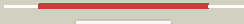








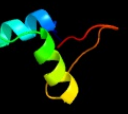

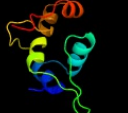










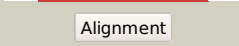





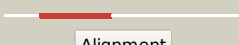



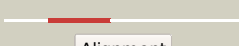









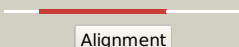




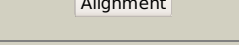


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2175c_(-)_2437454_2437894
Date	Mon Aug 5 13:25:30 BST 2019
Unique Job ID	da15fb5ebc3dcc04

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2kfsA_	 Alignment		100.0	100	PDB header: dna-binding protein Chain: A; PDB Molecule: conserved hypothetical regulatory protein; PDBTitle: nmr structure of rv2175c
2	c6fkgC_	 Alignment		98.4	18	PDB header: toxin Chain: C; PDB Molecule: rv1990c (mbca); PDBTitle: crystal structure of the m.tuberculosis mbct-mbca toxin-antitoxin2 complex.
3	c4j2nA_	 Alignment		97.8	27	PDB header: viral protein Chain: A; PDB Molecule: gp37; PDBTitle: crystal structure of mycobacteriophage pukovnik xis
4	c4j2nB_	 Alignment		97.7	27	PDB header: viral protein Chain: B; PDB Molecule: gp37; PDBTitle: crystal structure of mycobacteriophage pukovnik xis
5	c6amaO_	 Alignment		97.1	25	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
6	c2zhhA_	 Alignment		96.3	15	PDB header: transcription Chain: A; PDB Molecule: redox-sensitive transcriptional activator soxr; PDBTitle: crystal structure of soxr
7	c4r24B_	 Alignment		96.2	20	PDB header: transcription/dna Chain: B; PDB Molecule: hth-type transcriptional regulator tnra; PDBTitle: complete dissection of b. subtilis nitrogen homeostatic circuitry
8	c1y6uA_	 Alignment		95.6	11	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
9	c4r4eA_	 Alignment		95.6	17	PDB header: transcription regulator/dna Chain: A; PDB Molecule: hth-type transcriptional regulator glnr; PDBTitle: structure of glnr-dna complex
10	c5af3A_	 Alignment		95.3	24	PDB header: dna binding Chain: A; PDB Molecule: vapbc49; PDBTitle: x-ray crystal structure of rv2018 from mycobacterium tuberculosis
11	d1q06a_	 Alignment		94.3	18	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: DNA-binding N-terminal domain of transcription activators

12	c6gw6B_	 Alignment		94.1	17	PDB header: toxin Chain: B: PDB Molecule: xre antitoxin; PDBTitle: structure of the pseudomonas putida res-xre toxin-antitoxin complex
13	c5c8eC_	 Alignment		93.9	19	PDB header: transcription regulator/dna Chain: C: PDB Molecule: light-dependent transcriptional regulator carh; PDBTitle: crystal structure of thermus thermophilus carh bound to adenosylcobalamin and a 26-bp dna segment
14	c3gpvA_	 Alignment		93.7	14	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, merr family; PDBTitle: crystal structure of a transcriptional regulator, merr2 family from bacillus thuringiensis
15	d1biaa1	 Alignment		93.7	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Biotin repressor-like
16	d1r8ea1	 Alignment		93.6	15	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: DNA-binding N-terminal domain of transcription activators
17	c1z4hA_	 Alignment		93.5	18	PDB header: protein binding, dna binding protein Chain: A: PDB Molecule: tor inhibition protein; PDBTitle: the response regulator tori belongs to a new family of 2 atypical excisionase
18	c5i44E_	 Alignment		93.5	25	PDB header: dna binding protein/dna Chain: E: PDB Molecule: chromosome-anchoring protein raca; PDBTitle: structure of raca-dna complex; p21 form
19	c3hh0C_	 Alignment		93.1	16	PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulator, merr family; PDBTitle: crystal structure of a transcriptional regulator, merr family from 2 bacillus cereus
20	c2vz4A_	 Alignment		92.5	31	PDB header: transcription Chain: A: PDB Molecule: hth-type transcriptional activator tipa; PDBTitle: the n-terminal domain of merr-like protein tipal bound to promoter dna
21	d1r8da_	 Alignment	not modelled	92.2	22	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: DNA-binding N-terminal domain of transcription activators
22	c3gp4B_	 Alignment	not modelled	92.1	18	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, merr family; PDBTitle: crystal structure of putative merr family transcriptional regulator2 from listeria monocytogenes
23	c6sbsB_	 Alignment	not modelled	91.4	21	PDB header: transcription Chain: B: PDB Molecule: regulatory protein; PDBTitle: ytra from sulfolobus acidocaldarius, a gntr-family transcription2 factor
24	c3ucsB_	 Alignment	not modelled	91.4	12	PDB header: chaperone Chain: B: PDB Molecule: chaperone-modulator protein cbpm; PDBTitle: crystal structure of the complex between cbpa j-domain and cbpm
25	c2jmlA_	 Alignment	not modelled	91.3	14	PDB header: transcription Chain: A: PDB Molecule: dna binding domain/transcriptional regulator; PDBTitle: solution structure of the n-terminal domain of cara repressor
26	c4go1A_	 Alignment	not modelled	91.3	22	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator lsrr; PDBTitle: crystal structure of full length transcription repressor lsrr from e.2 coli.
27	c6d0hB_	 Alignment	not modelled	91.3	37	PDB header: toxin Chain: B: PDB Molecule: pars: cog5642 (duf2384) antitoxin; PDBTitle: part: prs adp-ribosylating toxin bound to cognate antitoxin pars
28	c3neuA_	 Alignment	not modelled	90.9	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lin1836 protein; PDBTitle: the crystal structure of a functionally-unknown protein lin1836 from 2 listeria innocua clip11262

29	c3by6C	Alignment	not modelled	90.5	16	PDB header: transcription regulator Chain: C: PDB Molecule: predicted transcriptional regulator; PDBTitle: crystal structure of a transcriptional regulator from oenococcus oeni
30	c6az6B	Alignment	not modelled	90.2	22	PDB header: transcription Chain: B: PDB Molecule: gntr family transcriptional regulator; PDBTitle: streptococcus agalactiae gntr
31	c4p96B	Alignment	not modelled	89.9	15	PDB header: transcription Chain: B: PDB Molecule: fatty acid metabolism regulator protein; PDBTitle: fadr, fatty acid responsive transcription factor from vibrio cholerae
32	c3fmsA	Alignment	not modelled	89.8	26	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, gntr family; PDBTitle: crystal structure of tm0439, a gntr transcriptional regulator
33	c2w48D	Alignment	not modelled	89.7	17	PDB header: transcription Chain: D: PDB Molecule: sorbitol operon regulator; PDBTitle: crystal structure of the full-length sorbitol operon2 regulator sorc from klebsiella pneumoniae
34	c5kvrA	Alignment	not modelled	89.6	25	PDB header: translation Chain: A: PDB Molecule: pyruvate dehydrogenase complex repressor; PDBTitle: x-ray crystal structure of a fragment (1-75) of a transcriptional2 regulator pdhr from escherichia coli cft073
35	c2hs5A	Alignment	not modelled	89.5	30	PDB header: transcription regulator Chain: A: PDB Molecule: putative transcriptional regulator gntr; PDBTitle: structural genomics, the crystal structure of a putative2 transcriptional regulator gntr from rhodococcus sp. rha1
36	c1e2xA	Alignment	not modelled	89.2	16	PDB header: transcriptional regulation Chain: A: PDB Molecule: fatty acid metabolism regulator protein; PDBTitle: fadr, fatty acid responsive transcription factor from e.2 coli
37	c6ep3B	Alignment	not modelled	88.8	18	PDB header: transcription Chain: B: PDB Molecule: lmo0651 protein; PDBTitle: lar controls the expression of the listeria monocytogenes agr system2 and mediates virulence.
38	c4hamA	Alignment	not modelled	88.6	23	PDB header: transcription Chain: A: PDB Molecule: lmo2241 protein; PDBTitle: crystal structure of transcriptional antiterminator from listeria2 monocytogenes egd-e
39	c4egzA	Alignment	not modelled	88.6	18	PDB header: transcription/dna Chain: A: PDB Molecule: arabinose metabolism transcriptional repressor; PDBTitle: crystal structure of arar(dbd) in complex with operator orr3
40	d3bwga1	Alignment	not modelled	88.4	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: GntR-like transcriptional regulators
41	c4r1hA	Alignment	not modelled	88.1	15	PDB header: transcription regulator Chain: A: PDB Molecule: lmo0741 protein; PDBTitle: gntr family transcriptional regulator from listeria monocytogenes
42	c3qaoA	Alignment	not modelled	87.8	28	PDB header: transcription regulator Chain: A: PDB Molecule: merr-like transcriptional regulator; PDBTitle: the crystal structure of the n-terminal domain of a merr-like2 transcriptional regulator from listeria monocytogenes egd-e
43	d1j5ya1	Alignment	not modelled	87.7	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Biotin repressor-like
44	c3bd1B	Alignment	not modelled	87.4	24	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
45	c3c7jA	Alignment	not modelled	87.3	27	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, gntr family; PDBTitle: crystal structure of transcriptional regulator (gntr family member)2 from pseudomonas syringae pv. tomato str. dc3000
46	c2du9A	Alignment	not modelled	87.3	16	PDB header: transcription Chain: A: PDB Molecule: predicted transcriptional regulators; PDBTitle: crystal structure of the transcriptional factor from c.glutamicum
47	c4lhfA	Alignment	not modelled	87.2	19	PDB header: viral protein Chain: A: PDB Molecule: regulatory protein cox; PDBTitle: crystal structure of a dna binding protein from phage p2
48	d1ku7a	Alignment	not modelled	86.9	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
49	d2p7vb1	Alignment	not modelled	86.8	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
50	c3bwgA	Alignment	not modelled	86.7	16	PDB header: transcription regulator Chain: A: PDB Molecule: uncharacterized hth-type transcriptional regulator yydk; PDBTitle: the crystal structure of possible transcriptional regulator yydk from2 bacillus subtilis subsp. subtilis str. 168
51	c3t72o	Alignment	not modelled	86.6	19	PDB header: transcription/dna Chain: O: PDB Molecule: pho box dna (strand 1); PDBTitle: phob(e)-sigma70(4)-(rnap-beta-flap-tip-helix)-dna transcription2 activation sub-complex
52	c3ihuA	Alignment	not modelled	86.4	25	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, gntr family; PDBTitle: crystal structure of dna binding protein (yp_298823.1) from ralstonia2 eutropha jmp134 at 1.92 a resolution
53	c5jaaB	Alignment	not modelled	86.0	12	PDB header: toxin Chain: B: PDB Molecule: antitoxin iga-2; PDBTitle: crystal structure of the higba2 toxin-antitoxin complex
						Fold: DNA/RNA-binding 3-helical bundle

54	d1hw1a1	Alignment	not modelled	85.3	16	Superfamily: "Winged helix" DNA-binding domain Family: GntR-like transcriptional regulators
55	c1r22B	Alignment	not modelled	85.3	27	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
56	d1ttya	Alignment	not modelled	85.3	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
57	c4p9fA	Alignment	not modelled	85.0	20	PDB header: transcription Chain: A: PDB Molecule: hth-type transcriptional regulator mcbr; PDBTitle: e. coli mcbr/yncc
58	d1s7oa	Alignment	not modelled	84.6	27	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: YlxM/p13-like
59	c5j9iH	Alignment	not modelled	84.4	12	PDB header: antitoxin Chain: H: PDB Molecule: antitoxin iga-2; PDBTitle: crystal structure of the higa2 antitoxin c-terminal domain
60	c3fmyA	Alignment	not modelled	84.3	12	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)
61	d1v4ra1	Alignment	not modelled	84.3	27	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: GntR-like transcriptional regulators
62	d1g2ha	Alignment	not modelled	84.0	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
63	c1g2hA	Alignment	not modelled	84.0	24	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulatory protein tyrr homolog; PDBTitle: solution structure of the dna-binding domain of the tyrr2 protein of haemophilus influenzae
64	d1ku3a	Alignment	not modelled	83.7	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
65	c2cfxD	Alignment	not modelled	83.6	7	PDB header: transcription Chain: D: PDB Molecule: hth-type transcriptional regulator lrpc; PDBTitle: structure of b.subtilis lrpc
66	d1xsva	Alignment	not modelled	83.6	27	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: YlxM/p13-like
67	c3f8mA	Alignment	not modelled	83.5	26	PDB header: transcription Chain: A: PDB Molecule: gntr-family protein transcriptional regulator; PDBTitle: crystal structure of phnf from mycobacterium smegmatis
68	d2ppxa1	Alignment	not modelled	83.4	4	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
69	c2ppxA	Alignment	not modelled	83.4	4	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein atu1735; PDBTitle: crystal structure of a hth xre-family like protein from agrobacterium2 tumefaciens
70	c3i4pA	Alignment	not modelled	83.3	10	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, asnc family; PDBTitle: crystal structure of asnc family transcriptional regulator from2 agrobacterium tumefaciens
71	c2di3A	Alignment	not modelled	82.9	19	PDB header: transcription Chain: A: PDB Molecule: bacterial regulatory proteins, gntr family; PDBTitle: crystal structure of the transcriptional factor cgl29152 from corynebacterium glutamicum
72	d2jn6a1	Alignment	not modelled	82.9	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Cgl2762-like
73	c2ewnA	Alignment	not modelled	82.9	18	PDB header: ligase, transcription Chain: A: PDB Molecule: bira bifunctional protein; PDBTitle: ecoli biotin repressor with co-repressor analog
74	d1fipa	Alignment	not modelled	82.7	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
75	c2e7xA	Alignment	not modelled	82.6	17	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
76	d2cg4a1	Alignment	not modelled	82.5	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
77	c3d6zA	Alignment	not modelled	82.5	15	PDB header: transcription regulator/dna Chain: A: PDB Molecule: multidrug-efflux transporter 1 regulator; PDBTitle: crystal structure of r275e mutant of bmrr bound to dna and rhodamine
78	c3t0yA	Alignment	not modelled	82.2	14	PDB header: transcription regulator/protein binding Chain: A: PDB Molecule: response regulator; PDBTitle: structure of the phyr anti-anti-sigma domain bound to the anti-sigma2 factor, nepr
79	c2ebyA	Alignment	not modelled	81.9	24	PDB header: transcription Chain: A: PDB Molecule: putative hth-type transcriptional regulator ybaq; PDBTitle: crystal structure of a hypothetical protein from e. coli
						Fold: DNA/RNA-binding 3-helical bundle

80	d1etxa_	Alignment	not modelled	81.8	17	Superfamily: Homeodomain-like Family: FIS-like
81	c3m1fC_	Alignment	not modelled	81.8	8	PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulator; PDBTitle: putative transcriptional regulator from staphylococcus aureus.
82	d2hs5a1	Alignment	not modelled	81.8	27	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: GntR-like transcriptional regulators
83	d1l1ga1	Alignment	not modelled	81.7	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
84	c2kpiA_	Alignment	not modelled	81.5	12	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
85	c21fwA_	Alignment	not modelled	81.3	23	PDB header: signaling protein Chain: A: PDB Molecule: phyr sigma-like domain; PDBTitle: nmr structure of the phyrsl-nepr complex from sphingomonas sp. fr1
86	d1r1ta_	Alignment	not modelled	81.1	27	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ArsR-like transcriptional regulators
87	d1adra_	Alignment	not modelled	81.0	16	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
88	c4zs8A_	Alignment	not modelled	80.7	18	PDB header: transcription Chain: A: PDB Molecule: hth-type transcriptional repressor dasr; PDBTitle: crystal structure of ligand-free, full length dasr
89	c2l4aA_	Alignment	not modelled	80.5	7	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
90	c2ia0A_	Alignment	not modelled	80.5	17	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)
91	d1mkma1	Alignment	not modelled	80.5	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Transcriptional regulator lclR, N-terminal domain
92	c3op9A_	Alignment	not modelled	80.4	28	PDB header: transcription regulator Chain: A: PDB Molecule: pli0006 protein; PDBTitle: crystal structure of transcriptional regulator from listeria innocua
93	c2vbzA_	Alignment	not modelled	79.9	23	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
94	c5tw1F_	Alignment	not modelled	79.8	19	PDB header: transcription activator/transferase/dna Chain: F: PDB Molecule: rna polymerase sigma factor sigma; PDBTitle: crystal structure of a mycobacterium smegmatis transcription2 initiation complex with rbpA
95	c2p6tH_	Alignment	not modelled	79.6	10	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
96	c2fjrB_	Alignment	not modelled	79.6	12	PDB header: transcription regulator Chain: B: PDB Molecule: repressor protein ci; PDBTitle: crystal structure of bacteriophage 186
97	c3vepA_	Alignment	not modelled	79.5	14	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
98	c3trbA_	Alignment	not modelled	79.4	20	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
99	d1umqa_	Alignment	not modelled	79.2	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
100	c1umqA_	Alignment	not modelled	79.2	13	PDB header: dna-binding protein Chain: A: PDB Molecule: photosynthetic apparatus regulatory protein; PDBTitle: solution structure and dna binding of the effector domain2 from the global regulator prra(rega) from r. sphaeroides:3 insights into dna binding specificity
101	c2o8xA_	Alignment	not modelled	79.2	19	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
102	c1bdhA_	Alignment	not modelled	79.1	17	PDB header: transcription/dna Chain: A: PDB Molecule: protein (purine repressor); PDBTitle: purine repressor mutant-hypoxanthine-palindromic operator2 complex
103	d1rp3a2	Alignment	not modelled	78.8	32	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
104	c3omtA_	Alignment	not modelled	78.7	12	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.
105	c2dhhA_	Alignment	not modelled	78.7	13	PDB header: transcriptional regulator Chain: A: PDB Molecule: putative hth-type transcriptional regulator

105	c2ubvA	Alignment	not modelled	78.7	15	ph0061; PDBTitle: crystal structure of ph0061
106	d1etob	Alignment	not modelled	78.6	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
107	d1ft9a1	Alignment	not modelled	78.6	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: CAP C-terminal domain-like
108	d2cyya1	Alignment	not modelled	78.5	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
109	c2m8gX	Alignment	not modelled	78.5	20	PDB header: transcription Chain: X: PDB Molecule: transcriptional regulator; PDBTitle: structure, function, and tethering of dna-binding domains in 542 transcriptional activators
110	c6f8sA	Alignment	not modelled	78.4	32	PDB header: toxin Chain: A: PDB Molecule: xre family transcriptional regulator; PDBTitle: toxin-antitoxin complex grata
111	c3hugA	Alignment	not modelled	78.3	23	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
112	c2xcjB	Alignment	not modelled	78.2	20	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
113	c1j5yA	Alignment	not modelled	78.1	19	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
114	d1i5za1	Alignment	not modelled	78.1	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: CAP C-terminal domain-like
115	c5ipmF	Alignment	not modelled	78.1	26	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
116	c6c05F	Alignment	not modelled	78.0	19	PDB header: transcription Chain: F: PDB Molecule: rna polymerase sigma factor siga; PDBTitle: mycobacterium tuberculosis rnap holo/rbpa in relaxed state
117	c2cg4B	Alignment	not modelled	77.7	10	PDB header: transcription Chain: B: PDB Molecule: regulatory protein asnc; PDBTitle: structure of e.coli asnc
118	c1u78A	Alignment	not modelled	77.7	8	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
119	d2cfxa1	Alignment	not modelled	77.7	7	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
120	c3kxaD	Alignment	not modelled	77.6	11	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of ngo0477 from neisseria gonorrhoeae