Phyre^2

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Description	P0CF42
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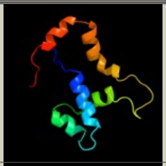
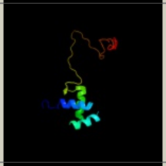
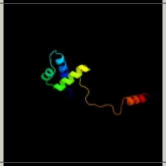
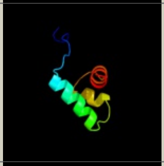
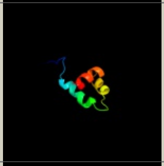
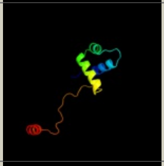
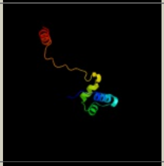
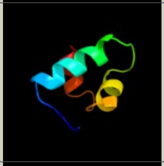
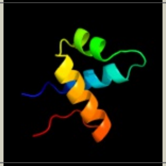
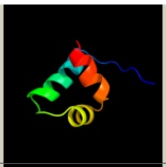
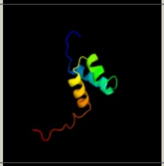
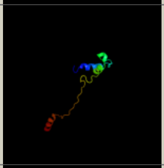
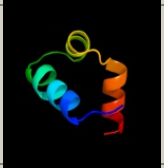
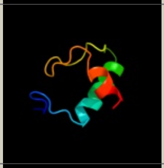
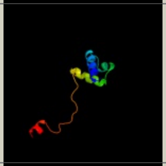
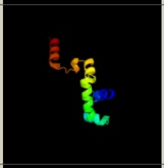
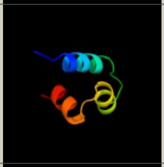
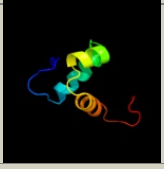
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2jn6a1	Alignment		99.7	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Cgl2762-like
2	c2rn7A_	Alignment		99.6	22	**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
3	c6paxA_	Alignment		98.4	13	**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
4	c1hlvA_	Alignment		98.4	34	**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
5	c2elhA_	Alignment		98.4	35	**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
6	d1pdnc_	Alignment		98.3	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
7	d1hlva1	Alignment		98.1	30	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Centromere-binding
8	c1u78A_	Alignment		98.1	5	**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
9	d1bw6a_	Alignment		98.0	33	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Centromere-binding
10	d6paxa1	Alignment		97.9	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
11	d1k78a1	Alignment		97.9	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain

12	c2gloA_	Alignment		97.8	18	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**brinker cg9653-pa; **PDBTitle:** solution structure of the brinker dna binding domain in2 complex with the omb enhancer
13	d2coba1	Alignment		97.7	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Psq domain
14	c2k27A_	Alignment		97.3	16	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**paired box protein pax-8; **PDBTitle:** solution structure of human pax8 paired box domain
15	c3hefB_	Alignment		96.9	17	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**gene 1 protein; **PDBTitle:** crystal structure of the bacteriophage sf6 terminase small2 subunit
16	c1iufA_	Alignment		96.6	19	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**centromere abp1 protein; **PDBTitle:** low resolution solution structure of the two dna-binding2 domains in schizosaccharomyces pombe abp1 protein
17	c3hosA_	Alignment		96.5	10	**PDB header:**transferase, dna binding protein/dna **Chain:** A: **PDB Molecule:**transposable element mariner, complete cds; **PDBTitle:** crystal structure of the mariner mos1 paired end complex with mg
18	c2w48D_	Alignment		96.3	24	**PDB header:**transcription **Chain:** D: **PDB Molecule:**sorbitol operon regulator; **PDBTitle:** crystal structure of the full-length sorbitol operon2 regulator sorc from klebsiella pneumoniae
19	d2ao9a1	Alignment		96.1	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Nanomeric phage protein-like
20	d2oa4a1	Alignment		96.0	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**TrpR-like **Family:**SPO1678-like
21	c2jrtA_	Alignment	not modelled	95.7	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** nmr solution structure of the protein coded by gene2 rhos4_12090 of rhodobacter sphaeroides. northeast3 structural genomics target rhr5
22	d1ntca_	Alignment	not modelled	95.5	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
23	d1fipa_	Alignment	not modelled	95.1	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
24	c1umqA_	Alignment	not modelled	95.1	16	**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
25	d1umqa_	Alignment	not modelled	95.1	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
26	d1etxa_	Alignment	not modelled	95.0	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
27	c3e7lD_	Alignment	not modelled	95.0	27	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** crystal structure of sigma54 activator ntrc4's dna binding2 domain
						PDB header:recombination/dna **Chain:** F: **PDB Molecule:**putative transposon tn552 dna-invertase

28	c2r0qF_	Alignment	not modelled	94.9	13	bin3; **PDBTitle:** crystal structure of a serine recombinase- dna regulatory2 complex
29	d1ijwc_	Alignment	not modelled	94.1	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
30	d1hcra_	Alignment	not modelled	93.6	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
31	c2gm4B_	Alignment	not modelled	93.4	13	**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
32	c2cg4B_	Alignment	not modelled	93.3	12	**PDB header:**transcription **Chain:** B: **PDB Molecule:**regulatory protein asnc; **PDBTitle:** structure of e.coli asnc
33	c1or7A_	Alignment	not modelled	93.3	9	**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
34	d1rp3a2	Alignment	not modelled	93.2	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
35	c3hugA_	Alignment	not modelled	93.0	19	**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
36	c2o8xA_	Alignment	not modelled	93.0	10	**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
37	c2oqgA_	Alignment	not modelled	92.7	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**possible transcriptional regulator, arsr family protein; **PDBTitle:** arsr-like transcriptional regulator from rhodococcus sp. rha1
38	c2kpjA_	Alignment	not modelled	92.7	17	**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
39	c2e7xA_	Alignment	not modelled	92.1	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
40	d1r1ua_	Alignment	not modelled	92.0	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ArsR-like transcriptional regulators
41	d1xsva_	Alignment	not modelled	91.9	8	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**YlxM/p13-like
42	d1r71a_	Alignment	not modelled	91.9	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**KorB DNA-binding domain-like **Family:**KorB DNA-binding domain-like
43	d1x57a1	Alignment	not modelled	91.8	18	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**EDF1-like
44	c2l0kA_	Alignment	not modelled	91.8	24	**PDB header:**transcription **Chain:** A: **PDB Molecule:**stage iii sporulation protein d; **PDBTitle:** nmr solution structure of a transcription factor spoiiid in complex2 with dna
45	c1r71B_	Alignment	not modelled	91.7	14	**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
46	c1rr7A_	Alignment	not modelled	91.7	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**middle operon regulator; **PDBTitle:** crystal structure of the middle operon regulator protein of2 bacteriophage mu
47	d1rr7a_	Alignment	not modelled	91.7	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Middle operon regulator, Mor
48	d2ezla_	Alignment	not modelled	91.6	31	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
49	d1etob_	Alignment	not modelled	91.6	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
50	d1ulya_	Alignment	not modelled	91.6	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Hypothetical protein PH1932
51	c2vz4A_	Alignment	not modelled	91.6	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**hth-type transcriptional activator tipa; **PDBTitle:** the n-terminal domain of merr-like protein tipal bound to2 promoter dna
52	d1or7a1	Alignment	not modelled	91.5	8	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
						Fold:DNA/RNA-binding 3-helical bundle

53	d2ecba1	Alignment	not modelled	91.5	13	**Superfamily:**Homeodomain-like **Family:**Homeodomain
54	c3i4pA_	Alignment	not modelled	91.5	13	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, asnc family; **PDBTitle:** crystal structure of asnc family transcriptional regulator from2 agrobacterium tumefaciens
55	c1rp3G_	Alignment	not modelled	91.4	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
56	d1ahdp_	Alignment	not modelled	91.3	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
57	c2pbxB_	Alignment	not modelled	91.3	16	**PDB header:**transcription **Chain:** B: **PDB Molecule:**hemagglutinin/protease regulatory protein; **PDBTitle:** vibrio cholerae hapr
58	c3t76A_	Alignment	not modelled	91.2	13	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator vanug; **PDBTitle:** crystal structure of transcriptional regulator vanug, form ii
59	c2p6tH_	Alignment	not modelled	91.2	19	**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
60	c2cfxD_	Alignment	not modelled	91.2	9	**PDB header:**transcription **Chain:** D: **PDB Molecule:**hth-type transcriptional regulator lrpc; **PDBTitle:** structure of b.subtilis lrpc
61	c2ao9H_	Alignment	not modelled	91.1	27	**PDB header:**structural genomics, unknown function **Chain:** H: **PDB Molecule:**phage protein; **PDBTitle:** structural genomics, the crystal structure of a phage protein2 (phbc6a51) from bacillus cereus atcc 14579
62	d1wh5a_	Alignment	not modelled	91.1	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
63	d1rzsa_	Alignment	not modelled	91.0	29	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
64	c2ia0A_	Alignment	not modelled	91.0	18	**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)
65	c1r22B_	Alignment	not modelled	90.9	13	**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
66	d1q06a_	Alignment	not modelled	90.8	15	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**DNA-binding N-terminal domain of transcription activators
67	d1nera_	Alignment	not modelled	90.7	19	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
68	c3b7hA_	Alignment	not modelled	90.5	14	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**prophage lp1 protein 11; **PDBTitle:** crystal structure of the prophage lp1 protein 11
69	c3op9A_	Alignment	not modelled	90.4	14	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**pli0006 protein; **PDBTitle:** crystal structure of transcriptional regulator from listeria innocua
70	d1r1ta_	Alignment	not modelled	90.3	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ArsR-like transcriptional regulators
71	d2craa1	Alignment	not modelled	90.1	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
72	d1jhga_	Alignment	not modelled	90.1	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**TrpR-like **Family:**Trp repressor, TrpR
73	d2b5aa1	Alignment	not modelled	89.8	8	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
74	c3narA_	Alignment	not modelled	89.7	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc fingers and homeoboxes protein 1; **PDBTitle:** crystal structure of zhx1 hd4 (zinc-fingers and homeoboxes protein 1,2 homeodomain 4)
75	c2vbzA_	Alignment	not modelled	89.6	14	**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
76	d1y9qa1	Alignment	not modelled	89.6	16	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Probable transcriptional regulator VC1968, N-terminal domain
77	c2jscB_	Alignment	not modelled	89.5	11	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator rv1994c/mt2050; **PDBTitle:** nmr structure of the cadmium metal-sensor cmtr from mycobacterium2 tuberculosis
78	c3mzyA_	Alignment	not modelled	89.5	8	**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

79	d1trra_	Alignment	not modelled	89.5	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**TrpR-like **Family:**Trp repressor, TrpR
80	c1i1gA_	Alignment	not modelled	89.2	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator lrpa; **PDBTitle:** crystal structure of the lrp-like transcriptional regulator from the2 archaeon pyrococcus furiosus
81	d2cuea1	Alignment	not modelled	89.1	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
82	d1g2ha_	Alignment	not modelled	89.0	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
83	d2cg4a1	Alignment	not modelled	88.6	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
84	d2e1oa1	Alignment	not modelled	88.5	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
85	d1e3oc1	Alignment	not modelled	88.5	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
86	d1r69a_	Alignment	not modelled	88.4	9	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
87	d1vz0a1	Alignment	not modelled	88.4	29	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**KorB DNA-binding domain-like **Family:**KorB DNA-binding domain-like
88	d1y7ya1	Alignment	not modelled	88.3	11	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
89	d1le8b_	Alignment	not modelled	88.3	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
90	c3f6oB_	Alignment	not modelled	88.1	9	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**probable transcriptional regulator, arsr family **PDBTitle:** crystal structure of arsr family transcriptional regulator,2 rha00566
91	c2kkoB_	Alignment	not modelled	88.1	13	**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.
92	c2e1cA_	Alignment	not modelled	88.1	12	**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
93	c2dmpA_	Alignment	not modelled	88.0	9	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**zinc fingers and homeoboxes protein 2; **PDBTitle:** solution structure of the third homeobox domain of zinc2 fingers and homeoboxes protein 2
94	c2da4A_	Alignment	not modelled	87.8	10	**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
95	c2dg7A_	Alignment	not modelled	87.7	21	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** crystal structure of the putative transcriptional regulator sco03372 from streptomyces coelicolor a3(2)
96	c2fjrB_	Alignment	not modelled	87.5	18	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**repressor protein ci; **PDBTitle:** crystal structure of bacteriophage 186
97	c2da5A_	Alignment	not modelled	87.5	13	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**zinc fingers and homeoboxes protein 3; **PDBTitle:** solution structure of the second homeobox domain of zinc2 fingers and homeoboxes protein 3 (triple homeobox 13 protein)
98	d1p7ia_	Alignment	not modelled	87.4	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
99	c3jthA_	Alignment	not modelled	87.4	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription activator hlyu; **PDBTitle:** crystal structure of a transcriptional regulator hlyu from2 vibrio vulnificus cmcp6
100	d1sq8a_	Alignment	not modelled	87.2	14	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
101	c2ewtA_	Alignment	not modelled	87.2	13	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**putative dna-binding protein; **PDBTitle:** crystal structure of the dna-binding domain of bldd
102	d1b0na2	Alignment	not modelled	87.2	31	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
103	d1gt0c1	Alignment	not modelled	87.2	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
						Fold:lambda repressor-like DNA-binding domains

104	d1adra_	Alignment	not modelled	87.2	11	**Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
105	d1bw5a_	Alignment	not modelled	87.1	7	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
106	c3cuoB_	Alignment	not modelled	87.1	15	**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
107	c3bs3A_	Alignment	not modelled	87.1	21	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**putative dna-binding protein; **PDBTitle:** crystal structure of a putative dna-binding protein from bacteroides2 fragilis
108	c2xcjB_	Alignment	not modelled	87.0	16	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**c protein; **PDBTitle:** crystal structure of p2 c, the immunity repressor of2 temperate e. coli phage p2
109	d1s7oa_	Alignment	not modelled	86.9	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**YlxM/p13-like
110	c2da1A_	Alignment	not modelled	86.8	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**alpha-fetoprotein enhancer binding protein; **PDBTitle:** solution structure of the first homeobox domain of at-2 binding transcription factor 1 (atbf1)
111	c3f6vA_	Alignment	not modelled	86.7	18	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**possible transcriptional regulator, arsr family **PDBTitle:** crystal structure of possible transcriptional regulator for2 arsenical resistance
112	d1biaa1	Alignment	not modelled	86.6	2	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Biotin repressor-like
113	c2l9rA_	Alignment	not modelled	86.5	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**homeobox protein nkx-3.1; **PDBTitle:** solution nmr structure of homeobox domain of homeobox protein nkx-3.12 from homo sapiens, northeast structural genomics consortium target3 hr6470a
114	c2w7nA_	Alignment	not modelled	86.5	14	**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
115	d2cyya1	Alignment	not modelled	86.4	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
116	c2dbbA_	Alignment	not modelled	86.4	9	**PDB header:**transcriptional regulator **Chain:** A: **PDB Molecule:**putative hth-type transcriptional regulator ph0061; **PDBTitle:** crystal structure of ph0061
117	c3bd1B_	Alignment	not modelled	86.4	25	**PDB header:**transcription **Chain:** B: **PDB Molecule:**cro protein; **PDBTitle:** structure of the cro protein from putative prophage element xfaso 1 in2 xylella fastidiosa strain ann-1
118	d1b8ia_	Alignment	not modelled	86.3	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
119	c3pqkD_	Alignment	not modelled	86.3	16	**PDB header:**transcription **Chain:** D: **PDB Molecule:**biofilm growth-associated repressor; **PDBTitle:** crystal structure of the transcriptional repressor bigr from xylella2 fastidiosa
120	d1yrnb_	Alignment	not modelled	86.2	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain