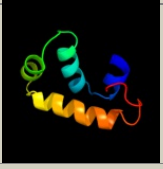
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1or7A_	Alignment		99.9	19	**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
2	c2q1zA_	Alignment		99.9	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**rpoe, ecf sige; **PDBTitle:** crystal structure of rhodobacter sphaeroides sige in complex with the2 anti-sigma chrr
3	c1rp3G_	Alignment		99.9	16	**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
4	c3mzyA_	Alignment		99.7	17	**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
5	c2a6eF_	Alignment		99.6	14	**PDB header:**transferase **Chain:** F: **PDB Molecule:**rna polymerase sigma factor rpod; **PDBTitle:** crystal structure of the t. thermophilus rna polymerase2 holoenzyme
6	c1l9uH_	Alignment		99.6	16	**PDB header:**transcription **Chain:** H: **PDB Molecule:**sigma factor siga; **PDBTitle:** thermus aquaticus rna polymerase holoenzyme at 4 a2 resolution
7	d1or7a2	Alignment		99.5	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
8	d1or7b2	Alignment		99.5	16	**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	c2o7gA_	Alignment		99.4	25	**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
10	c3hugA_	Alignment		99.4	23	**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
11	c3iydF_	Alignment		99.3	12	**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

12	d1h3la_	Alignment		99.3	20	**Fold:**Sigma2 domain of RNA polymerase sigma factors **Superfamily:**Sigma2 domain of RNA polymerase sigma factors **Family:**Sigma2 domain of RNA polymerase sigma factors
13	d1rp3a2	Alignment		99.3	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
14	d1or7a1	Alignment		99.1	27	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
15	c2o8xA_	Alignment		99.1	34	**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
16	d1s7oa_	Alignment		99.1	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**YlxM/p13-like
17	d1xsva_	Alignment		99.1	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**YlxM/p13-like
18	c3n0rA_	Alignment		99.0	16	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator; **PDBTitle:** structure of the phyr stress response regulator at 1.25 angstrom2 resolution
19	d1smyf2	Alignment		98.9	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
20	d1ttya_	Alignment		98.8	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
21	d1ku7a_	Alignment	not modelled	98.7	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
22	d1ku3a_	Alignment	not modelled	98.7	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
23	d1rp3a3	Alignment	not modelled	98.7	16	**Fold:**Sigma2 domain of RNA polymerase sigma factors **Superfamily:**Sigma2 domain of RNA polymerase sigma factors **Family:**Sigma2 domain of RNA polymerase sigma factors
24	d2p7vb1	Alignment	not modelled	98.5	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
25	c3t72o_	Alignment	not modelled	98.5	14	**PDB header:**transcription/dna **Chain:** O: **PDB Molecule:**pho box dna (strand 1); **PDBTitle:** phob(e)-sigma70(4)-(rnap-betha-flap-tip-helix)-dna transcription2 activation sub-complex
26	c1ku2A_	Alignment	not modelled	98.3	15	**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
27	d1yioa1	Alignment	not modelled	98.2	25	**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)
28	c3qp5C_	Alignment	not modelled	97.9	25	**PDB header:**transcription **Chain:** C: **PDB Molecule:**cvir transcriptional regulator; **PDBTitle:** crystal structure of cvir bound to antagonist chlorolactone (cl)
						PDB header:transcription

29	c3sztB_	Alignment	not modelled	97.9	26	**Chain:** B: **PDB Molecule:**quorum-sensing control repressor; **PDBTitle:** quorum sensing control repressor, qscr, bound to n-3-oxo-dodecanoyl-l-2 homoserine lactone
30	c1x3uA_	Alignment	not modelled	97.9	23	**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
31	d1a04a1	Alignment	not modelled	97.9	26	**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)
32	c2rnjA_	Alignment	not modelled	97.8	24	**PDB header:**transcription **Chain:** A: **PDB Molecule:**response regulator protein vrar; **PDBTitle:** nmr structure of the s. aureus vrar dna binding domain
33	c2q0oA_	Alignment	not modelled	97.8	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
34	c1h0mD_	Alignment	not modelled	97.8	27	**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
35	c1zljE_	Alignment	not modelled	97.8	30	**PDB header:**transcription **Chain:** E: **PDB Molecule:**dormancy survival regulator; **PDBTitle:** crystal structure of the mycobacterium tuberculosis hypoxic2 response regulator dosr c-terminal domain
36	c2krfB_	Alignment	not modelled	97.8	22	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulatory protein coma; **PDBTitle:** nmr solution structure of the dna binding domain of competence protein2 a
37	d1p4wa_	Alignment	not modelled	97.7	26	**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)
38	d1l3la1	Alignment	not modelled	97.6	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)
39	d1fsea_	Alignment	not modelled	97.6	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)
40	c3cloC_	Alignment	not modelled	97.6	23	**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 thetaiotaomicron vpi-5482 at 2.04 a resolution
41	c3c3wB_	Alignment	not modelled	97.5	29	**PDB header:**transcription **Chain:** B: **PDB Molecule:**two component transcriptional regulatory protein devr; **PDBTitle:** crystal structure of the mycobacterium tuberculosis hypoxic response2 regulator dosr
42	c3klnC_	Alignment	not modelled	97.4	26	**PDB header:**transcription **Chain:** C: **PDB Molecule:**transcriptional regulator, luxr family; **PDBTitle:** vibrio cholerae vpst
43	d1smyf3	Alignment	not modelled	97.3	9	**Fold:**Sigma2 domain of RNA polymerase sigma factors **Superfamily:**Sigma2 domain of RNA polymerase sigma factors **Family:**Sigma2 domain of RNA polymerase sigma factors
44	d1ku2a2	Alignment	not modelled	97.3	9	**Fold:**Sigma2 domain of RNA polymerase sigma factors **Superfamily:**Sigma2 domain of RNA polymerase sigma factors **Family:**Sigma2 domain of RNA polymerase sigma factors
45	c2jpcA_	Alignment	not modelled	97.3	25	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**ssrb; **PDBTitle:** ssrb dna binding protein
46	c1rnlA_	Alignment	not modelled	97.2	23	**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
47	c1zn2A_	Alignment	not modelled	97.2	26	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**response regulatory protein; **PDBTitle:** low resolution structure of response regulator styr
48	d1siga_	Alignment	not modelled	96.7	9	**Fold:**Sigma2 domain of RNA polymerase sigma factors **Superfamily:**Sigma2 domain of RNA polymerase sigma factors **Family:**Sigma2 domain of RNA polymerase sigma factors
49	c1u78A_	Alignment	not modelled	96.6	18	**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
50	c6paxA_	Alignment	not modelled	96.2	23	**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
51	d1pdnc_	Alignment	not modelled	96.2	26	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
52	c2cfxD_	Alignment	not modelled	96.0	21	**PDB header:**transcription **Chain:** D: **PDB Molecule:**hth-type transcriptional regulator lrpc; **PDBTitle:** structure of b.subtilis lrpc
53	c2cg4B_	Alignment	not modelled	95.7	21	**PDB header:**transcription **Chain:** B: **PDB Molecule:**regulatory protein asnc; **PDBTitle:** structure of e.coli asnc
54	c2vbzA_	Alignment	not modelled	95.7	31	**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
55	c2dbbA_	Alignment	not modelled	95.7	18	**PDB header:**transcriptional regulator **Chain:** A: **PDB Molecule:**putative hth-type transcriptional regulator ph0061; **PDBTitle:** crystal structure of ph0061
56	d2cg4a1	Alignment	not modelled	95.4	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
57	d1k78a1	Alignment	not modelled	95.4	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
58	c2p6tH_	Alignment	not modelled	95.2	18	**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
59	d2cfxa1	Alignment	not modelled	95.2	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
60	c2elhA_	Alignment	not modelled	95.1	14	**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
61	c2ia0A_	Alignment	not modelled	94.9	28	**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)
62	d1i1ga1	Alignment	not modelled	94.9	28	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
63	c1i1gA_	Alignment	not modelled	94.8	28	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator lrpa; **PDBTitle:** crystal structure of the lrp-like transcriptional regulator from the2 archaeon pyrococcus furiosus
64	c2e1cA_	Alignment	not modelled	94.8	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	c2e7xA_	Alignment	not modelled	94.7	14	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**150aa long hypothetical transcriptional regulator; **PDBTitle:** structure of the lrp/asnc like transcriptional regulator from2 sulfolobus tokodaii 7 complexed with its cognate ligand
66	d1trra_	Alignment	not modelled	94.7	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**TrpR-like **Family:**Trp repressor, TrpR
67	c3i4pA_	Alignment	not modelled	94.6	24	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, asnc family; **PDBTitle:** crystal structure of asnc family transcriptional regulator from2 agrobacterium tumefaciens
68	c2l4aA_	Alignment	not modelled	94.5	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
69	d2cyya1	Alignment	not modelled	94.4	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
70	d6paxa1	Alignment	not modelled	94.4	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
71	d1jhga_	Alignment	not modelled	94.4	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**TrpR-like **Family:**Trp repressor, TrpR
72	d2jn6a1	Alignment	not modelled	94.4	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Cgl2762-like
73	d2d1ha1	Alignment	not modelled	93.7	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**TrmB-like
74	c3frwF_	Alignment	not modelled	93.4	24	**PDB header:**structural genomics, unknown function **Chain:** F: **PDB Molecule:**putative trp repressor protein; **PDBTitle:** crystal structure of putative trpr protein from ruminococcus obeum
75	c2gqqB_	Alignment	not modelled	93.1	21	**PDB header:**transcription **Chain:** B: **PDB Molecule:**leucine-responsive regulatory protein; **PDBTitle:** crystal structure of e. coli leucine-responsive regulatory protein2 (lrp)
76	c3korD_	Alignment	not modelled	93.1	21	**PDB header:**transcription **Chain:** D: **PDB Molecule:**possible trp repressor; **PDBTitle:** crystal structure of a putative trp repressor from staphylococcus2 aureus
77	c2w7nA_	Alignment	not modelled	93.0	20	**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
78	d1biaa1	Alignment	not modelled	92.9	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Biotin repressor-like
79	d1r1ua_	Alignment	not modelled	92.8	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ArsR-like transcriptional regulators
						PDB header:transcription regulator

80	c2k27A_	Alignment	not modelled	92.7	23	**Chain:** A: **PDB Molecule:**paired box protein pax-8; **PDBTitle:** solution structure of human pax8 paired box domain
81	c1r22B_	Alignment	not modelled	92.3	24	**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
82	c2gm4B_	Alignment	not modelled	92.3	26	**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
83	c2r0qF_	Alignment	not modelled	92.2	16	**PDB header:**recombination/dna **Chain:** F: **PDB Molecule:**putative transposon tn552 dna-invertase bin3; **PDBTitle:** crystal structure of a serine recombinase- dna regulatory2 complex
84	d1uxca_	Alignment	not modelled	92.0	33	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
85	d1hlva1	Alignment	not modelled	92.0	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Centromere-binding
86	c2da4A_	Alignment	not modelled	91.6	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein dkfzp686k21156; **PDBTitle:** solution structure of the homeobox domain of the2 hypothetical protein, dkfzp686k21156
87	c2oqgA_	Alignment	not modelled	91.6	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**possible transcriptional regulator, arsr family protein; **PDBTitle:** arsr-like transcriptional regulator from rhodococcus sp. rha1
88	c2rn7A_	Alignment	not modelled	91.3	23	**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
89	c3r0aB_	Alignment	not modelled	91.3	13	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** possible transcriptional regulator from methanosarcina mazei go1 (gi2 21227196)
90	d2hsga1	Alignment	not modelled	91.2	22	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
91	d1vz0a1	Alignment	not modelled	91.1	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**KorB DNA-binding domain-like **Family:**KorB DNA-binding domain-like
92	c3nqoB_	Alignment	not modelled	90.9	21	**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
93	c3tgnA_	Alignment	not modelled	90.9	30	**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
94	d1rr7a_	Alignment	not modelled	90.8	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Middle operon regulator, Mor
95	c1rr7A_	Alignment	not modelled	90.8	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**middle operon regulator; **PDBTitle:** crystal structure of the middle operon regulator protein of2 bacteriophage mu
96	d2r5yb1	Alignment	not modelled	90.8	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
97	c2wteB_	Alignment	not modelled	90.7	11	**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.
98	d1jhfa1	Alignment	not modelled	90.7	27	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**LexA repressor, N-terminal DNA-binding domain
99	d1uxda_	Alignment	not modelled	90.5	31	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
100	d1r1ta_	Alignment	not modelled	90.5	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ArsR-like transcriptional regulators
101	d1qpza1	Alignment	not modelled	90.2	20	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
102	d1lcda_	Alignment	not modelled	89.8	26	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
103	c1hlvA_	Alignment	not modelled	89.3	13	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**major centromere autoantigen b; **PDBTitle:** crystal structure of cenp-b(1-129) complexed with the cenp-2 b box dna
104	c3cuoB_	Alignment	not modelled	89.1	16	**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
105	d2p4wa1	Alignment	not modelled	89.0	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**PF1790-like

106	c1kgsA_	Alignment	not modelled	89.0	13	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna binding response regulator d; **PDBTitle:** crystal structure at 1.50 a of an ompr/phob homolog from thermotoga2 maritima
107	c2x4hA_	Alignment	not modelled	88.8	26	**PDB header:**transcription **Chain:** A: **PDB Molecule:**hypothetical protein sso2273; **PDBTitle:** crystal structure of the hypothetical protein sso2273 from2 sulfolobus solfataricus
108	c3pvpA_	Alignment	not modelled	88.8	16	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**chromosomal replication initiator protein dnaa; **PDBTitle:** structure of mycobacterium tuberculosis dnaa-dbd in complex with box22 dna
109	c2kkoB_	Alignment	not modelled	88.7	14	**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.
110	d1r71a_	Alignment	not modelled	88.3	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**KorB DNA-binding domain-like **Family:**KorB DNA-binding domain-like
111	c2lk2A_	Alignment	not modelled	88.3	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**homeobox protein tgif1; **PDBTitle:** solution nmr structure of homeobox domain (171-248) of human homeobox2 protein tgif1, northeast structural genomics consortium target3 hr4411b
112	c3jthA_	Alignment	not modelled	88.2	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription activator hlyu; **PDBTitle:** crystal structure of a transcriptional regulator hlyu from2 vibrio vulnificus cmcp6
113	d1efaa1	Alignment	not modelled	88.2	26	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
114	c1r71B_	Alignment	not modelled	88.2	16	**PDB header:**transcription/dna **Chain:** B: **PDB Molecule:**transcriptional repressor protein korb; **PDBTitle:** crystal structure of the dna binding domain of korb in2 complex with the operator dna
115	c3f6oB_	Alignment	not modelled	87.8	19	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**probable transcriptional regulator, arsr family **PDBTitle:** crystal structure of arsr family transcriptional regulator,2 rha00566
116	d2bjca1	Alignment	not modelled	87.7	31	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
117	d1j5ya1	Alignment	not modelled	87.5	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Biotin repressor-like
118	d1ku9a_	Alignment	not modelled	87.5	30	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**DNA-binding protein Mj223
119	c2zkzC_	Alignment	not modelled	87.4	16	**PDB header:**transcription **Chain:** C: **PDB Molecule:**transcriptional repressor pagr; **PDBTitle:** crystal structure of the transcriptional repressor pagr of bacillus2 anthracis
120	c2l8nA_	Alignment	not modelled	87.4	26	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional repressor cytr; **PDBTitle:** nmr structure of the cytidine repressor dna binding domain in presence2 of operator half-site dna