
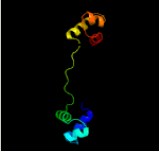



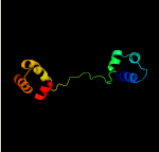

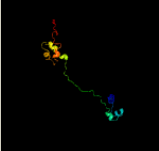
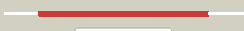
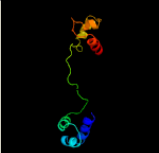





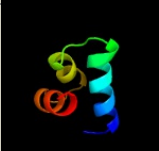








Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3636 (-)_4075931_4076278
Date	Fri Aug 9 18:20:32 BST 2019
Unique Job ID	257864240f5a4703

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1u78A_	 Alignment		99.5	18	PDB header: dna binding protein/dna Chain: A: PDB Molecule: transposable element tc3 transposase; PDBTitle: structure of the bipartite dna-binding domain of tc32 transposase bound to transposon dna
2	c6paxA_	 Alignment		99.1	22	PDB header: gene regulation/dna Chain: A: PDB Molecule: homeobox protein pax-6; PDBTitle: crystal structure of the bipartite dna-binding domain-dna2 complex reveals a general model for pax protein-dna3 interactions
3	d1pdnc_	 Alignment		98.9	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
4	c2k27A_	 Alignment		98.5	24	PDB header: transcription regulator Chain: A: PDB Molecule: paired box protein pax-8; PDBTitle: solution structure of human pax8 paired box domain
5	c3hosA_	 Alignment		98.1	17	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
6	c1hlvA_	 Alignment		97.8	25	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
7	c4go1A_	 Alignment		97.8	28	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator Isrr; PDBTitle: crystal structure of full length transcription repressor Isrr from e.2 coli.
8	d1k78a1	 Alignment		97.8	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
9	d6paxa1	 Alignment		97.6	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
10	c2w48D_	 Alignment		97.5	26	PDB header: transcription Chain: D: PDB Molecule: sorbitol operon regulator; PDBTitle: crystal structure of the full-length sorbitol operon2 regulator sorc from klebsiella pneumoniae
11	c2r0qF_	 Alignment		97.3	26	PDB header: recombination/dna Chain: F: PDB Molecule: putative transposon tn552 dna-invertase bin3; PDBTitle: crystal structure of a serine recombinase- dna regulatory2 complex

12	c1r71B_	Alignment		97.3	13	PDB header: transcription/dna Chain: B: PDB Molecule: transcriptional repressor protein korb; PDBTitle: crystal structure of the dna binding domain of korb in complex with2 the operator dna
13	c2mqkA_	Alignment		97.2	18	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent target dna activator b; PDBTitle: solution structure of n terminal domain of the mub aaa+ atpase
14	d1r71a_	Alignment		97.2	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: KorB DNA-binding domain-like Family: KorB DNA-binding domain-like
15	c2gm4B_	Alignment		97.2	21	PDB header: recombination, dna Chain: B: PDB Molecule: transposon gamma-delta resolvase; PDBTitle: an activated, tetrameric gamma-delta resolvase: hin chimera bound to2 cleaved dna
16	c3hugA_	Alignment		96.9	25	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 sigI
17	c5chhA_	Alignment		96.9	20	PDB header: transcription Chain: A: PDB Molecule: arac family transcriptional regulator; PDBTitle: crystal structure of transcriptional regulator cdpr from pseudomonas2 aeruginosa
18	c5fgmA_	Alignment		96.8	28	PDB header: hydrolase Chain: A: PDB Molecule: ecf rna polymerase sigma factor sigr; PDBTitle: streptomyces coelicolor sigr region 4
19	d1tc3c_	Alignment		96.8	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Recombinase DNA-binding domain
20	c2o8xA_	Alignment		96.8	25	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
21	d1or7a1	Alignment	not modelled	96.8	31	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
22	d1xsva_	Alignment	not modelled	96.8	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: YlxM/p13-like
23	c2elhA_	Alignment	not modelled	96.8	13	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
24	c4lfuA_	Alignment	not modelled	96.8	37	PDB header: dna binding protein Chain: A: PDB Molecule: regulatory protein sdia; PDBTitle: crystal structure of escherichia coli sdia in the space group c2
25	c3sztB_	Alignment	not modelled	96.7	23	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
26	d1rp3a2	Alignment	not modelled	96.6	31	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
27	d2jn6a1	Alignment	not modelled	96.6	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Cgl2762-like
28	c3vepA_	Alignment	not modelled	96.5	25	PDB header: membrane protein/transcription Chain: A: PDB Molecule: probable rna polymerase sigma-d factor; PDBTitle: crystal structure of sigd4 in complex with its negative regulator rsda PDB header: transcription regulator

29	c2kpiA	Alignment	not modelled	96.5	15	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
30	c2lvsA	Alignment	not modelled	96.5	37	PDB header: dna binding protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: nmr solution structure of a crispr repeat binding protein
31	d1hlva1	Alignment	not modelled	96.5	28	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Centromere-binding
32	c2q0oA	Alignment	not modelled	96.5	20	PDB header: transcription Chain: A: PDB Molecule: probable transcriptional activator protein trar; PDBTitle: crystal structure of an anti-activation complex in bacterial quorum2 sensing
33	c3fmyA	Alignment	not modelled	96.5	16	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)
34	c4fcyA	Alignment	not modelled	96.5	14	PDB header: dna binding protein/dna Chain: A: PDB Molecule: transposase; PDBTitle: crystal structure of the bacteriophage mu transposome
35	c5z7iC	Alignment	not modelled	96.4	31	PDB header: dna binding protein/dna Chain: C: PDB Molecule: cell cycle regulatory protein gcrA; PDBTitle: caulobacter crescentus gcrA dna-binding domain(dbd)in complex with2 unmethylated dsdna
36	d1p4wa	Alignment	not modelled	96.4	30	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators)
37	c3vdoA	Alignment	not modelled	96.4	22	PDB header: dna binding protein/protein binding Chain: A: PDB Molecule: rna polymerase sigma factor sigK; PDBTitle: structure of extra-cytoplasmic function(ecf) sigma factor sigK in2 complex with its negative regulator rskA from mycobacterium3 tuberculosis
38	d1a04a1	Alignment	not modelled	96.4	30	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators)
39	c5j9iH	Alignment	not modelled	96.4	16	PDB header: antitoxin Chain: H: PDB Molecule: antitoxin iga-2; PDBTitle: crystal structure of the higa2 antitoxin c-terminal domain
40	c1x3uA	Alignment	not modelled	96.3	31	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
41	d1s7oa	Alignment	not modelled	96.3	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: YlxM/p13-like
42	c4j2nB	Alignment	not modelled	96.3	19	PDB header: viral protein Chain: B: PDB Molecule: gp37; PDBTitle: crystal structure of mycobacteriophage pukovnik xis
43	c4cxfA	Alignment	not modelled	96.3	22	PDB header: transcription Chain: A: PDB Molecule: rna polymerase sigma factor cnrH; PDBTitle: structure of cnrH in complex with the cytosolic domain of cnry
44	c2ppxA	Alignment	not modelled	96.3	22	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
45	d2ppxa1	Alignment	not modelled	96.3	22	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
46	c2krfB	Alignment	not modelled	96.3	21	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulatory protein coma; PDBTitle: nmr solution structure of the dna binding domain of competence protein2 a
47	c1zljE	Alignment	not modelled	96.3	26	PDB header: transcription Chain: E: PDB Molecule: dormancy survival regulator; PDBTitle: crystal structure of the mycobacterium tuberculosis hypoxic2 response regulator dosR c-terminal domain
48	c1or7A	Alignment	not modelled	96.3	31	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
49	c6in7B	Alignment	not modelled	96.2	33	PDB header: transcription Chain: B: PDB Molecule: rna polymerase sigma-h factor; PDBTitle: crystal structure of alga in complex with muca(cyto)
50	c5o8yG	Alignment	not modelled	96.2	31	PDB header: transcription Chain: G: PDB Molecule: transcriptional regulatory protein rcsB; PDBTitle: conformational dynamism for dna interaction in salmonella typhimurium2 rcsB response regulator.
51	c5uxxC	Alignment	not modelled	96.2	19	PDB header: dna binding protein/unknown function Chain: C: PDB Molecule: rna polymerase sigma factor; PDBTitle: co-crystal structure of the sigma factor rpoE in complex with the2 anti-sigma factor nepr from bartonella quintana
52	c1h0mD	Alignment	not modelled	96.2	26	PDB header: transcription/dna Chain: D: PDB Molecule: transcriptional activator protein trar; PDBTitle: three-dimensional structure of the quorum sensing protein trar bound2 to its autoinducer and to its target dna
53	c6jqSA	Alignment	not modelled	96.1	24	PDB header: dna binding protein Chain: A: PDB Molecule: dna-binding response regulator; PDBTitle: structure of transcription factor, gere
54	c2kpiA	Alignment	not modelled	96.1	17	PDB header: transcription regulator/protein binding Chain: A: PDB Molecule: response regulator;

54	c3vya_	Alignment	not modelled	96.1	17	PDBTitle: structure of the phyr anti-anti-sigma domain bound to the anti-sigma2 factor, nepr PDB header: transcription Chain: B: PDB Molecule: two component transcriptional regulatory protein devr;
55	c3c3wB_	Alignment	not modelled	96.1	26	PDBTitle: crystal structure of the mycobacterium tuberculosis hypoxic response2 regulator dosr PDB header: rna binding protein Chain: A: PDB Molecule: rna polymerase sigma-h factor;
56	c3mzyA_	Alignment	not modelled	96.1	14	PDBTitle: the crystal structure of the rna polymerase sigma-h factor from2 fusobacterium nucleatum to 2.5a 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)
57	d1yioa1	Alignment	not modelled	96.1	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Biotin repressor-like
58	d1biaa1	Alignment	not modelled	96.1	10	PDB header: dna binding protein Chain: A: PDB Molecule: putative dna-binding protein;
59	c3bs3A_	Alignment	not modelled	96.0	17	PDBTitle: crystal structure of a putative dna-binding protein from bacteroides2 fragilis PDB header: transcription Chain: F: PDB Molecule: ecf rna polymerase sigma factor sigh;
60	c5zx3F_	Alignment	not modelled	96.0	28	PDBTitle: mycobacterium tuberculosis rna polymerase holoenzyme with ecf sigma2 factor sigma h PDB header: transcription Chain: G: PDB Molecule: rna polymerase sigma factor sigma-28 (flia);
61	c1rp3G_	Alignment	not modelled	96.0	31	PDBTitle: cocrystal structure of the flagellar sigma/anti-sigma complex, sigma-2 28/flgm PDB header: dna binding protein Chain: B: PDB Molecule: hth-type transcriptional regulator mqsa (ygit/b3021);
62	c3gn5B_	Alignment	not modelled	96.0	16	PDBTitle: structure of the e. coli protein mqsa (ygit/b3021) Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
63	d2b5aa1	Alignment	not modelled	96.0	13	PDB header: transcription Chain: A: PDB Molecule: putative rna polymerase ecf-subfamily sigma factor;
64	c6c03A_	Alignment	not modelled	96.0	25	PDBTitle: the crystal structure streptomyces venezuelae rsbn-bldn complex PDB header: dna binding protein Chain: A: PDB Molecule: sleeping beauty transposase;
65	c2m8eA_	Alignment	not modelled	96.0	24	PDBTitle: nmr structure of the pai subdomain of sleeping beauty transposase PDB header: toxin Chain: B: PDB Molecule: antitoxin iga-2;
66	c5jaaB_	Alignment	not modelled	96.0	23	PDBTitle: crystal structure of the higba2 toxin-antitoxin complex PDB header: transferase/dna Chain: F: PDB Molecule: ecf rna polymerase sigma factor sigl;
67	c6dvdF_	Alignment	not modelled	96.0	25	PDBTitle: crystal structure of mycobacterium tuberculosis transcription2 initiation complex(ecf sigma factor I) with 6 nt spacer and bromine3 labelled in position "-11 PDB header: transcription regulator Chain: C: PDB Molecule: positive transcription regulator evga;
68	c5f64C_	Alignment	not modelled	96.0	20	PDBTitle: putative positive transcription regulator (sensor evgs) from shigella2 flexneri 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)
69	d1fsea_	Alignment	not modelled	96.0	26	PDB header: dna binding protein Chain: A: PDB Molecule: centromere abp1 protein;
70	c1iufA_	Alignment	not modelled	96.0	17	PDBTitle: low resolution solution structure of the two dna-binding2 domains in schizosaccharomyces pombe abp1 protein PDB header: signal transduction protein Chain: A: PDB Molecule: nitrate/nitrite response regulator protein narl;
71	c1rnlA_	Alignment	not modelled	96.0	34	PDBTitle: the nitrate/nitrite response regulator protein narl from narl PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein;
72	c3omtA_	Alignment	not modelled	95.9	14	PDBTitle: putative antitoxin component, chu_2935 protein, from xre family from2 prevotella buccae. PDB header: transcription Chain: C: PDB Molecule: cvir transcriptional regulator;
73	c3qp5C_	Alignment	not modelled	95.9	38	PDBTitle: crystal structure of cvir bound to antagonist chlorolactone (cl) PDB header: transcription Chain: A: PDB Molecule: response regulator protein vrar;
74	c2rnjA_	Alignment	not modelled	95.9	21	PDBTitle: nmr structure of the s. aureus vrar dna binding domain PDB header: structural protein Chain: A: PDB Molecule: prophage lp1 protein 11;
75	c3b7hA_	Alignment	not modelled	95.8	17	PDBTitle: crystal structure of the prophage lp1 protein 11 PDB header: viral protein Chain: A: PDB Molecule: gp37;
76	c4j2nA_	Alignment	not modelled	95.8	19	PDBTitle: crystal structure of mycobacteriophage pukovnik xis PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator clgr;
77	c5woqA_	Alignment	not modelled	95.8	11	PDBTitle: crystal structure of an xre family protein transcriptional regulator2 from mycobacterium smegmatis PDB header: dna binding protein/dna Chain: O: PDB Molecule: putative dna-binding protein;
78	c6amaO_	Alignment	not modelled	95.8	21	PDBTitle: structure of s. coelicolor/s. venezuelae bldc-smea-ssfa complex to2 3.09 angstrom PDB header: transcription Chain: A: PDB Molecule: response regulator protein vrar;
79	c4if4A_	Alignment	not modelled	95.8	21	PDBTitle: structure of s. coelicolor/s. venezuelae bldc-smea-ssfa complex to2 3.09 angstrom PDB header: transcription Chain: A: PDB Molecule: response regulator protein vrar;

79	c4t4A	Alignment	not modelled	95.8	31	PDBTitle: crystal structure of the magnesium and beryll fluoride-activated vrrar2 from staphylococcus aureus
80	d1adra	Alignment	not modelled	95.8	13	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
81	c1y9qA	Alignment	not modelled	95.8	18	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
82	d1l3a1	Alignment	not modelled	95.8	24	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)
83	d1vz0a1	Alignment	not modelled	95.7	29	Fold: DNA/RNA-binding 3-helical bundle Superfamily: KorB DNA-binding domain-like Family: KorB DNA-binding domain-like
84	d1utxa	Alignment	not modelled	95.7	24	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
85	c3vk0B	Alignment	not modelled	95.7	18	PDB header: dna binding protein Chain: B: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of hypothetical transcription factor nhtf from2 heisseria
86	d1y9qa1	Alignment	not modelled	95.7	18	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Probable transcriptional regulator VC1968, N-terminal domain
87	d1r69a	Alignment	not modelled	95.7	11	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
88	c5hevC	Alignment	not modelled	95.7	37	PDB header: transcription Chain: C: PDB Molecule: response regulator protein vrrar; PDBTitle: crystal structure of the beryll fluoride-activated liar from2 enterococcus faecium
89	c2bnoA	Alignment	not modelled	95.7	16	PDB header: oxidoreductase Chain: A: PDB Molecule: epoxidase; PDBTitle: the structure of hydroxypropylphosphonic acid epoxidase from s.2 wedmorenis.
90	d2o38a1	Alignment	not modelled	95.7	15	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE1354
91	c2o38A	Alignment	not modelled	95.7	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: putative xre family transcriptional regulator
92	c5wurB	Alignment	not modelled	95.6	25	PDB header: metal binding protein Chain: B: PDB Molecule: ecf rna polymerase sigma factor sigw; PDBTitle: crystal structure of sigw in complex with its anti-sigma rsiw, an2 oxidized form
93	c2lfwA	Alignment	not modelled	95.6	11	PDB header: signaling protein Chain: A: PDB Molecule: phyr sigma-like domain; PDBTitle: nmr structure of the phyrsl-nepr complex from sphingomonas sp. fr1
94	d1j5ya1	Alignment	not modelled	95.6	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Biotin repressor-like
95	c3klnC	Alignment	not modelled	95.6	35	PDB header: transcription Chain: C: PDB Molecule: transcriptional regulator, luxr family; PDBTitle: vibrio cholerae vpst
96	c3op9A	Alignment	not modelled	95.6	20	PDB header: transcription regulator Chain: A: PDB Molecule: pli0006 protein; PDBTitle: crystal structure of transcriptional regulator from listeria innocua
97	c2xcjB	Alignment	not modelled	95.6	21	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
98	c4hyeB	Alignment	not modelled	95.5	23	PDB header: transcription activator Chain: B: PDB Molecule: response regulator; PDBTitle: crystal structure of a response regulator spr1814 from streptococcus2 pneumoniae reveals unique interdomain contacts among narl family3 proteins
99	c3ivpD	Alignment	not modelled	95.5	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.
100	c5byhM	Alignment	not modelled	95.5	15	PDB header: transferase Chain: M: PDB Molecule: rna polymerase sigma-54 factor; PDBTitle: crystal structure of escherichia coli rna polymerase - sigma542 holoenzyme complex
101	c5ipmF	Alignment	not modelled	95.5	17	PDB header: transcription, transferase/dna/rna Chain: F: PDB Molecule: rna polymerase sigma factor rpos; PDBTitle: sigmas-transcription initiation complex with 4-nt nascent rna
102	c2zhha	Alignment	not modelled	95.5	12	PDB header: transcription Chain: A: PDB Molecule: redox-sensitive transcriptional activator soxr; PDBTitle: crystal structure of soxr
103	c3f52A	Alignment	not modelled	95.5	15	PDB header: transcription activator Chain: A: PDB Molecule: clp gene regulator (clgr); PDBTitle: crystal structure of the clp gene regulator clgr from c. glutamicum
104	d1sq8a	Alignment	not modelled	95.5	16	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
						PDB header: dna binding protein

105	c2jpcA_	Alignment	not modelled	95.4	25	Chain: A: PDB Molecule: ssrb; PDBTitle: ssrb dna binding protein
106	c3clcC_	Alignment	not modelled	95.4	11	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
107	d2icta1	Alignment	not modelled	95.4	19	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
108	c3eusB_	Alignment	not modelled	95.4	16	PDB header: dna binding protein Chain: B: PDB Molecule: dna-binding protein; PDBTitle: the crystal structure of the dna binding protein from silicibacter2 pomeroyi
109	d1ttya_	Alignment	not modelled	95.4	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
110	c2cg4B_	Alignment	not modelled	95.4	18	PDB header: transcription Chain: B: PDB Molecule: regulatory protein asnc; PDBTitle: structure of e.coli asnc
111	d1bw6a_	Alignment	not modelled	95.3	28	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Centromere-binding
112	c1b0nA_	Alignment	not modelled	95.3	15	PDB header: transcription regulator Chain: A: PDB Molecule: protein (sinr protein); PDBTitle: sinr protein/sini protein complex
113	d1y7ya1	Alignment	not modelled	95.3	18	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
114	d2croa_	Alignment	not modelled	95.3	11	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
115	d2cg4a1	Alignment	not modelled	95.3	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
116	c3t76A_	Alignment	not modelled	95.2	10	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator vanug; PDBTitle: crystal structure of transcriptional regulator vanug, form ii
117	c3kxaD_	Alignment	not modelled	95.2	17	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of ngo0477 from neisseria gonorrhoeae
118	c2ef8A_	Alignment	not modelled	95.2	21	PDB header: transcription regulator Chain: A: PDB Molecule: putative transcription factor; PDBTitle: crystal structure of c.ecot38is
119	c2q1za_	Alignment	not modelled	95.2	19	PDB header: transcription Chain: A: PDB Molecule: rpoe, ecf sige; PDBTitle: crystal structure of rhodobacter sphaeroides sige in complex with the2 anti-sigma chrr
120	c3m1fC_	Alignment	not modelled	95.2	22	PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulator; PDBTitle: putative transcriptional regulator from staphylococcus aureus.