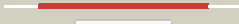
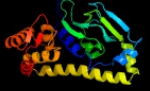


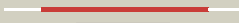






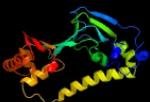












Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1675c_(-)_1900248_1900982
Date	Fri Aug 2 13:30:27 BST 2019
Unique Job ID	8a0c457a5ab64f50

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5w5aB	 Alignment		100.0	98	PDB header: transcription Chain: B: PDB Molecule: hth-type transcriptional regulator cmr; PDBTitle: crystal structure of mycobacterium tuberculosis crp-fnr family2 transcription factor cmr (rv1675c)
2	c3dv8A	 Alignment		100.0	16	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, crp/fnr family; PDBTitle: crystal structure of a putative transcriptional regulator of the2 crp/fnr family (eubrec_1222) from eubacterium rectale atcc 33656 at3 2.55 a resolution
3	c4ev0A	 Alignment		100.0	20	PDB header: transcription activator Chain: A: PDB Molecule: transcription regulator, crp family; PDBTitle: crystal structure of thermus thermophilus catabolite activator protein
4	c3fx3A	 Alignment		100.0	20	PDB header: camp-binding protein Chain: A: PDB Molecule: cyclic nucleotide-binding protein; PDBTitle: structure of a putative camp-binding regulatory protein from2 silicibacter pomeroyi dss-3
5	c5e44A	 Alignment		100.0	16	PDB header: transcription Chain: A: PDB Molecule: fnr regulator; PDBTitle: crystal structure of holo-fnr of a. fischeri
6	c1zybA	 Alignment		100.0	15	PDB header: transcription regulator Chain: A: PDB Molecule: transcription regulator, crp family; PDBTitle: crystal structure of transcription regulator from bacteroides2 thetaiotaomicron vpi-5482 at 2.15 a resolution
7	c3e97A	 Alignment		100.0	20	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, crp/fnr family; PDBTitle: crystal structure of transcriptional regulator of crp/fnr family2 (yp_604437.1) from deinococcus geothermalis dsm 11300 at 1.86 a3 resolution
8	c3d0sA	 Alignment		100.0	25	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulatory protein; PDBTitle: camp receptor protein from m.tuberculosis, camp-free form
9	c2bgcA	 Alignment		100.0	13	PDB header: transcription Chain: A: PDB Molecule: prfa; PDBTitle: prfa-g145s, a constitutive active mutant of the2 transcriptional regulator in l.monocytogenes
10	c3e6dA	 Alignment		100.0	10	PDB header: transcription regulation Chain: A: PDB Molecule: cyclic nucleotide-binding protein; PDBTitle: crystal structure of cprk c200s
11	c2h6bA	 Alignment		100.0	11	PDB header: dna binding protein Chain: A: PDB Molecule: chlorophenol reduction gene k; PDBTitle: crystal structure of oxidized cprk in complex with o-2 chlorophenolacetic acid

12	c3iwzB_	Alignment		100.0	15	PDB header: transcription Chain: B: PDB Molecule: catabolite activation-like protein; PDBTitle: the c-di-gmp responsive global regulator clp links cell-cell signaling2 to virulence gene expression in xanthomonas campestris
13	c1ft9A_	Alignment		100.0	19	PDB header: transcription Chain: A: PDB Molecule: carbon monoxide oxidation system transcription PDBTitle: structure of the reduced (feii) co-sensing protein from r.2 rubrum
14	c2gauA_	Alignment		100.0	21	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, crp/fnr family; PDBTitle: crystal structure of transcriptional regulator, crp/fnr family from2 porphyromonas gingivalis (apc80792), structural genomics, mcsg
15	c2oz6A_	Alignment		100.0	15	PDB header: dna binding protein Chain: A: PDB Molecule: virulence factor regulator; PDBTitle: crystal structure of virulence factor regulator from pseudomonas2 aeruginosa in complex with camp
16	c3dkwB_	Alignment		100.0	16	PDB header: transcription regulator Chain: B: PDB Molecule: dnr protein; PDBTitle: crystal structure of dnr from pseudomonas aeruginosa.
17	c2fmyB_	Alignment		100.0	14	PDB header: dna binding protein Chain: B: PDB Molecule: carbon monoxide oxidation system transcription regulator PDBTitle: co-dependent transcription factor coa from carboxydotherrmus2 hydrogenoformans (imidazole-bound form)
18	c3kccA_	Alignment		100.0	19	PDB header: transcription Chain: A: PDB Molecule: catabolite gene activator; PDBTitle: crystal structure of d138l mutant of catabolite gene activator protein
19	c4rfaA_	Alignment		100.0	15	PDB header: transcription regulator Chain: A: PDB Molecule: lmo0740 protein; PDBTitle: crystal structure of cyclic nucleotide-binding domain containing2 protein from listeria monocytogenes egd-e
20	c2zcwA_	Alignment		100.0	20	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, fnr/crp family; PDBTitle: crystal structure of ttha1359, a transcriptional regulator,2 crp/fnr family from thermus thermophilus hb8
21	c2zdbA_	Alignment	not modelled	100.0	16	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, crp family; PDBTitle: crystal structure of tthb099, a transcriptional regulator crp family2 from thermus thermophilus hb8
22	c3la2A_	Alignment	not modelled	100.0	20	PDB header: transcription Chain: A: PDB Molecule: global nitrogen regulator; PDBTitle: crystal structure of ntca in complex with 2-oxoglutarate
23	c1zreB_	Alignment	not modelled	100.0	18	PDB header: gene regulation/dna Chain: B: PDB Molecule: catabolite gene activator; PDBTitle: 4 crystal structures of cap-dna with all base-pair substitutions at2 position 6, cap-[6g;17c]icap38 dna
24	c4i2oA_	Alignment	not modelled	99.9	14	PDB header: transcription regulator/dna Chain: A: PDB Molecule: fixk2 protein; PDBTitle: the structure of fixk2 from bradyrhizobium japonicum
25	c4avcA_	Alignment	not modelled	99.7	22	PDB header: transferase Chain: A: PDB Molecule: lysine acetyltransferase; PDBTitle: crystal structure of protein lysine acetyltransferase rv09982 in complex with acetyl coa and camp
26	c5v30B_	Alignment	not modelled	99.7	15	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of the sensor domain of the transcriptional2 regulator hcpr from porphyromonas gingivalis
27	c3gydA_	Alignment	not modelled	99.7	13	PDB header: dna binding protein Chain: A: PDB Molecule: cyclic nucleotide-binding domain; PDBTitle: crystal structure of a cyclic nucleotide-binding domain (mfla_1926)2 from methylobacillus flagellatus kt at 1.79 a resolution
28	d1zyba2	Alignment	not modelled	99.7	11	Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain
						PDB header: transferase

29	c4orfA_	Alignment	not modelled	99.7	22	Chain: A: PDB Molecule: acetyltransferase pat; PDBTitle: camp-binding acyltransferase from mycobacterium smegmatis, mutant r95k
30	d3e5ua2	Alignment	not modelled	99.7	10	Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain
31	c2pqqD_	Alignment	not modelled	99.7	22	PDB header: transcription Chain: D: PDB Molecule: putative transcriptional regulator; PDBTitle: structural genomics, the crystal structure of the n-terminal domain of2 a transcriptional regulator from streptomyces coelicolor a3(2)
32	d1ft9a2	Alignment	not modelled	99.7	18	Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: CO-sensing protein CooA, N-terminal domain
33	d2gaua2	Alignment	not modelled	99.7	21	Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain
34	d2oz6a2	Alignment	not modelled	99.7	11	Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain
35	d2h6ca2	Alignment	not modelled	99.7	10	Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain
36	d1cx4a1	Alignment	not modelled	99.7	18	Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain
37	d1o5la1	Alignment	not modelled	99.6	17	Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain
38	c1o5IA_	Alignment	not modelled	99.6	17	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, crp family; PDBTitle: crystal structure of transcriptional regulator (tm1171) from2 thermotoga maritima at 2.30 a resolution
39	c3dn7A_	Alignment	not modelled	99.6	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: cyclic nucleotide binding regulatory protein; PDBTitle: cyclic nucleotide binding regulatory protein from cytophaga2 hutchinsonii.
40	d1i5za2	Alignment	not modelled	99.6	14	Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain
41	c5jonA_	Alignment	not modelled	99.6	20	PDB header: transport protein Chain: A: PDB Molecule: maltose-binding periplasmic protein,potassium/sodium PDBTitle: crystal structure of the unliganded form of hcn2 cnbd
42	c4kg1A_	Alignment	not modelled	99.6	19	PDB header: lyase Chain: A: PDB Molecule: diguanylate cyclase; PDBTitle: cgmp-responsive diguanylate cyclase
43	d1cx4a2	Alignment	not modelled	99.6	20	Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain
44	c4chwB_	Alignment	not modelled	99.6	23	PDB header: transport protein Chain: B: PDB Molecule: cyclic nucleotide-gated potassium channel mll3241; PDBTitle: the electron crystallography structure of the camp-free potassium2 channel mlok1
45	c2z69A_	Alignment	not modelled	99.6	15	PDB header: transcription regulator Chain: A: PDB Molecule: dnr protein; PDBTitle: crystal structure of the sensor domain of the transcriptional2 regulator dnr from pseudomonas aeruginosa
46	c3mdpA_	Alignment	not modelled	99.6	20	PDB header: nucleotide binding protein Chain: A: PDB Molecule: cyclic nucleotide-binding domain (cnmp-bd) protein; PDBTitle: crystal structure of a putative cyclic nucleotide-binding protein2 (gmet_1532) from geobacter metallireducens gs-15 at 1.90 a resolution
47	c5bv6A_	Alignment	not modelled	99.6	16	PDB header: transferase Chain: A: PDB Molecule: cgmp-dependent protein kinase 2; PDBTitle: pkg ii's carboxyl terminal cyclic nucleotide binding domain (cnb-b) in2 a complex with cgmp
48	c3idcB_	Alignment	not modelled	99.5	18	PDB header: transferase Chain: B: PDB Molecule: camp-dependent protein kinase type ii-beta regulatory PDBTitle: crystal structure of (102-265)riib:c holoenzyme of camp-dependent2 protein kinase
49	c5d1iB_	Alignment	not modelled	99.5	21	PDB header: unknown function Chain: B: PDB Molecule: cyclic nucleotide-binding protein; PDBTitle: structure of cyclic nucleotide-binding-like protein from brucella2 abortus bv. 1 str. 9-941
50	d2gaua1	Alignment	not modelled	99.5	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: CAP C-terminal domain-like
51	d2coha1	Alignment	not modelled	99.5	29	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: CAP C-terminal domain-like
52	d1ne6a2	Alignment	not modelled	99.5	25	Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain
53	c3j4qC_	Alignment	not modelled	99.5	18	PDB header: transferase Chain: C: PDB Molecule: camp-dependent protein kinase type ii-alpha regulatory PDBTitle: pseudo-atomic model of the akap18-pka complex in a bent conformation2 derived from electron microscopy
						Fold: Double-stranded beta-helix

54	d1vp6a_	Alignment	not modelled	99.5	23	Superfamily: cAMP-binding domain-like Family: cAMP-binding domain
55	c5t3nB_	Alignment	not modelled	99.5	20	PDB header: transferase Chain: B: PDB Molecule: camp-dependent protein kinase regulatory subunit; PDBTitle: sp-2cl-camps bound to pkar cbd2
56	d2coha2	Alignment	not modelled	99.5	17	Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain
57	c2byvE_	Alignment	not modelled	99.4	14	PDB header: regulation Chain: E: PDB Molecule: rap guanine nucleotide exchange factor 4; PDBTitle: structure of the camp responsive exchange factor epac2 in2 its auto-inhibited state
58	d1ft9a1	Alignment	not modelled	99.4	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: CAP C-terminal domain-like
59	d1ne6a1	Alignment	not modelled	99.4	18	Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain
60	c1o7fA_	Alignment	not modelled	99.4	14	PDB header: regulation Chain: A: PDB Molecule: camp-dependent rap1 guanine-nucleotide exchange PDBTitle: crystal structure of the regulatory domain of epac2
61	d2h6ca1	Alignment	not modelled	99.4	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: CAP C-terminal domain-like
62	c4myiA_	Alignment	not modelled	99.4	18	PDB header: transferase Chain: A: PDB Molecule: cgmp-dependent protein kinase, putative; PDBTitle: crystal structure of pvx_084705
63	d2bgca1	Alignment	not modelled	99.4	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: CAP C-terminal domain-like
64	c5v4sB_	Alignment	not modelled	99.4	20	PDB header: transport protein Chain: B: PDB Molecule: transporter, cation channel family / cyclic nucleotide- PDBTitle: cryoem structure of a prokaryotic cyclic nucleotide-gated ion channel
65	d1o7fa2	Alignment	not modelled	99.4	13	Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain
66	c6cjtB_	Alignment	not modelled	99.4	23	PDB header: transport protein Chain: B: PDB Molecule: sthk cyclic nucleotide-gated potassium channel; PDBTitle: structure of the sthk cyclic nucleotide-gated potassium channel in2 complex with cgmp
67	c3pvbB_	Alignment	not modelled	99.4	17	PDB header: transferase Chain: B: PDB Molecule: camp-dependent protein kinase type i-alpha regulatory PDBTitle: crystal structure of (73-244)ria:c holoenzyme of camp-dependent2 protein kinase
68	c5c8wB_	Alignment	not modelled	99.4	13	PDB header: transferase Chain: B: PDB Molecule: cgmp-dependent protein kinase 2; PDBTitle: pkg ii's amino terminal cyclic nucleotide binding domain (cnb-a) in a2 complex with cgmp
69	c5u6pA_	Alignment	not modelled	99.3	20	PDB header: transport protein Chain: A: PDB Molecule: potassium/sodium hyperpolarization-activated cyclic PDBTitle: structure of the human hcn1 hyperpolarization-activated cyclic2 nucleotide-gated ion channel in complex with camp
70	c4f8aA_	Alignment	not modelled	99.3	19	PDB header: membrane protein, transport protein Chain: A: PDB Molecule: potassium voltage-gated channel subfamily h member 1; PDBTitle: cyclic nucleotide binding-homology domain from mouse eag1 potassium2 channel
71	d3e5ua1	Alignment	not modelled	99.3	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: CAP C-terminal domain-like
72	c2n7gA_	Alignment	not modelled	99.3	17	PDB header: membrane protein Chain: A: PDB Molecule: potassium voltage-gated channel subfamily h member 2; PDBTitle: structure of the cyclic nucleotide-binding homology domain of the herg2 channel
73	c1cx4A_	Alignment	not modelled	99.3	18	PDB header: signaling protein Chain: A: PDB Molecule: camp-dependent protein kinase regulatory subunit PDBTitle: crystal structure of a deletion mutant of the type ii beta2 regulatory subunit of camp-dependent protein kinase
74	c3ogjD_	Alignment	not modelled	99.3	16	PDB header: transferase Chain: D: PDB Molecule: prkg1 protein; PDBTitle: crystal structure of partial apo (92-227) of cgmp-dependent protein2 kinase
75	c2ptmA_	Alignment	not modelled	99.3	19	PDB header: transport protein Chain: A: PDB Molecule: hyperpolarization-activated (ih) channel; PDBTitle: structure and rearrangements in the carboxy-terminal region of spih2 channels
76	d1wgpA_	Alignment	not modelled	99.3	18	Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain
77	c3otfA_	Alignment	not modelled	99.3	19	PDB header: transport protein Chain: A: PDB Molecule: potassium/sodium hyperpolarization-activated cyclic PDBTitle: structural basis for the camp-dependent gating in human hcn4 channel
78	d2oz6a1	Alignment	not modelled	99.3	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: CAP C-terminal domain-like

79	c4d7sB_	Alignment	not modelled	99.3	24	PDB header: transport protein Chain: B: PDB Molecule: sthk_cnbd_cgmp; PDBTitle: structure of the sthk carboxy-terminal region in complex with cgmp
80	c6g52H_	Alignment	not modelled	99.3	15	PDB header: metal transport Chain: H: PDB Molecule: metal transporter cnm4; PDBTitle: crystal structure of the cnm4 binding domain of the magnesium2 transporter cnm4
81	c4dinB_	Alignment	not modelled	99.2	25	PDB header: transferase/transport protein Chain: B: PDB Molecule: camp-dependent protein kinase type i-beta regulatory PDBTitle: novel localization and quaternary structure of the pka ri beta2 holoenzyme
82	d1o7fa3	Alignment	not modelled	99.2	23	Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain
83	c3cf6E_	Alignment	not modelled	99.2	22	PDB header: signaling protein/gtp-binding protein Chain: E: PDB Molecule: rap guanine nucleotide exchange factor (gef) 4; PDBTitle: structure of epac2 in complex with cyclic-amp and rap
84	d1q3ea_	Alignment	not modelled	99.2	21	Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain
85	d1i5za1	Alignment	not modelled	99.2	29	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: CAP C-terminal domain-like
86	c3uknC_	Alignment	not modelled	99.2	20	PDB header: transport protein, membrane protein Chain: C: PDB Molecule: novel protein similar to vertebrate potassium voltage-gated PDBTitle: structure of the c-linker/cnbd of zelk channels in c 2 2 21 space2 group
87	c5va1A_	Alignment	not modelled	99.2	25	PDB header: transport protein Chain: A: PDB Molecule: potassium voltage-gated channel subfamily h member 2; PDBTitle: cryo-em structure of the human ether-a-go-go related k+ channel
88	c4lloE_	Alignment	not modelled	99.2	26	PDB header: transport protein Chain: E: PDB Molecule: potassium voltage-gated channel subfamily h member 1; PDBTitle: structure of the eag domain-cnbd complex of the mouse eag1 channel
89	c5k71A_	Alignment	not modelled	99.2	27	PDB header: metal transport/calcium binding protein Chain: A: PDB Molecule: potassium voltage-gated channel subfamily h member 1; PDBTitle: single particle cryo-em structure of the voltage-gated k+ channel eag12 bound to the channel inhibitor calmodulin
90	c5h3oA_	Alignment	not modelled	99.2	17	PDB header: transport protein Chain: A: PDB Molecule: cyclic nucleotide-gated cation channel; PDBTitle: structure of a eukaryotic cyclic nucleotide-gated channel
91	c3of1A_	Alignment	not modelled	99.2	22	PDB header: transferase Chain: A: PDB Molecule: camp-dependent protein kinase regulatory subunit; PDBTitle: crystal structure of bcy1, the yeast regulatory subunit of pka
92	c3tnqA_	Alignment	not modelled	99.2	18	PDB header: transferase Chain: A: PDB Molecule: camp-dependent protein kinase type ii-beta regulatory PDBTitle: structure and allostery of the pka riib tetrameric holoenzyme
93	c6ftfB_	Alignment	not modelled	99.2	23	PDB header: signaling protein Chain: B: PDB Molecule: protein kinase a regulatory subunit, putative; PDBTitle: regulatory subunit of a camp-independent protein kinase a from2 trypanosoma cruzi at 1.09 a resolution
94	c5kbfA_	Alignment	not modelled	99.1	21	PDB header: transferase Chain: A: PDB Molecule: camp-dependent protein kinase regulatory subunit, putative; PDBTitle: camp bound pfpka-r (141-441)
95	c5j3uA_	Alignment	not modelled	99.1	18	PDB header: transferase Chain: A: PDB Molecule: protein kinase a; PDBTitle: co-crystal structure of the regulatory domain of toxoplasma gondii pka2 with camp
96	c2d93A_	Alignment	not modelled	99.0	18	PDB header: signaling protein Chain: A: PDB Molecule: rap guanine nucleotide exchange factor 6; PDBTitle: solution structure of the cnm4 binding domain of human rap2 guanine nucleotide exchange factor 6
97	c3shrA_	Alignment	not modelled	99.0	18	PDB header: transferase Chain: A: PDB Molecule: cgmp-dependent protein kinase 1; PDBTitle: crystal structure of cgmp-dependent protein kinase reveals novel site2 of interchain communication
98	c1rgsA_	Alignment	not modelled	99.0	17	PDB header: kinase Chain: A: PDB Molecule: camp dependent protein kinase; PDBTitle: regulatory subunit of camp dependent protein kinase
99	c4i11A_	Alignment	not modelled	99.0	13	PDB header: metal transport Chain: A: PDB Molecule: agap007709-pa; PDBTitle: structure of the c-linker/cnbd of agerg channels
100	d1zyba1	Alignment	not modelled	98.3	26	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: CAP C-terminal domain-like
101	c5zc2B_	Alignment	not modelled	97.7	15	PDB header: flavoprotein Chain: B: PDB Molecule: p-hydroxyphenylacetate 3-hydroxylase, reductase component; PDBTitle: acinetobacter baumannii p-hydroxyphenylacetate 3-hydroxylase (hpah),2 reductase component (c1)
102	c2x4hA_	Alignment	not modelled	97.6	16	PDB header: transcription Chain: A: PDB Molecule: hypothetical protein sso2273; PDBTitle: crystal structure of the hypothetical protein sso2273 from2 sulfobolbus solfataricus

103	d2hr3a1	Alignment	not modelled	97.6	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
104	c1fx7C	Alignment	not modelled	97.5	19	PDB header: signaling protein Chain: C: PDB Molecule: iron-dependent repressor ider; PDBTitle: crystal structure of the iron-dependent regulator (ider) from2 mycobacterium tuberculosis
105	d2fxaa1	Alignment	not modelled	97.5	8	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
106	c5jbrA	Alignment	not modelled	97.5	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein bcav_2135; PDBTitle: crystal structure of uncharacterized protein bcav_2135 from2 beutenbergia cavernae
107	c3zplE	Alignment	not modelled	97.4	16	PDB header: transcription/dna Chain: E: PDB Molecule: putative marr-family transcriptional repressor; PDBTitle: crystal structure of sco3205, a marr family transcriptional regulator2 from streptomyces coelicolor, in complex with dna
108	c5cviB	Alignment	not modelled	97.4	14	PDB header: transcription regulator Chain: B: PDB Molecule: slor; PDBTitle: structure of the manganese regulator slor
109	c1g3wA	Alignment	not modelled	97.4	14	PDB header: gene regulation Chain: A: PDB Molecule: diphtheria toxin repressor; PDBTitle: cd-cys102ser dtxr
110	c4q77B	Alignment	not modelled	97.4	5	PDB header: dna binding protein Chain: B: PDB Molecule: hth-type transcriptional regulator rot; PDBTitle: crystal structure of the full-length sorbitol operon2 genes in2 staphylococcus aureus
111	c2w48D	Alignment	not modelled	97.4	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
112	c2h09A	Alignment	not modelled	97.4	22	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator mntr; PDBTitle: crystal structure of diphtheria toxin repressor like protein2 from e. coli
113	c1f5tA	Alignment	not modelled	97.4	14	PDB header: transcription/dna Chain: A: PDB Molecule: diphtheria toxin repressor; PDBTitle: diphtheria tox repressor (c102d mutant) complexed with2 nickel and dtxr consensus binding sequence
114	d2fbha1	Alignment	not modelled	97.4	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
115	d3broa1	Alignment	not modelled	97.4	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
116	c2pexA	Alignment	not modelled	97.4	15	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator ohrr; PDBTitle: structure of reduced c22s ohrr from xanthomonas campestris
117	c2fxaB	Alignment	not modelled	97.4	8	PDB header: transcription Chain: B: PDB Molecule: protease production regulatory protein hpr; PDBTitle: structure of the protease production regulatory protein hpr from2 bacillus subtilis.
118	c2it0A	Alignment	not modelled	97.4	18	PDB header: transcription/dna Chain: A: PDB Molecule: iron-dependent repressor ider; PDBTitle: crystal structure of a two-domain ider-dna complex crystal2 form ii
119	c4nb5D	Alignment	not modelled	97.3	14	PDB header: dna binding protein Chain: D: PDB Molecule: dna binding protein; PDBTitle: crystal structure of a transcriptional regulator
120	c3zmdD	Alignment	not modelled	97.3	12	PDB header: transcription Chain: D: PDB Molecule: putative transcriptional regulator; PDBTitle: crystal structure of absc, a marr family transcriptional2 regulator from streptomyces coelicolor