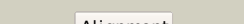
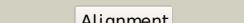
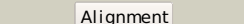


Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P0A6R3
Date	Thu Jan 5 11:03:44 GMT 2012
Unique Job ID	0264b442c21122ce

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1etob_	 Alignment		99.9	100	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
2	d1fipa_	 Alignment		99.8	99	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
3	d1etxa_	 Alignment		99.8	96	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
4	d1ntca_	 Alignment		99.6	28	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
5	c3e7lD_	 Alignment		99.4	19	PDB header: transcription regulator Chain: D: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigma54 activator ntrc4's dna binding2 domain
6	d1umqa_	 Alignment		99.4	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
7	c1umqA_	 Alignment		99.4	19	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
8	d1g2ha_	 Alignment		99.4	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
9	c3onqB_	 Alignment		96.7	16	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: regulator of polyketide synthase expression; PDBTitle: crystal structure of regulator of polyketide synthase expression2 bad_0249 from bifidobacterium adolescentis
10	d2cg4a1	 Alignment		94.9	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
11	dlixca1	 Alignment		94.6	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: LysR-like transcriptional regulators

12	d2cyya1	Alignment		94.5	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
13	d2coba1	Alignment		94.5	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Psq domain
14	c1u78A_	Alignment		94.2	20	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
15	d1b9ma1	Alignment		94.2	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: N-terminal domain of molybdate-dependent transcriptional regulator ModE
16	d1i1ga1	Alignment		94.1	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
17	d2esna1	Alignment		93.9	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: LysR-like transcriptional regulators
18	c2ijlB_	Alignment		93.8	11	PDB header: transcription Chain: B: PDB Molecule: molybdenum-binding transcriptional repressor; PDBTitle: the structure of a putative mode from agrobacterium tumefaciens.
19	c2p6tH_	Alignment		93.7	12	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
20	c2r0qF_	Alignment		93.6	21	PDB header: recombination/dna Chain: F: PDB Molecule: putative transposon tn552 dna-invertase bin3; PDBTitle: crystal structure of a serine recombinase- dna regulatory2 complex
21	c2esnC_	Alignment	not modelled	93.6	16	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: probable transcriptional regulator; PDBTitle: the crystal structure of probable transcriptional regulator pa04772 from pseudomonas aeruginosa
22	c2cg4B_	Alignment	not modelled	93.6	17	PDB header: transcription Chain: B: PDB Molecule: regulatory protein asnc; PDBTitle: structure of e.coli asnc
23	d2jn6a1	Alignment	not modelled	93.6	27	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Cgl2762-like
24	c3m1eA_	Alignment	not modelled	93.5	14	PDB header: transcription regulator Chain: A: PDB Molecule: hth-type transcriptional regulator benm; PDBTitle: crystal structure of benm_dbd
25	d2cfxa1	Alignment	not modelled	93.4	5	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
26	c2dbbA_	Alignment	not modelled	93.2	17	PDB header: transcriptional regulator Chain: A: PDB Molecule: putative hth-type transcriptional regulator ph0061; PDBTitle: crystal structure of ph0061
27	c3fzvC_	Alignment	not modelled	93.1	13	PDB header: transcription regulator Chain: C: PDB Molecule: probable transcriptional regulator; PDBTitle: crystal structure of pa01 protein, putative lysr family2 transcriptional regulator from pseudomonas aeruginosa
28	c3fzjC_	Alignment	not modelled	93.1	10	PDB header: transcription regulator Chain: C: PDB Molecule: lysr type regulator of tsambcd; PDBTitle: tsar low resolution crystal structure, tetragonal form
						PDB header: transcription

29	c1b9nA_	Alignment	not modelled	93.0	16	Chain: A: PDB Molecule: protein (mode); PDBTitle: regulator from escherichia coli
30	c2ia0A_	Alignment	not modelled	93.0	15	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)
31	c1iz1B_	Alignment	not modelled	92.9	16	PDB header: dna binding protein Chain: B: PDB Molecule: lysr-type regulatory protein; PDBTitle: crystal structure of cbnr, a lysr family transcriptional2 regulator
32	c3t1bB_	Alignment	not modelled	92.5	13	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator, lysr family; PDBTitle: crystal structure of the full-length aphb n100e variant
33	c3rqia_	Alignment	not modelled	92.5	28	PDB header: transcription Chain: A: PDB Molecule: response regulator protein; PDBTitle: crystal structure of a response regulator protein from burkholderia2 pseudomallei with a phosphorylated aspartic acid, calcium ion and3 citrate
34	c2l4aA_	Alignment	not modelled	92.5	10	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
35	c2vbzA_	Alignment	not modelled	92.3	12	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
36	c2e7xA_	Alignment	not modelled	92.1	20	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
37	c2e1cA_	Alignment	not modelled	91.9	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
38	c1ilgA_	Alignment	not modelled	91.9	24	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator lrpA; PDBTitle: crystal structure of the lrp-like transcriptional regulator from the2 archaeon pyrococcus furiosus
39	c1z4hA_	Alignment	not modelled	91.0	9	PDB header: protein binding, dna binding protein Chain: A: PDB Molecule: tor inhibition protein; PDBTitle: the response regulator tori belongs to a new family of2 atypical excisionase
40	c2cfxD_	Alignment	not modelled	91.0	5	PDB header: transcription Chain: D: PDB Molecule: hth-type transcriptional regulator lrpC; PDBTitle: structure of b.subtilis lrpC
41	c3hhgF_	Alignment	not modelled	90.7	16	PDB header: transcription regulator Chain: F: PDB Molecule: transcriptional regulator, lysr family; PDBTitle: structure of crga, a lysr-type transcriptional regulator from2 neisseria meningitidis.
42	c2auwB_	Alignment	not modelled	90.5	21	PDB header: unknown function Chain: B: PDB Molecule: hypothetical protein ne0471; PDBTitle: crystal structure of putative dna binding protein ne0471 from2 nitrosomonas europaea atcc 19718
43	c6paxA_	Alignment	not modelled	90.3	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
44	c3ispA_	Alignment	not modelled	90.3	13	PDB header: transcription Chain: A: PDB Molecule: hth-type transcriptional regulator PDBTitle: crystal structure of argp from mycobacterium tuberculosis
45	d1pdnc_	Alignment	not modelled	89.7	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
46	c3lsgD_	Alignment	not modelled	89.6	15	PDB header: transcription regulator Chain: D: PDB Molecule: two-component response regulator yesn; PDBTitle: the crystal structure of the c-terminal domain of the two-2 component response regulator yesn from fusobacterium3 nucleatum subsp. nucleatum atcc 25586
47	c3i4pA_	Alignment	not modelled	88.9	10	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, asnc family; PDBTitle: crystal structure of asnc family transcriptional regulator from2 agrobacterium tumefaciens
48	d2auwa1	Alignment	not modelled	88.8	19	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE0471 C-terminal domain-like
49	c2gqgB_	Alignment	not modelled	88.5	10	PDB header: transcription Chain: B: PDB Molecule: leucine-responsive regulatory protein; PDBTitle: crystal structure of e. coli leucine-responsive regulatory protein2 (lrp)
50	c2k9sA_	Alignment	not modelled	88.2	8	PDB header: transcription Chain: A: PDB Molecule: arabinose operon regulatory protein; PDBTitle: solution structure of dna binding domain of e. coli arac
51	d1rzsa_	Alignment	not modelled	87.8	23	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
52	c3mk1B_	Alignment	not modelled	86.7	23	PDB header: transcription regulator Chain: B: PDB Molecule: hth-type transcriptional regulator gadx; PDBTitle: crystal structure of dna-binding transcriptional dual regulator from2 escherichia coli k-12
53	c3b7hA_	Alignment	not modelled	85.6	21	PDB header: structural protein Chain: A: PDB Molecule: prophage lp1 protein 11; PDBTitle: crystal structure of the prophage lp1 protein 11
54	c3mkyP_	Alignment	not modelled	85.6	15	PDB header: dna binding protein/dna Chain: P: PDB Molecule: protein sobp;

						PDBTitle: structure of sobp(155-323)-18mer dna complex, i23 form
55	c1hlvA	Alignment	not modelled	85.2	19	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
56	c3gbgA	Alignment	not modelled	85.1	21	PDB header: transcription regulator Chain: A: PDB Molecule: tcp pilus virulence regulatory protein; PDBTitle: crystal structure of toxT from vibrio cholerae o395
57	d1vz0a1	Alignment	not modelled	84.8	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: KorB DNA-binding domain-like Family: KorB DNA-binding domain-like
58	c3bd1B	Alignment	not modelled	84.5	11	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
59	c2gm4B	Alignment	not modelled	84.3	19	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
60	c3mkzU	Alignment	not modelled	83.3	15	PDB header: dna-binding protein/dna Chain: U: PDB Molecule: protein sobp; PDBTitle: structure of sobp(155-272)-18mer complex, p21 form
61	c2rn7A	Alignment	not modelled	83.2	23	PDB header: unknown function Chain: A: PDB Molecule: is629 orfa; PDBTitle: nmr solution structure of tpe protein from shigella2 flexneri. northeast structural genomics target sfr125
62	c3oouA	Alignment	not modelled	82.9	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lin2118 protein; PDBTitle: the structure of a protein with unknwn function from listeria innocua
63	c1bl0A	Alignment	not modelled	82.5	11	PDB header: transcription/dna Chain: A: PDB Molecule: protein (multiple antibiotic resistance protein); PDBTitle: multiple antibiotic resistance protein (mara)/dna complex
64	c3oioA	Alignment	not modelled	82.4	22	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator (arac-type dna-binding domain- PDBTitle: crystal structure of transcriptional regulator (arac-type dna-binding2 domain-containing proteins) from chromobacterium violaceum
65	c1r71B	Alignment	not modelled	82.3	10	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
66	c3t76A	Alignment	not modelled	82.3	14	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator vanug; PDBTitle: crystal structure of transcriptional regulator vanug, form ii
67	c3cecA	Alignment	not modelled	82.3	12	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
68	d1r71a	Alignment	not modelled	81.9	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: KorB DNA-binding domain-like Family: KorB DNA-binding domain-like
69	d1r69a	Alignment	not modelled	81.8	13	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
70	d2o38a1	Alignment	not modelled	81.4	32	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE1354
71	c2o38A	Alignment	not modelled	81.4	32	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: putative xre family transcriptional regulator
72	d1j5ya1	Alignment	not modelled	81.0	5	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Biotin repressor-like
73	d1hlva1	Alignment	not modelled	80.8	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Centromere-binding
74	d2icta1	Alignment	not modelled	80.7	12	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
75	c1zgwA	Alignment	not modelled	80.2	18	PDB header: transcription regulator/dna Chain: A: PDB Molecule: ada polyprotein; PDBTitle: nmr structure of e. coli ada protein in complex with dna
76	c2kfsA	Alignment	not modelled	80.0	17	PDB header: dna-binding protein Chain: A: PDB Molecule: conserved hypothetical regulatory protein; PDBTitle: nmr structure of rv2175c
77	c3mn2B	Alignment	not modelled	79.7	8	PDB header: transcription regulator Chain: B: PDB Molecule: probable arac family transcriptional regulator; PDBTitle: the crystal structure of a probable arac family transcriptional2 regulator from rhodopseudomonas palustris cga009
78	c2fjrB	Alignment	not modelled	79.6	14	PDB header: transcription regulator Chain: B: PDB Molecule: repressor protein ci; PDBTitle: crystal structure of bacteriophage 186
79	c2xciB	Alignment	not modelled	79.1	17	PDB header: viral protein Chain: B: PDB Molecule: c protein;

79	c2AcjB_	Alignment	not modelled	79.1	17	PDBTitle: crystal structure of p2 c, the immunity repressor of2 temperate e. coli phage p2 PDB header: transcription/membrane protein
80	c3hugA_	Alignment	not modelled	77.9	21	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
81	d1sq8a_	Alignment	not modelled	77.8	13	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
82	d2a6ca1	Alignment	not modelled	77.8	17	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE1354
83	c1y6uA_	Alignment	not modelled	77.7	17	PDB header: dna binding protein Chain: A: PDB Molecule: excisionase from transposon tn916; PDBTitle: the structure of the excisionase (xis) protein from2 conjugative transposon tn916 provides insights into the3 regulation of heterobivalent tyrosine recombinases
84	c3omtA_	Alignment	not modelled	77.3	18	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.
85	d1utxa_	Alignment	not modelled	77.0	18	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
86	d2d1ha1	Alignment	not modelled	76.8	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: TrmB-like
87	d1mkma1	Alignment	not modelled	76.6	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Transcriptional regulator IclR, N-terminal domain
88	d1b0na2	Alignment	not modelled	75.5	11	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
89	c3cuoB_	Alignment	not modelled	75.5	11	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
90	d1adra_	Alignment	not modelled	74.9	11	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
91	d1xsva_	Alignment	not modelled	74.8	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: YlxM/p13-like
92	c2ebyA_	Alignment	not modelled	74.6	13	PDB header: transcription Chain: A: PDB Molecule: putative hth-type transcriptional regulator ybaq; PDBTitle: crystal structure of a hypothetical protein from e. coli
93	d2ao9a1	Alignment	not modelled	74.5	47	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Nanomeric phage protein-like
94	d1vega_	Alignment	not modelled	73.9	17	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
95	c2w48D_	Alignment	not modelled	73.9	33	PDB header: transcription Chain: D: PDB Molecule: sorbitol operon regulator; PDBTitle: crystal structure of the full-length sorbitol operon2 regulator sorc from klebsiella pneumoniae
96	d1y7ya1	Alignment	not modelled	73.6	17	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
97	d1i3ja_	Alignment	not modelled	73.3	24	Fold: DNA-binding domain of intron-encoded endonucleases Superfamily: DNA-binding domain of intron-encoded endonucleases Family: DNA-binding domain of intron-encoded endonucleases
98	c2gloA_	Alignment	not modelled	73.2	33	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
99	c3trbA_	Alignment	not modelled	73.0	12	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
100	d1a04a1	Alignment	not modelled	72.9	21	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)
101	c2oqgA_	Alignment	not modelled	72.8	11	PDB header: transcription Chain: A: PDB Molecule: possible transcriptional regulator, arsr family protein; PDBTitle: arsr-like transcriptional regulator from rhodococcus sp. rha1
102	d1k78a1	Alignment	not modelled	72.7	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
103	d1biaa1	Alignment	not modelled	72.7	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Biotin repressor-like
104	c2elhA_	Alignment	not modelled	72.6	17	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 PDB header: transcription

105	c2jmlA_	Alignment	not modelled	72.6	38	Chain: A: PDB Molecule: dna binding domain/transcriptional regulator; PDBTitle: solution structure of the n-terminal domain of cara repressor
106	d2p4wa1	Alignment	not modelled	72.5	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: PF1790-like
107	c1j5yA_	Alignment	not modelled	72.3	5	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, biotin repressor family; PDBTitle: crystal structure of transcriptional regulator (tm1602) from2 thermotoga maritima at 2.3 a resolution
108	c2kjpA_	Alignment	not modelled	72.2	16	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
109	d1rp3a2	Alignment	not modelled	72.1	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
110	d1x57a1	Alignment	not modelled	71.8	10	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: EDF1-like
111	c3r0aB_	Alignment	not modelled	71.8	10	PDB header: transcription regulator Chain: B: PDB Molecule: putative transcriptional regulator; PDBTitle: possible transcriptional regulator from methanosarcina mazei go1 (gi2 21227196)
112	c3bs3A_	Alignment	not modelled	71.7	14	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
113	d1bw6a_	Alignment	not modelled	71.5	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Centromere-binding
114	d1r1ta_	Alignment	not modelled	70.8	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ArsR-like transcriptional regulators
115	d1l1ib_	Alignment	not modelled	70.8	10	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
116	d1s7oa_	Alignment	not modelled	70.7	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: YlxM/p13-like
117	d6paxa1	Alignment	not modelled	70.4	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
118	c3f6wE_	Alignment	not modelled	70.2	20	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
119	c2wteB_	Alignment	not modelled	69.8	27	PDB header: antiviral protein Chain: B: PDB Molecule: csa3; PDBTitle: the structure of the crispr-associated protein, csa3, from2 sulfobolus solfataricus at 1.8 angstrom resolution.
120	d2croa_	Alignment	not modelled	69.6	18	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors