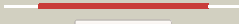
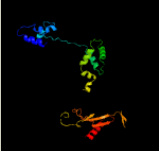


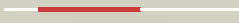


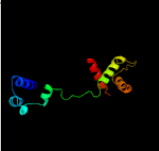

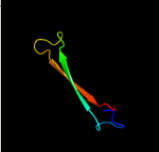



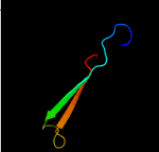



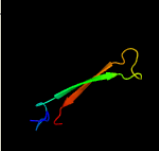

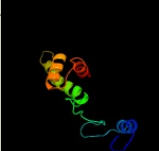






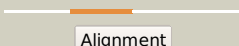

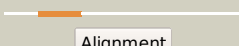

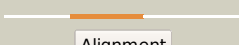

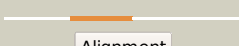

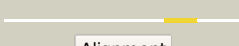
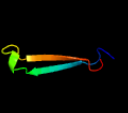
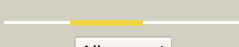



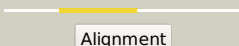
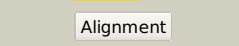
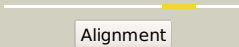
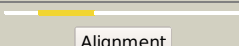
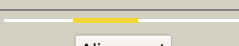
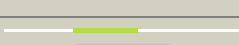
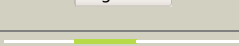
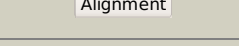
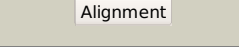


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2086 (-) _2343319_2343924
Date	Mon Aug 5 13:25:20 BST 2019
Unique Job ID	b93a7f8362868e9c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4fcyA_	 Alignment		97.1	14	PDB header: dna binding protein/dna Chain: A: PDB Molecule: transposase; PDBTitle: crystal structure of the bacteriophage mu transpososome
2	c1u78A_	 Alignment		95.3	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
3	d1pdnc_	 Alignment		94.7	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
4	c6paxA_	 Alignment		94.4	14	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
5	c1c0mA_	 Alignment		88.8	21	PDB header: transferase Chain: A: PDB Molecule: protein (integrase); PDBTitle: crystal structure of rsv two-domain integrase
6	c3hefB_	 Alignment		87.2	17	PDB header: viral protein Chain: B: PDB Molecule: gene 1 protein; PDBTitle: crystal structure of the bacteriophage sf6 terminase small subunit
7	d1asua_	 Alignment		85.8	20	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
8	c2ahqA_	 Alignment		84.6	24	PDB header: transcription Chain: A: PDB Molecule: rna polymerase sigma factor rpon; PDBTitle: solution structure of the c-terminal rpon domain of sigma-2 54 from aquifex aeolicus
9	d1c0ma2	 Alignment		84.0	19	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
10	c6gh5M_	 Alignment		83.1	14	PDB header: transcription Chain: M: PDB Molecule: rna polymerase sigma-54 factor, rna polymerase sigma-54 PDBTitle: cryo-em structure of bacterial rna polymerase-sigma54 holoenzyme2 transcription open complex
11	c5nwtM_	 Alignment		82.1	22	PDB header: transferase Chain: M: PDB Molecule: rna polymerase sigma-54 factor, rna polymerase sigma-54 PDBTitle: crystal structure of escherichia coli rna polymerase - sigma542 holoenzyme complex

12	d1aoya	 Alignment		81.8	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Arginine repressor (ArgR), N-terminal DNA-binding domain
13	c5unkA	 Alignment		81.5	17	PDB header: dna binding protein Chain: A: PDB Molecule: sleeping beauty transposase; PDBTitle: nmr structure of the red subdomain of the sleeping beauty transposase
14	c5byhM	 Alignment		81.0	22	PDB header: transferase Chain: M: PDB Molecule: rna polymerase sigma-54 factor; PDBTitle: crystal structure of escherichia coli rna polymerase - sigma542 holoenzyme complex
15	d1rzsa	 Alignment		80.9	22	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
16	c2mt3A	 Alignment		80.6	19	PDB header: transcription Chain: A: PDB Molecule: rna polymerase sigma-54 factor; PDBTitle: structure of -24 dna binding domain of sigma 54 from e.coli
17	c2o8kA	 Alignment		80.3	24	PDB header: transcription/dna Chain: A: PDB Molecule: rna polymerase sigma factor rpon; PDBTitle: nmr structure of the sigma-54 rpon domain bound to the-242 promoter element
18	c5cz1B	 Alignment		79.2	3	PDB header: hydrolase Chain: B: PDB Molecule: integrase; PDBTitle: crystal structure of the catalytic core domain of mmtv integrase
19	c5ui5I	 Alignment		77.3	19	PDB header: transcription/dna Chain: I: PDB Molecule: rna polymerase sigma factor rpon; PDBTitle: crystal structure of aquifex aeolicus sigman bound to promoter dna
20	c3v4gA	 Alignment		75.3	12	PDB header: dna binding protein Chain: A: PDB Molecule: arginine repressor; PDBTitle: 1.60 angstrom resolution crystal structure of an arginine repressor2 from vibrio vulnificus cmcp6
21	c3ereD	 Alignment	not modelled	74.3	15	PDB header: dna binding protein/dna Chain: D: PDB Molecule: arginine repressor; PDBTitle: crystal structure of the arginine repressor protein from mycobacterium2 tuberculosis in complex with the dna operator
22	d2p5ka1	 Alignment	not modelled	73.8	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Arginine repressor (ArgR), N-terminal DNA-binding domain
23	d1cxqa	 Alignment	not modelled	73.5	22	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
24	d2jn6a1	 Alignment	not modelled	72.4	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Cgl2762-like
25	d1b4aa1	 Alignment	not modelled	70.4	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Arginine repressor (ArgR), N-terminal DNA-binding domain
26	c1b4aA	 Alignment	not modelled	69.9	17	PDB header: repressor Chain: A: PDB Molecule: arginine repressor; PDBTitle: structure of the arginine repressor from bacillus stearothermophilus
27	d1f9na1	 Alignment	not modelled	69.9	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Arginine repressor (ArgR), N-terminal DNA-binding domain
28	d1jhfa1	 Alignment	not modelled	68.4	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: LexA repressor, N-terminal DNA-binding domain
29	c2in6A	 Alignment	not modelled	64.0	24	PDB header: hydrolase Chain: A: PDB Molecule: dna-3-methyladenine glycosidase;

29	c2j9uA	Alignment	not modelled	64.0	24	PDBTitle: crystal structure of a 3-methyladenine dna glycosylase i from2 staphylococcus aureus
30	d1nkua	Alignment	not modelled	63.3	24	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: 3-Methyladenine DNA glycosylase I (Tag)
31	c3oouA	Alignment	not modelled	56.6	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lin2118 protein; PDBTitle: the structure of a protein with unkown function from listeria innocua
32	c3hosA	Alignment	not modelled	50.4	20	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
33	c2k9sA	Alignment	not modelled	48.7	6	PDB header: transcription Chain: A: PDB Molecule: arabinose operon regulatory protein; PDBTitle: solution structure of dna binding domain of e. coli arac
34	c2k27A	Alignment	not modelled	47.4	13	PDB header: transcription regulator Chain: A: PDB Molecule: paired box protein pax-8; PDBTitle: solution structure of human pax8 paired box domain
35	c3oioA	Alignment	not modelled	47.2	11	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
36	c2o03A	Alignment	not modelled	47.2	13	PDB header: gene regulation Chain: A: PDB Molecule: probable zinc uptake regulation protein furb; PDBTitle: crystal structure of furb from m. tuberculosis- a zinc uptake2 regulator
37	c4j2nB	Alignment	not modelled	46.3	21	PDB header: viral protein Chain: B: PDB Molecule: gp37; PDBTitle: crystal structure of mycobacteriophage pukovnik xis
38	c3mkIB	Alignment	not modelled	45.2	13	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
39	d2fq4a1	Alignment	not modelled	45.1	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
40	d1bl0a1	Alignment	not modelled	44.6	7	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: AraC type transcriptional activator
41	d1mzba	Alignment	not modelled	44.4	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: FUR-like
42	c5fd6A	Alignment	not modelled	44.2	13	PDB header: transcription Chain: A: PDB Molecule: ferric uptake regulation protein; PDBTitle: zinc-bound manganese uptake regulator
43	d2g3ba1	Alignment	not modelled	43.7	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
44	c3jcaE	Alignment	not modelled	43.6	7	PDB header: viral protein Chain: E: PDB Molecule: integrase; PDBTitle: core model of the mouse mammary tumor virus intasome
45	c2fu4B	Alignment	not modelled	43.5	15	PDB header: dna binding protein Chain: B: PDB Molecule: ferric uptake regulation protein; PDBTitle: crystal structure of the dna binding domain of e.coli fur (ferric2 uptake regulator)
46	d1d5ya1	Alignment	not modelled	41.6	6	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: AraC type transcriptional activator
47	c2fe3B	Alignment	not modelled	41.4	15	PDB header: dna binding protein Chain: B: PDB Molecule: peroxide operon regulator; PDBTitle: the crystal structure of bacillus subtilis perr-zn reveals a novel2 zn(cys)4 structural redox switch
48	d3c07a1	Alignment	not modelled	41.3	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
49	c2r0qF	Alignment	not modelled	41.2	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
50	c2rn7A	Alignment	not modelled	40.6	12	PDB header: unknown function Chain: A: PDB Molecule: is629 orfa; PDBTitle: nmr solution structure of tnpε protein from shigella2 flexneri. northeast structural genomics target sfr125
51	c4j2nA	Alignment	not modelled	39.7	18	PDB header: viral protein Chain: A: PDB Molecule: gp37; PDBTitle: crystal structure of mycobacteriophage pukovnik xis
52	c4razB	Alignment	not modelled	39.3	13	PDB header: metal binding protein Chain: B: PDB Molecule: dna-binding transcriptional dual regulator of siderophore PDBTitle: crystal structure of magnetospirillum gryphiswaldense msr-1 holo-fur
53	c2iu5A	Alignment	not modelled	37.1	15	PDB header: transcription Chain: A: PDB Molecule: hth-type dhaklm operon transcriptional activator dhas; PDBTitle: dihydroxyacetone kinase operon activator dhas
54	c5ijzH	Alignment	not modelled	37.0	14	PDB header: oxidoreductase Chain: H: PDB Molecule: nadp-specific glutamate dehydrogenase; PDBTitle: crystal structure of glutamate dehydrogenase(gdh) from

						corynebacterium2 glutamicum
55	d1mkma1	Alignment	not modelled	36.7	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Transcriptional regulator IclR, N-terminal domain
56	c5nbcD	Alignment	not modelled	36.6	17	PDB header: dna binding protein Chain: D: PDB Molecule: ferric uptake regulation protein; PDBTitle: structure of prokaryotic transcription factors
57	c5ejkG	Alignment	not modelled	36.6	22	PDB header: transferase/dna Chain: G: PDB Molecule: gag-pro-pol polyprotein; PDBTitle: crystal structure of the rous sarcoma virus intasome
58	c5xviA	Alignment	not modelled	36.5	14	PDB header: oxidoreductase Chain: A: PDB Molecule: glutamate dehydrogenase; PDBTitle: crystal structure of aspergillus niger apo- glutamate dehydrogenase
59	c6dk4A	Alignment	not modelled	35.9	13	PDB header: metal transport Chain: A: PDB Molecule: ferric uptake regulation protein; PDBTitle: crystal structure of campylobacter jejuni peroxide stress regulator
60	c3p9a1	Alignment	not modelled	35.4	13	PDB header: dna binding protein Chain: I: PDB Molecule: dna-packaging protein gp3; PDBTitle: an atomic view of the nonameric small terminase subunit of 2 bacteriophage p22
61	c3mwmA	Alignment	not modelled	34.2	10	PDB header: transcription Chain: A: PDB Molecule: putative metal uptake regulation protein; PDBTitle: graded expression of zinc-responsive genes through two regulatory2 zinc-binding sites in zur
62	c1bl0A	Alignment	not modelled	33.1	7	PDB header: transcription/dna Chain: A: PDB Molecule: protein (multiple antibiotic resistance protein); PDBTitle: multiple antibiotic resistance protein (mara)/dna complex
63	d1ui5a1	Alignment	not modelled	32.7	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
64	d2iu5a1	Alignment	not modelled	32.4	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
65	d2o7ta1	Alignment	not modelled	30.8	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
66	c5vl9D	Alignment	not modelled	30.3	21	PDB header: transcription/dna Chain: D: PDB Molecule: regulatory protein tetr; PDBTitle: crystal structure of eilr in complex with eilo dna element
67	c2guhA	Alignment	not modelled	30.1	12	PDB header: transcription Chain: A: PDB Molecule: putative tetr-family transcriptional regulator; PDBTitle: crystal structure of the putative tetr-family transcriptional2 regulator from rhodococcus sp. rha1
68	d2fx0a1	Alignment	not modelled	30.0	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
69	d1pb6a1	Alignment	not modelled	29.9	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
70	d1etxa	Alignment	not modelled	29.8	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
71	c6fkqC	Alignment	not modelled	29.8	9	PDB header: toxin Chain: C: PDB Molecule: rv1990c (mbca); PDBTitle: crystal structure of the m.tuberculosis mbct-mbca toxin-antitoxin2 complex.
72	d2vkea1	Alignment	not modelled	29.7	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
73	c4i7hA	Alignment	not modelled	29.7	13	PDB header: transcription Chain: A: PDB Molecule: peroxide stress sensing regulator; PDBTitle: structural basis for peroxide sensing and gene regulation by perr from2 streptococcus pyogenes
74	c5nl9B	Alignment	not modelled	29.6	8	PDB header: dna binding protein Chain: B: PDB Molecule: transcriptional regulator (fur family); PDBTitle: crystal structure of a peroxide stress regulator from leptospira2 interrogans
75	d1umqa	Alignment	not modelled	29.6	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
76	c1umqA	Alignment	not modelled	29.6	21	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
77	c2w57A	Alignment	not modelled	28.8	13	PDB header: metal transport Chain: A: PDB Molecule: ferric uptake regulation protein; PDBTitle: crystal structure of the vibrio cholerae ferric uptake2 regulator (fur) reveals structural rearrangement of the3 dna-binding domains
78	c6amaO	Alignment	not modelled	28.8	8	PDB header: dna binding protein/dna Chain: O: PDB Molecule: putative dna-binding protein; PDBTitle: structure of s. coelicolor/s. venezuelae bldc-smea-ssfa complex to2 3.09 angstrom
79	c2xigA	Alignment	not modelled	28.6	3	PDB header: transcription Chain: A: PDB Molecule: ferric uptake regulation protein; PDBTitle: the structure of the helicobacter pylori ferric uptake2 regulator fur reveals three functional metal binding sites PDB header: structural genomics, unknown function

80	c3o60A_	Alignment	not modelled	28.5	6	Chain: A: PDB Molecule: lin0861 protein; PDBTitle: the crystal structure of lin0861 from listeria innocua to 2.8a
81	c4l5eA_	Alignment	not modelled	28.4	20	PDB header: protein binding Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of a. aeolicus ntrc1 dna binding domain
82	c2qkoA_	Alignment	not modelled	28.3	5	PDB header: transcription Chain: A: PDB Molecule: possible transcriptional regulator, tetr family protein; PDBTitle: crystal structure of transcriptional regulator rha06399 from2 rhodococcus sp. rha1
83	d1bgva1	Alignment	not modelled	28.1	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
84	d2fbqa1	Alignment	not modelled	27.3	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
85	d1stza1	Alignment	not modelled	27.0	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Heat-inducible transcription repressor HrcA, N-terminal domain
86	c3cwrA_	Alignment	not modelled	26.2	14	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, tetr family; PDBTitle: crystal structure of transcriptional regulator of tetr family2 (yp_425770.1) from rhodospirillum rubrum atcc 11170 at 1.50 a3 resolution
87	c2m8eA_	Alignment	not modelled	26.2	22	PDB header: dna binding protein Chain: A: PDB Molecule: sleeping beauty transposase; PDBTitle: nmr structure of the pai subdomain of sleeping beauty transposase
88	c2of7A_	Alignment	not modelled	25.7	11	PDB header: transcription Chain: A: PDB Molecule: putative tetr-family transcriptional regulator; PDBTitle: structural genomics, the crystal structure of a tetr-family2 transcriptional regulator from streptomyces coelicolor a3
89	c2elhA_	Alignment	not modelled	25.6	9	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
90	c3eupA_	Alignment	not modelled	25.6	14	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, tetr family; PDBTitle: the crystal structure of the transcriptional regulator, tetr family2 from cytophaga hutchinsonii
91	c3kkcB_	Alignment	not modelled	25.3	9	PDB header: transcription regulator Chain: B: PDB Molecule: tetr family transcriptional regulator; PDBTitle: the crystal structure of tetr transcriptional regulator from2 streptococcus agalactiae 2603v
92	c4etsB_	Alignment	not modelled	25.2	5	PDB header: metal binding protein Chain: B: PDB Molecule: ferric uptake regulation protein; PDBTitle: crystal structure of campylobacter jejuni ferric uptake regulator
93	d1ntca_	Alignment	not modelled	25.2	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
94	d2i10a1	Alignment	not modelled	24.9	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
95	c4oojB_	Alignment	not modelled	24.8	19	PDB header: unknown function Chain: B: PDB Molecule: sidc, interaptin; PDBTitle: crystal structure of the n-terminal domain of the legionella2 pneumophila protein sidc at 2.4a resolution
96	d2o3fa1	Alignment	not modelled	24.8	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: RpiR-like
97	c2o3fC_	Alignment	not modelled	24.8	16	PDB header: transcription Chain: C: PDB Molecule: putative hth-type transcriptional regulator ybbh; PDBTitle: structural genomics, the crystal structure of the n-2 terminal domain of the putative transcriptional regulator3 ybbh from bacillus subtilis subsp. subtilis str. 168.
98	d1z0xa1	Alignment	not modelled	24.1	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
99	c5dajB_	Alignment	not modelled	24.1	18	PDB header: transcription regulator Chain: B: PDB Molecule: nald; PDBTitle: crystal structure of nald, the secondary repressor of mexab-oprm2 multidrug efflux pump in pseudomonas aeruginosa
100	c4mtdA_	Alignment	not modelled	24.0	10	PDB header: dna binding protein/dna Chain: A: PDB Molecule: zinc uptake regulation protein; PDBTitle: zinc uptake regulator complexed with zinc and dna
101	d1j5ya1	Alignment	not modelled	23.9	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Biotin repressor-like
102	c1bvuf_	Alignment	not modelled	23.9	22	PDB header: oxidoreductase Chain: F: PDB Molecule: protein (glutamate dehydrogenase); PDBTitle: glutamate dehydrogenase from thermococcus litoralis
103	c3e7ID_	Alignment	not modelled	23.8	11	PDB header: transcription regulator Chain: D: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigma54 activator ntrc4's dna binding2 domain
104	c2xroE_	Alignment	not modelled	23.7	18	PDB header: dna-binding protein/dna Chain: E: PDB Molecule: hth-type transcriptional regulator ttgv; PDBTitle: crystal structure of ttgv in complex with its dna operator
105	d1fipa_	Alignment	not modelled	23.6	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like

					Family: FIS-like
106	d2d6ya1	Alignment	not modelled	22.9	9 Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
107	c2dg7A	Alignment	not modelled	22.5	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)
108	c4zuzA	Alignment	not modelled	21.9	19 PDB header: phosphate binding protein Chain: A: PDB Molecule: sidc; PDBTitle: sidc 1-871
109	d1t56a1	Alignment	not modelled	20.8	19 Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
110	c3eyyA	Alignment	not modelled	20.6	18 PDB header: transport Chain: A: PDB Molecule: putative iron uptake regulatory protein; PDBTitle: structural basis for the specialization of nur, a nickel-2 specific fur homologue, in metal sensing and dna3 recognition
111	c3w6vA	Alignment	not modelled	20.4	20 PDB header: transcription activator/dna Chain: A: PDB Molecule: adpa; PDBTitle: crystal structure of the dna-binding domain of adpa, the global2 transcriptional factor, in complex with a target dna