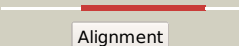

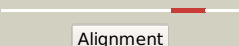

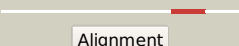

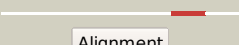

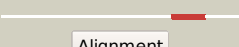

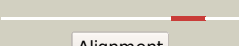













Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2370c_(-)_2650255_2651568
Date	Mon Aug 5 13:25:52 BST 2019
Unique Job ID	24fbcc49fe377483

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3onqB_	 Alignment		100.0	14	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: regulator of polyketide synthase expression; PDBTitle: crystal structure of regulator of polyketide synthase expression2 bad_0249 from bifidobacterium adolescentis
2	d1ntca_	 Alignment		97.3	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
3	d1fipa_	 Alignment		97.2	26	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
4	c1umqA_	 Alignment		97.1	35	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
5	d1umqa_	 Alignment		97.1	35	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
6	c3m1eA_	 Alignment		97.0	20	PDB header: transcription regulator Chain: A: PDB Molecule: hth-type transcriptional regulator benm; PDBTitle: crystal structure of benm_dbd
7	c5fo5A_	 Alignment		97.0	23	PDB header: transcription Chain: A: PDB Molecule: hth-type transcriptional regulator metr; PDBTitle: structure of the dna-binding domain of escherichia coli methionine2 biosynthesis regulator metr
8	c5z4yB_	 Alignment		96.9	18	PDB header: dna binding protein Chain: B: PDB Molecule: cys regulon transcriptional activator; PDBTitle: crystal structure of pacysb ntd domain with space group p4
9	c2m8gX_	 Alignment		96.8	23	PDB header: transcription Chain: X: PDB Molecule: transcriptional regulator; PDBTitle: structure, function, and tethering of dna-binding domains in 542 transcriptional activators
10	c2esnC_	 Alignment		96.8	20	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: probable transcriptional regulator; PDBTitle: the crystal structure of probable transcriptional regulator pa04772 from pseudomonas aeruginosa
11	d1letxa_	 Alignment		96.8	29	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like

12	d1etob_	Alignment		96.8	26	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
13	d2esna1	Alignment		96.8	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: LysR-like transcriptional regulators
14	c1iz1B_	Alignment		96.7	20	PDB header: dna binding protein Chain: B: PDB Molecule: lysr-type regulatory protein; PDBTitle: crystal structure of cbnr, a lysr family transcriptional2 regulator
15	c3t1bB_	Alignment		96.7	14	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator, lysr family; PDBTitle: crystal structure of the full-length aphb n100e variant
16	c3ispA_	Alignment		96.7	15	PDB header: transcription Chain: A: PDB Molecule: hth-type transcriptional regulator PDBTitle: crystal structure of argp from mycobacterium tuberculosis
17	c5y9sD_	Alignment		96.7	23	PDB header: transcription Chain: D: PDB Molecule: vv2_1132; PDBTitle: crystal structure of vv2_1132, a lysr family transcriptional regulator
18	d1b9ma1	Alignment		96.6	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: N-terminal domain of molybdate-dependent transcriptional regulator ModE
19	c1z1jE_	Alignment		96.5	16	PDB header: transcription Chain: E: PDB Molecule: dormancy survival regulator; PDBTitle: crystal structure of the mycobacterium tuberculosis hypoxic2 response regulator dosr c-terminal domain
20	c3fzjC_	Alignment		96.5	23	PDB header: transcription regulator Chain: C: PDB Molecule: lysr type regulator of tsambcd; PDBTitle: tsar low resolution crystal structure, tetragonal form
21	c1b9nA_	Alignment	not modelled	96.4	11	PDB header: transcription Chain: A: PDB Molecule: protein (mode); PDBTitle: regulator from escherichia coli
22	c3k1nB_	Alignment	not modelled	96.4	20	PDB header: transcription Chain: B: PDB Molecule: hth-type transcriptional regulator benm; PDBTitle: crystal structure of full-length benm
23	c1g2hA_	Alignment	not modelled	96.3	13	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
24	d1g2ha_	Alignment	not modelled	96.3	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
25	d1ixca1	Alignment	not modelled	96.3	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: LysR-like transcriptional regulators
26	c4pziA_	Alignment	not modelled	96.3	25	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, lysr family; PDBTitle: 1.60 angstrom resolution crystal structure of a transcriptional2 regulator of the lysr family from eggerthella lenta dsm 2243
27	c5y2vA_	Alignment	not modelled	96.3	18	PDB header: transcription Chain: A: PDB Molecule: rubisco operon transcriptional regulator; PDBTitle: strcutrue of the full-length ccmr complexed with 2-og from2 synechocystis pcc6803
28	c5m7nA_	Alignment	not modelled	96.2	25	PDB header: signaling protein Chain: A: PDB Molecule: nitrogen assimilation regulatory protein; PDBTitle: crystal structure of ntrx from brucella abortus in complex with atp2 processed with the crystaldirect automated mounting and

						cryo-cooling3 technology
29	c4l5eA_	Alignment	not modelled	96.2	22	PDB header: protein binding Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of a. aeolicus ntrc1 dna binding domain
30	c5ydwB_	Alignment	not modelled	96.1	23	PDB header: dna binding protein Chain: B: PDB Molecule: cell density-dependent motility repressor; PDBTitle: full-length structure of hpyt from salmonella typhimuriuma2 (hypochlorite-specific lysr-type transcriptional regulator)
31	c3e7lD_	Alignment	not modelled	96.1	13	PDB header: transcription regulator Chain: D: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigma54 activator ntrc4's dna binding2 domain
32	c3fzvC_	Alignment	not modelled	96.1	11	PDB header: transcription regulator Chain: C: PDB Molecule: probable transcriptional regulator; PDBTitle: crystal structure of pa01 protein, putative lysr family2 transcriptional regulator from pseudomonas aeruginosa
33	c3hhgF_	Alignment	not modelled	95.9	21	PDB header: transcription regulator Chain: F: PDB Molecule: transcriptional regulator, lysr family; PDBTitle: structure of crga, a lysr-type transcriptional regulator from2 heisseria meningitidis.
34	c3hugA_	Alignment	not modelled	95.8	19	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
35	c6g4rE_	Alignment	not modelled	95.7	26	PDB header: transcription Chain: E: PDB Molecule: hydrogen peroxide-inducible genes activator; PDBTitle: corynebacterium glutamicum oxyr c206s mutant, h2o2-bound
36	c4lfuA_	Alignment	not modelled	95.5	22	PDB header: dna binding protein Chain: A: PDB Molecule: regulatory protein sdiA; PDBTitle: crystal structure of escherichia coli sdiA in the space group c2
37	d1or7a1	Alignment	not modelled	95.4	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
38	c3qp5C_	Alignment	not modelled	95.3	10	PDB header: transcription Chain: C: PDB Molecule: cvir transcriptional regulator; PDBTitle: crystal structure of cvir bound to antagonist chlorolactone (cl)
39	d1a04a1	Alignment	not modelled	95.3	12	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)
40	d1rp3a2	Alignment	not modelled	95.3	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
41	c1ojlD_	Alignment	not modelled	95.2	30	PDB header: response regulator Chain: D: PDB Molecule: transcriptional regulatory protein zrar; PDBTitle: crystal structure of a sigma54-activator suggests the mechanism for2 the conformational switch necessary for sigma54 binding
42	c2ijlB_	Alignment	not modelled	95.1	7	PDB header: transcription Chain: B: PDB Molecule: molybdenum-binding transcriptional repressor; PDBTitle: the structure of a putative mode from agrobacterium tumefaciens.
43	c6c03A_	Alignment	not modelled	95.0	17	PDB header: transcription Chain: A: PDB Molecule: putative rna polymerase ecf-subfamily sigma factor; PDBTitle: the crystal structure streptomyces venezuelae rsbn-bldn complex
44	c3sztB_	Alignment	not modelled	94.9	14	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
45	c2rnjA_	Alignment	not modelled	94.3	15	PDB header: transcription Chain: A: PDB Molecule: response regulator protein vrar; PDBTitle: nmr structure of the s. aureus vrar dna binding domain
46	c3vepA_	Alignment	not modelled	94.3	13	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
47	d1l3la1	Alignment	not modelled	94.1	18	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)
48	c6dvdF_	Alignment	not modelled	94.1	19	PDB header: transferase/dna Chain: F: PDB Molecule: ecf rna polymerase sigma factor sigI; PDBTitle: crystal structure of mycobacterium tuberculosis transcription2 initiation complex(ecf sigma factor I) with 6 nt spacer and bromine3 labelled in position "-11
49	d1p4wa_	Alignment	not modelled	94.1	17	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)
50	d1fsea_	Alignment	not modelled	94.0	15	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)
51	c5fgmA_	Alignment	not modelled	94.0	20	PDB header: hydrolase Chain: A: PDB Molecule: ecf rna polymerase sigma factor sigr; PDBTitle: streptomyces coelicolor sigr region 4
52	c6jqsA_	Alignment	not modelled	93.8	8	PDB header: dna binding protein Chain: A: PDB Molecule: dna-binding response regulator; PDBTitle: structure of transcription factor, gere

53	c2o8xA	Alignment	not modelled	93.8	14	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
54	c2krfB	Alignment	not modelled	93.8	15	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulatory protein coma; PDBTitle: nmr solution structure of the dna binding domain of competence protein2 a
55	c2q0a	Alignment	not modelled	93.6	21	PDB header: transcription Chain: A: PDB Molecule: probable transcriptional activator protein trar; PDBTitle: crystal structure of an anti-activation complex in bacterial quorum2 sensing
56	c1h0mD	Alignment	not modelled	93.2	18	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
57	d1yioa1	Alignment	not modelled	93.2	15	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)
58	c2e1cA	Alignment	not modelled	93.0	7	PDB header: transcription/dna Chain: A: PDB Molecule: putative hth-type transcriptional regulator ph1519; PDBTitle: structure of putative hth-type transcriptional regulator ph1519/dna2 complex
59	c5zx3F	Alignment	not modelled	92.9	21	PDB header: transcription Chain: F: PDB Molecule: ecf rna polymerase sigma factor sigh; PDBTitle: mycobacterium tuberculosis rna polymerase holoenzyme with ecf sigma2 factor sigma h
60	c6in7B	Alignment	not modelled	92.7	14	PDB header: transcription Chain: B: PDB Molecule: rna polymerase sigma-h factor; PDBTitle: crystal structure of algu in complex with muca(cyto)
61	c3t0yA	Alignment	not modelled	92.7	22	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
62	c1x3uA	Alignment	not modelled	92.6	11	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
63	c6ideA	Alignment	not modelled	92.6	13	PDB header: transcription/dna Chain: A: PDB Molecule: transcriptional regulator luxr family; PDBTitle: crystal structure of the vibrio cholera vqma-ligand-dna complex2 provides molecular mechanisms for drug design
64	c2cfxD	Alignment	not modelled	92.6	5	PDB header: transcription Chain: D: PDB Molecule: hth-type transcriptional regulator lrpc; PDBTitle: structure of b.subtilis lrpc
65	d2cg4a1	Alignment	not modelled	92.3	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
66	c5o8yG	Alignment	not modelled	92.0	21	PDB header: transcription Chain: G: PDB Molecule: transcriptional regulatory protein rcsb; PDBTitle: conformational dynamism for dna interaction in salmonella typhimurium2 rcsb response regulator.
67	c1or7A	Alignment	not modelled	92.0	12	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
68	c4x6gG	Alignment	not modelled	91.8	23	PDB header: dna binding protein Chain: G: PDB Molecule: oxyr; PDBTitle: full-length oxyr c199d from pseudomonas aeruginosa
69	c2vzbA	Alignment	not modelled	91.8	12	PDB header: dna-binding protein Chain: A: PDB Molecule: transcriptional regulatory protein; PDBTitle: feast or famine regulatory protein (rv3291c)from m.2 tuberculosis complexed with l-tryptophan
70	d1xsva	Alignment	not modelled	91.6	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: YlxM/p13-like
71	d2jn6a1	Alignment	not modelled	91.6	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Cgl2762-like
72	d1lga1	Alignment	not modelled	91.5	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
73	d1s7oa	Alignment	not modelled	91.5	7	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: YlxM/p13-like
74	c2lfwA	Alignment	not modelled	91.2	15	PDB header: signaling protein Chain: A: PDB Molecule: phyr sigma-like domain; PDBTitle: nmr structure of the phyrsl-nepr complex from sphingomonas sp. fr1
75	c3vdoA	Alignment	not modelled	91.0	13	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
76	c2jpcA	Alignment	not modelled	90.8	23	PDB header: dna binding protein Chain: A: PDB Molecule: ssrb; PDBTitle: ssrb dna binding protein
77	c3cloC	Alignment	not modelled	90.7	20	PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of putative transcriptional regulator containing a2 luxr dna binding domain (np_811094.1) from bacteroides3 thetaiotaomicron vpi-5482 at 2.04 a resolution
						PDB header: transcription

78	c2cg4B_	Alignment	not modelled	90.7	12	Chain: B: PDB Molecule: regulatory protein asnc; PDBTitle: structure of e.coli asnc
79	c2l4aA_	Alignment	not modelled	90.7	6	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
80	c2dbbA_	Alignment	not modelled	90.6	23	PDB header: transcriptional regulator Chain: A: PDB Molecule: putative lth-type transcriptional regulator ph0061; PDBTitle: crystal structure of ph0061
81	c4czdA_	Alignment	not modelled	90.5	15	PDB header: lyase Chain: A: PDB Molecule: putative transcriptional regulator, asnc family; PDBTitle: sirohaem decarboxylase ahba/b - an enzyme with structural homology2 to the lrp/asnc transcription factor family that is part of the3 alternative haem biosynthesis pathway.
82	c2e7xA_	Alignment	not modelled	90.5	15	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
83	c2p6tH_	Alignment	not modelled	90.0	16	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
84	d2cfxa1	Alignment	not modelled	90.0	3	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
85	c1i1gA_	Alignment	not modelled	89.4	9	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator lrpA; PDBTitle: crystal structure of the lrp-like transcriptional regulator from the2 archaeon pyrococcus furiosus
86	c4if4A_	Alignment	not modelled	89.1	16	PDB header: transcription Chain: A: PDB Molecule: response regulator protein vrrA; PDBTitle: crystal structure of the magnesium and beryllium-activated vrrA2 from staphylococcus aureus
87	c3i4pA_	Alignment	not modelled	89.0	15	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, asnc family; PDBTitle: crystal structure of asnc family transcriptional regulator from2 agrobacterium tumefaciens
88	c2q1zA_	Alignment	not modelled	88.9	8	PDB header: transcription Chain: A: PDB Molecule: rpoe, ecf sigE; PDBTitle: crystal structure of rhodobacter sphaeroides sigE in complex with the2 anti-sigma chrr
89	c5f64C_	Alignment	not modelled	88.9	16	PDB header: transcription regulator Chain: C: PDB Molecule: positive transcription regulator evgA; PDBTitle: putative positive transcription regulator (sensor evgs) from shigella2 flexneri
90	d2cyya1	Alignment	not modelled	88.6	8	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
91	c5z7iC_	Alignment	not modelled	88.1	18	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
92	c1u78A_	Alignment	not modelled	87.9	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
93	d2coba1	Alignment	not modelled	87.6	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Psq domain
94	c3mzyA_	Alignment	not modelled	87.4	13	PDB header: rna binding protein Chain: A: PDB Molecule: rna polymerase sigma-h factor; PDBTitle: the crystal structure of the rna polymerase sigma-h factor from2 fusobacterium nucleatum to 2.5a
95	c4cxfA_	Alignment	not modelled	86.9	15	PDB header: transcription Chain: A: PDB Molecule: rna polymerase sigma factor cnrh; PDBTitle: structure of cnrh in complex with the cytosolic domain of cnry
96	c4pccC_	Alignment	not modelled	86.9	12	PDB header: transcription Chain: C: PDB Molecule: possible transcriptional regulatory protein (probably PDBTitle: crystal structure of mtbaldr (rv2779c)
97	c3hyiA_	Alignment	not modelled	86.3	15	PDB header: transcription regulator Chain: A: PDB Molecule: protein duf199/whia; PDBTitle: crystal structure of full-length duf199/whia from thermatoga maritima
98	c5wurB_	Alignment	not modelled	86.3	10	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
99	c2gqqB_	Alignment	not modelled	85.4	12	PDB header: transcription Chain: B: PDB Molecule: leucine-responsive regulatory protein; PDBTitle: crystal structure of e. coli leucine-responsive regulatory protein2 (lrp)
100	d1smyf2	Alignment	not modelled	84.8	8	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
101	c4czdD_	Alignment	not modelled	84.8	18	PDB header: lyase Chain: D: PDB Molecule: putative transcriptional regulator, asnc family; PDBTitle: sirohaem decarboxylase ahba/b - an enzyme with structural homology2 to the lrp/asnc transcription factor family that is part of the3 alternative haem biosynthesis pathway.
102	c2rn7A_	Alignment	not modelled	84.2	16	PDB header: unknown function Chain: A: PDB Molecule: is629 orfA; PDBTitle: nmr solution structure of tnpe protein from shigella2 flexneri. northeast structural genomics target sfr125 PDB header: transcription

103	c5hevC_	Alignment	not modelled	84.1	16	Chain: C; PDB Molecule: response regulator protein vvar; PDBTitle: crystal structure of the beryllium-fluoride-activated liar from <i>2 enterococcus faecium</i>
104	c5ae5A_	Alignment	not modelled	84.0	17	PDB header: transcription Chain: A; PDB Molecule: lysr-type regulatory protein; PDBTitle: structures of inactive and activated dntr provide conclusive evidence ² for the mechanism of action of lysr transcription factors
105	c5uxxC_	Alignment	not modelled	83.9	15	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 the ² anti-sigma factor nepr from <i>bartonella quintana</i>
106	c2ia0A_	Alignment	not modelled	83.3	20	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: putative hth-type transcriptional regulator pf0864; PDBTitle: transcriptional regulatory protein pf0864 from <i>pyrococcus furiosus</i> a2 member of the asnc family (pf0864)
107	c3klnC_	Alignment	not modelled	82.8	13	PDB header: transcription Chain: C; PDB Molecule: transcriptional regulator, luxr family; PDBTitle: <i>vibrio cholerae</i> vpst
108	c4yn8A_	Alignment	not modelled	79.7	15	PDB header: dna binding protein Chain: A; PDB Molecule: response regulator chra; PDBTitle: crystal structure of response regulator chra in heme-sensing two2 component system
109	c6amaO_	Alignment	not modelled	79.6	17	PDB header: dna binding protein/dna Chain: O; PDB Molecule: putative dna-binding protein; PDBTitle: structure of <i>s. coelicolor/s. venezuelae</i> bldc-smea-ssfa complex to2 3.09 angstrom
110	c1zn2A_	Alignment	not modelled	79.5	15	PDB header: transcription regulator Chain: A; PDB Molecule: response regulatory protein; PDBTitle: low resolution structure of response regulator styR
111	c1rp3G_	Alignment	not modelled	79.2	14	PDB header: transcription Chain: G; PDB Molecule: rna polymerase sigma factor sigma-28 (fliA); PDBTitle: cocrystal structure of the flagellar sigma/anti-sigma complex, sigma-2 28/flgM
112	d1ttya_	Alignment	not modelled	79.1	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
113	c5xe7A_	Alignment	not modelled	78.6	15	PDB header: dna binding protein Chain: A; PDB Molecule: ecf rna polymerase sigma factor sigJ; PDBTitle: crystal structure of mycobacterium tuberculosis extracytoplasmic ² function sigma factor sigJ
114	d1ku7a_	Alignment	not modelled	77.3	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
115	c4ch7A_	Alignment	not modelled	76.3	21	PDB header: transcription Chain: A; PDB Molecule: nird-like protein; PDBTitle: crystal structure of the siroheme decarboxylase nirdI
116	d1i3ja_	Alignment	not modelled	74.9	19	Fold: DNA-binding domain of intron-encoded endonucleases Superfamily: DNA-binding domain of intron-encoded endonucleases Family: DNA-binding domain of intron-encoded endonucleases
117	c3c3wB_	Alignment	not modelled	74.6	12	PDB header: transcription Chain: B; PDB Molecule: two component transcriptional regulatory protein devr; PDBTitle: crystal structure of the mycobacterium tuberculosis hypoxic response ² regulator dosR
118	c5chhA_	Alignment	not modelled	74.5	16	PDB header: transcription Chain: A; PDB Molecule: arac family transcriptional regulator; PDBTitle: crystal structure of transcriptional regulator cdpr from <i>pseudomonas</i> 2 <i>aeruginosa</i>
119	d1q06a_	Alignment	not modelled	74.2	16	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: DNA-binding N-terminal domain of transcription activators
120	d2auwa1	Alignment	not modelled	74.1	14	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE0471 C-terminal domain-like