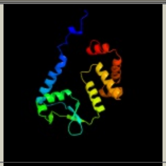
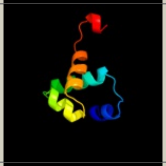
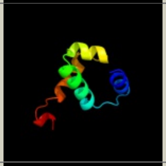
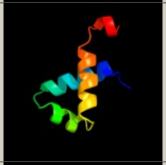
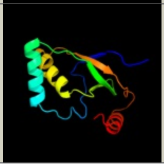
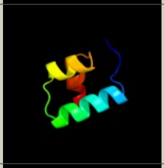
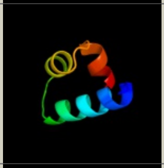
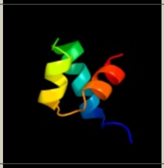
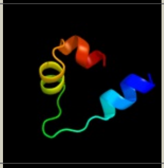
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P77174
Date	Thu Jan 5 12:25:59 GMT 2012
Unique Job ID	7f3c96e86f1a1294

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1vz0B_	Alignment		100.0	18	**PDB header:**nuclear protein **Chain:** B: **PDB Molecule:**chromosome partitioning protein parb; **PDBTitle:** chromosome segregation protein spo0j from thermus2 thermophilus
2	d1vk1a_	Alignment		99.9	14	**Fold:**ParB/Sulfiredoxin **Superfamily:**ParB/Sulfiredoxin **Family:**Hypothetical protein PF0380
3	d1vz0a2	Alignment		99.9	23	**Fold:**ParB/Sulfiredoxin **Superfamily:**ParB/Sulfiredoxin **Family:**ParB-like nuclease domain
4	d1xw3a1	Alignment		99.8	18	**Fold:**ParB/Sulfiredoxin **Superfamily:**ParB/Sulfiredoxin **Family:**Sulfiredoxin-like
5	d2b6fa1	Alignment		99.8	17	**Fold:**ParB/Sulfiredoxin **Superfamily:**ParB/Sulfiredoxin **Family:**Sulfiredoxin-like
6	d1r71a_	Alignment		99.3	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**KorB DNA-binding domain-like **Family:**KorB DNA-binding domain-like
7	c1r71B_	Alignment		99.3	20	**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
8	d1vz0a1	Alignment		98.7	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**KorB DNA-binding domain-like **Family:**KorB DNA-binding domain-like
9	c3mkyP_	Alignment		98.0	6	**PDB header:**dna binding protein/dna **Chain:** P: **PDB Molecule:**protein sopb; **PDBTitle:** structure of sopb(155-323)-18mer dna complex, i23 form
10	c3mkzU_	Alignment		97.9	6	**PDB header:**dna-binding protein/dna **Chain:** U: **PDB Molecule:**protein sopb; **PDBTitle:** structure of sopb(155-272)-18mer complex, p21 form
11	d2hwja1	Alignment		97.5	9	**Fold:**ParB/Sulfiredoxin **Superfamily:**ParB/Sulfiredoxin **Family:**Atu1540-like

12	c2w48D_	Alignment		96.3	21	**PDB header:**transcription **Chain:** D: **PDB Molecule:**sorbitol operon regulator; **PDBTitle:** crystal structure of the full-length sorbitol operon2 regulator sorc from klebsiella pneumoniae
13	c1u78A_	Alignment		95.6	7	**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
14	c2x48B_	Alignment		93.7	21	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**cag38821; **PDBTitle:** orf 55 from sulfolobus islandicus rudivirus 1
15	c2elhA_	Alignment		93.7	5	**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
16	d1pdnc_	Alignment		93.5	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
17	c3ivpD_	Alignment		93.4	13	**PDB header:**dna binding protein **Chain:** D: **PDB Molecule:**putative transposon-related dna-binding protein; **PDBTitle:** the structure of a possible transposon-related dna-binding protein2 from clostridium difficile 630.
18	d2o38a1	Alignment		93.3	12	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**NE1354
19	c2o38A_	Alignment		93.3	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** putative xre family transcriptional regulator
20	d2a6ca1	Alignment		93.1	24	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**NE1354
21	d1k78a1	Alignment	not modelled	93.1	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
22	c3eusB_	Alignment	not modelled	92.7	12	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**dna-binding protein; **PDBTitle:** the crystal structure of the dna binding protein from silicibacter2 pomeroyi
23	d2ofya1	Alignment	not modelled	92.4	10	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
24	c3e7lD_	Alignment	not modelled	92.3	15	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** crystal structure of sigma54 activator ntrc4's dna binding2 domain
25	c3dnvB_	Alignment	not modelled	92.2	16	**PDB header:**transcription/dna **Chain:** B: **PDB Molecule:**hth-type transcriptional regulator hipb; **PDBTitle:** mdt protein
26	c1umqA_	Alignment	not modelled	91.8	13	**PDB header:**dna-binding protein **Chain:** A: **PDB Molecule:**photosynthetic apparatus regulatory protein; **PDBTitle:** solution structure and dna binding of the effector domain2 from the global regulator prra(rega) from r. sphaeroides:3 insights into dna binding specificity
27	d1umqa_	Alignment	not modelled	91.8	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
28	c3pxpA_	Alignment	not modelled	91.8	13	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**helix-turn-helix domain protein; **PDBTitle:** crystal structure of a pas and dna binding domain containing protein2 (caur 2278) from chloroflexus aurantiacus j-

						10-fl at 2.30 a3 resolution
29	d1hlva1	Alignment	not modelled	91.7	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Centromere-binding
30	c3t76A_	Alignment	not modelled	91.7	9	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator vanug; **PDBTitle:** crystal structure of transcriptional regulator vanug, form ii
31	d1a9xa1	Alignment	not modelled	91.5	21	**Fold:**Carbamoyl phosphate synthetase, large subunit connection domain **Superfamily:**Carbamoyl phosphate synthetase, large subunit connection domain **Family:**Carbamoyl phosphate synthetase, large subunit connection domain
32	c6paxA_	Alignment	not modelled	91.5	20	**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
33	c1y9qA_	Alignment	not modelled	91.4	9	**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
34	d1bw6a_	Alignment	not modelled	91.3	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Centromere-binding
35	d6paxa1	Alignment	not modelled	91.0	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
36	d1fipa_	Alignment	not modelled	90.7	5	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
37	c2jvlA_	Alignment	not modelled	90.4	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**trmbf1; **PDBTitle:** nmr structure of the c-terminal domain of mbf1 of trichoderma reesei
38	d1etob_	Alignment	not modelled	90.3	5	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
39	c3op9A_	Alignment	not modelled	90.3	17	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**pli0006 protein; **PDBTitle:** crystal structure of transcriptional regulator from listeria innocua
40	c2ef8A_	Alignment	not modelled	90.3	10	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**putative transcription factor; **PDBTitle:** crystal structure of c.ecot38is
41	c3f6wE_	Alignment	not modelled	90.2	21	**PDB header:**dna binding protein **Chain:** E: **PDB Molecule:**xre-family like protein; **PDBTitle:** xre-family like protein from pseudomonas syringae pv. tomato str.2 dc3000
42	d1y7ya1	Alignment	not modelled	90.2	20	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
43	c2bnoA_	Alignment	not modelled	90.1	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**epoxidase; **PDBTitle:** the structure of hydroxypropylphosphonic acid epoxidase2 from s. wedmorenis.
44	d1ntca_	Alignment	not modelled	90.0	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
45	c3fmyA_	Alignment	not modelled	90.0	13	**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 (ygit/b3021)
46	c2gm4B_	Alignment	not modelled	90.0	20	**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
47	d1rioa_	Alignment	not modelled	89.7	17	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
48	c3omtA_	Alignment	not modelled	89.7	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.
49	c2ppxA_	Alignment	not modelled	89.7	4	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein atu1735; **PDBTitle:** crystal structure of a hth xre-family like protein from agrobacterium2 tumefaciens
50	d2ppxa1	Alignment	not modelled	89.7	4	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
51	c2r0qF_	Alignment	not modelled	89.5	31	**PDB header:**recombination/dna **Chain:** F: **PDB Molecule:**putative transposon tn552 dna-invertase bin3; **PDBTitle:** crystal structure of a serine recombinase- dna regulatory2 complex
52	c3b7hA_	Alignment	not modelled	89.3	24	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**prophage lp1 protein 11; **PDBTitle:** crystal structure of the prophage lp1 protein 11
53	d1etxa_	Alignment	not modelled	89.2	5	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
54	c3bs3A_	Alignment	not modelled	88.9	11	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**putative dna-binding protein;

54	c3bs3A_	Alignment	not modelled	88.9	11	**PDBTitle:** crystal structure of a putative dna-binding protein from bacteroides2 fragilis
55	c3cecA_	Alignment	not modelled	88.4	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative antidote protein of plasmid maintenance system; **PDBTitle:** crystal structure of a putative antidote protein of plasmid2 maintenance system (npun_f2943) from nostoc punctiforme pcc 73102 at3 1.60 a resolution
56	c2q0oA_	Alignment	not modelled	88.3	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**probable transcriptional activator protein trar; **PDBTitle:** crystal structure of an anti-activation complex in bacterial quorum2 sensing
57	c3f52A_	Alignment	not modelled	88.3	9	**PDB header:**transcription activator **Chain:** A: **PDB Molecule:**clp gene regulator (clgr); **PDBTitle:** crystal structure of the clp gene regulator clgr from c. glutamicum
58	d1utxa_	Alignment	not modelled	88.1	4	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
59	c1b0nA_	Alignment	not modelled	88.0	6	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**protein (sinr protein); **PDBTitle:** sinr protein/sini protein complex
60	c3clcC_	Alignment	not modelled	88.0	9	**PDB header:**transcription regulator/dna **Chain:** C: **PDB Molecule:**regulatory protein; **PDBTitle:** crystal structure of the restriction-modification controller protein2 c.esp1396i tetramer in complex with its natural 35 base-pair operator
61	d1sq8a_	Alignment	not modelled	87.9	26	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
62	d1r69a_	Alignment	not modelled	87.9	21	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
63	d2b5aa1	Alignment	not modelled	87.8	9	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
64	c3sztB_	Alignment	not modelled	87.4	17	**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
65	d1y9qa1	Alignment	not modelled	87.3	9	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Probable transcriptional regulator VC1968, N-terminal domain
66	c2ebyA_	Alignment	not modelled	87.3	24	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative hth-type transcriptional regulator ybaq; **PDBTitle:** crystal structure of a hypothetical protein from e. coli
67	c3kxaD_	Alignment	not modelled	87.3	14	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of ngo0477 from neisseria gonorrhoeae
68	d1x57a1	Alignment	not modelled	87.2	7	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**EDF1-like
69	d1adra_	Alignment	not modelled	87.0	17	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
70	d1b0na2	Alignment	not modelled	86.9	10	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
71	d2jn6a1	Alignment	not modelled	86.8	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Cgl2762-like
72	d2icta1	Alignment	not modelled	86.8	19	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
73	c3mlfC_	Alignment	not modelled	86.5	18	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**transcriptional regulator; **PDBTitle:** putative transcriptional regulator from staphylococcus aureus.
74	d1lmb3_	Alignment	not modelled	86.5	18	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
75	c2cg4B_	Alignment	not modelled	86.3	15	**PDB header:**transcription **Chain:** B: **PDB Molecule:**regulatory protein asnc; **PDBTitle:** structure of e.coli asnc
76	d1g2ha_	Alignment	not modelled	86.1	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
77	d1fsea_	Alignment	not modelled	86.0	18	**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)
78	c3trbA_	Alignment	not modelled	85.9	15	**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
79	d1tc3c_	Alignment	not modelled	85.7	7	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
						PDB header:viral protein

80	c2xcjB_	Alignment	not modelled	85.5	9	**Chain:** B: **PDB Molecule:**c protein; **PDBTitle:** crystal structure of p2 c, the immunity repressor of2 temperate e. coli phage p2
81	c1zljE_	Alignment	not modelled	85.4	11	**PDB header:**transcription **Chain:** E: **PDB Molecule:**dormancy survival regulator; **PDBTitle:** crystal structure of the mycobacterium tuberculosis hypoxic2 response regulator dosr c-terminal domain
82	d1llib_	Alignment	not modelled	85.2	15	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
83	c2ewtA_	Alignment	not modelled	85.0	15	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**putative dna-binding protein; **PDBTitle:** crystal structure of the dna-binding domain of bldd
84	c3hugA_	Alignment	not modelled	85.0	15	**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
85	d2cg4a1	Alignment	not modelled	84.9	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
86	c3mzyA_	Alignment	not modelled	84.6	14	**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
87	d2croa_	Alignment	not modelled	84.5	6	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
88	c2kpjA_	Alignment	not modelled	84.4	8	**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
89	c3gn5B_	Alignment	not modelled	84.4	15	**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)
90	c2fjrB_	Alignment	not modelled	84.3	9	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**repressor protein ci; **PDBTitle:** crystal structure of bacteriophage 186
91	c2p6tH_	Alignment	not modelled	84.1	21	**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
92	d2cyya1	Alignment	not modelled	84.0	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
93	c1x3uA_	Alignment	not modelled	83.9	14	**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
94	d1a04a1	Alignment	not modelled	83.9	19	**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)
95	c1rp3G_	Alignment	not modelled	83.8	14	**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
96	d2r1jl1	Alignment	not modelled	83.8	17	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
97	c2dbbA_	Alignment	not modelled	83.8	15	**PDB header:**transcriptional regulator **Chain:** A: **PDB Molecule:**putative hth-type transcriptional regulator ph0061; **PDBTitle:** crystal structure of ph0061
98	c2krfB_	Alignment	not modelled	83.6	9	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulatory protein coma; **PDBTitle:** nmr solution structure of the dna binding domain of competence protein2 a
99	c3qp5C_	Alignment	not modelled	83.4	9	**PDB header:**transcription **Chain:** C: **PDB Molecule:**cvir transcriptional regulator; **PDBTitle:** crystal structure of cvir bound to antagonist chlorolactone (cl)
100	c3frwF_	Alignment	not modelled	83.2	8	**PDB header:**structural genomics, unknown function **Chain:** F: **PDB Molecule:**putative trp repressor protein; **PDBTitle:** crystal structure of putative trpr protein from ruminococcus obeum
101	d1nera_	Alignment	not modelled	83.1	5	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
102	d1l3la1	Alignment	not modelled	83.0	11	**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)
103	c2vbzA_	Alignment	not modelled	83.0	22	**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
104	d1rp3a1	Alignment	not modelled	82.9	36	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma3 domain
105	d1p4wa	Alignment	not modelled	82.8	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response

105	d1p4wa_	Alignment	not modelled	82.8	14	regulators **Family:**GerE-like (LuxR/UhpA family of transcriptional regulators)
106	c2k27A_	Alignment	not modelled	82.8	18	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**paired box protein pax-8; **PDBTitle:** solution structure of human pax8 paired box domain
107	c2wusR_	Alignment	not modelled	82.4	9	**PDB header:**structural protein **Chain:** R: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** bacterial actin mreb assembles in complex with cell shape2 protein rodz
108	c1hlvA_	Alignment	not modelled	82.2	12	**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
109	c1h0mD_	Alignment	not modelled	82.2	11	**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
110	d1s7oa_	Alignment	not modelled	82.2	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**YlxM/p13-like
111	c3i4pA_	Alignment	not modelled	82.1	18	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, asnc family; **PDBTitle:** crystal structure of asnc family transcriptional regulator from2 agrobacterium tumefaciens
112	c2jpcA_	Alignment	not modelled	81.9	20	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**ssrb; **PDBTitle:** ssrb dna binding protein
113	d1trra_	Alignment	not modelled	81.2	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**TrpR-like **Family:**Trp repressor, TrpR
114	c3fymA_	Alignment	not modelled	81.2	13	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** the 1a structure of ymfm, a putative dna-binding membrane2 protein from staphylococcus aureus
115	d2d1ha1	Alignment	not modelled	81.0	5	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**TrmB-like
116	c3korD_	Alignment	not modelled	80.4	15	**PDB header:**transcription **Chain:** D: **PDB Molecule:**possible trp repressor; **PDBTitle:** crystal structure of a putative trp repressor from staphylococcus2 aureus
117	c3bdnB_	Alignment	not modelled	80.4	15	**PDB header:**transcription/dna **Chain:** B: **PDB Molecule:**lambda repressor; **PDBTitle:** crystal structure of the lambda repressor
118	c2ia0A_	Alignment	not modelled	80.4	13	**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)
119	c1or7A_	Alignment	not modelled	79.8	8	**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
120	d1i1ga1	Alignment	not modelled	79.7	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain