
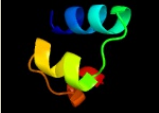
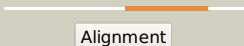

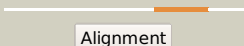

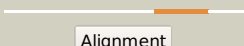
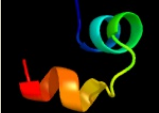
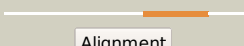

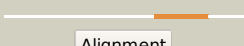

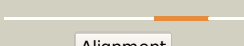




















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2664 (-) _2982107_2982361
Date	Wed Aug 7 12:50:31 BST 2019
Unique Job ID	a3424459122bfc11

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1u78A_	 Alignment		88.2	9	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	d1s7oa_	 Alignment		87.7	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: YlxM/p13-like
3	c2e7xA_	 Alignment		86.6	14	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
4	c2ia0A_	 Alignment		85.8	14	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)
5	c1i1gA_	 Alignment		85.2	28	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator lrpA; PDBTitle: crystal structure of the lrp-like transcriptional regulator from the2 archaeon pyrococcus furiosus
6	c2cfxD_	 Alignment		84.7	10	PDB header: transcription Chain: D: PDB Molecule: hth-type transcriptional regulator lrpC; PDBTitle: structure of b.subtilis lrpC
7	c4pccC_	 Alignment		84.6	19	PDB header: transcription Chain: C: PDB Molecule: possible transcriptional regulatory protein (probably PDBTitle: crystal structure of mtbaldr (rv2779c)
8	c2vzbA_	 Alignment		84.5	19	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
9	c2p6tH_	 Alignment		84.0	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
10	c3i4pA_	 Alignment		82.7	14	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, asnc family; PDBTitle: crystal structure of asnc family transcriptional regulator from2 agrobacterium tumefaciens
11	c2x48B_	 Alignment		82.5	24	PDB header: viral protein Chain: B: PDB Molecule: cag38821; PDBTitle: orf 55 from sulfolobus islandicus rudivirus 1

12	c2e1cA	Alignment		82.4	14	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
13	d1dwka1	Alignment		82.3	8	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Cyanase N-terminal domain
14	c2dbbA	Alignment		82.3	29	PDB header: transcriptional regulator Chain: A; PDB Molecule: putative hth-type transcriptional regulator ph0061; PDBTitle: crystal structure of ph0061
15	c3hugA	Alignment		81.7	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
16	c2cg4B	Alignment		80.9	14	PDB header: transcription Chain: B; PDB Molecule: regulatory protein asnc; PDBTitle: structure of e.coli asnc
17	c3vepA	Alignment		80.7	15	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
18	c1p8cD	Alignment		80.4	12	PDB header: structural genomics, unknown function Chain: D; PDB Molecule: conserved hypothetical protein; PDBTitle: crystal structure of tm1620 (apc4843) from thermotoga2 maritima
19	c5uk3J	Alignment		79.0	9	PDB header: lyase Chain: J; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of cyanase from t. urticae
20	c1or7A	Alignment		78.5	9	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
21	c2l4aA	Alignment	not modelled	78.3	10	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
22	d1xsva	Alignment	not modelled	77.6	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: YlxM/p13-like
23	d1rp3a2	Alignment	not modelled	77.0	6	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
24	c3e7ID	Alignment	not modelled	76.9	22	PDB header: transcription regulator Chain: D; PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigma54 activator ntrc4's dna binding2 domain
25	d1v7ba1	Alignment	not modelled	76.9	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
26	c3vwbA	Alignment	not modelled	76.1	20	PDB header: transcription/dna Chain: A; PDB Molecule: virulence regulon transcriptional activator virb; PDBTitle: crystal structure of virb core domain (se-met derivative) complexed2 with the cis-acting site (5-bru modifications) upstream ic sb promoter
27	c4czdD	Alignment	not modelled	75.9	15	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.
28	c6in7B	Alignment	not modelled	74.9	15	PDB header: transcription Chain: B; PDB Molecule: rna polymerase sigma-h factor;

						PDBTitle: crystal structure of algu in complex with muca(cyto)
29	c2iv1J_	Alignment	not modelled	74.0	9	PDB header: lyase Chain: J; PDB Molecule: cyanate hydratase; PDBTitle: site directed mutagenesis of key residues involved in the catalytic2 mechanism of cyanase
30	c3t72o_	Alignment	not modelled	73.3	24	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
31	d1vz0a1	Alignment	not modelled	73.2	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: KorB DNA-binding domain-like Family: KorB DNA-binding domain-like
32	d2cg4a1	Alignment	not modelled	72.6	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
33	c3rkaA_	Alignment	not modelled	72.2	19	PDB header: ligase Chain: A; PDB Molecule: biotin-[acetyl-coa-carboxylase] ligase; PDBTitle: structural characterisation of staphylococcus aureus biotin protein2 ligase
34	c1vz0B_	Alignment	not modelled	71.7	18	PDB header: nuclear protein Chain: B; PDB Molecule: chromosome-partitioning protein spo0j; PDBTitle: chromosome segregation protein spo0j from thermus thermophilus
35	c2gqgB_	Alignment	not modelled	71.4	8	PDB header: transcription Chain: B; PDB Molecule: leucine-responsive regulatory protein; PDBTitle: crystal structure of e. coli leucine-responsive regulatory protein2 (lrp)
36	d2vkea1	Alignment	not modelled	70.9	27	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
37	d2p7vb1	Alignment	not modelled	70.5	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
38	c4czdA_	Alignment	not modelled	70.2	20	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.
39	c6fkgC_	Alignment	not modelled	69.5	11	PDB header: toxin Chain: C; PDB Molecule: rv1990c (mbca); PDBTitle: crystal structure of the m.tuberculosis mbct-mbca toxin-antitoxin2 complex.
40	d1ku3a_	Alignment	not modelled	69.1	28	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
41	c6c05F_	Alignment	not modelled	68.6	33	PDB header: transcription Chain: F; PDB Molecule: rna polymerase sigma factor siga; PDBTitle: mycobacterium tuberculosis rnap holo/rbpa in relaxed state
42	c5wurB_	Alignment	not modelled	68.0	19	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
43	d2cfxa1	Alignment	not modelled	67.5	8	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
44	c5zx3F_	Alignment	not modelled	66.8	27	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
45	c5xazD_	Alignment	not modelled	66.2	28	PDB header: dna binding protein Chain: D; PDB Molecule: gamma-butyrolactone receptor protein; PDBTitle: crystal structure of full length native tylp, a tetr regulator from2 streptomyces fradiae
46	d1ilga1	Alignment	not modelled	65.6	28	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
47	d1ku7a_	Alignment	not modelled	65.6	27	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
48	c5tw1F_	Alignment	not modelled	65.2	33	PDB header: transcription activator/transferase/dna Chain: F; PDB Molecule: rna polymerase sigma factor siga; PDBTitle: crystal structure of a mycobacterium smegmatis transcription2 initiation complex with rbpa
49	c5dxzA_	Alignment	not modelled	65.1	23	PDB header: dna binding protein Chain: A; PDB Molecule: tetr family transcriptional regulator; PDBTitle: crystal of amtr from corynebacterium glutamicum
50	d1ttya_	Alignment	not modelled	64.7	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
51	d1or7a1	Alignment	not modelled	64.2	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
52	c3npiB_	Alignment	not modelled	63.4	23	PDB header: gene regulation Chain: B; PDB Molecule: tetr family regulatory protein; PDBTitle: crystal structure of a tetr family regulatory protein (dip1788) from2 corynebacterium diphtheriae at 2.96 a resolution
53	d2cyya1	Alignment	not modelled	63.0	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
						PDB header: transcription regulator

54	c3g7rB_	Alignment	not modelled	62.9	19	Chain: B: PDB Molecule: putative transcriptional regulator; PDBTitle: crystal structure of sco4454, a tetr-family transcriptional regulator2 from streptomyces coelicolor
55	c2qibA_	Alignment	not modelled	62.3	19	PDB header: transcription Chain: A: PDB Molecule: tetr-family transcriptional regulator; PDBTitle: crystal structure of tetr-family transcriptional regulator from2 streptomyces coelicolor
56	c2qeuA_	Alignment	not modelled	62.1	12	PDB header: lyase Chain: A: PDB Molecule: putative carboxymuconolactone decarboxylase; PDBTitle: crystal structure of putative carboxymuconolactone decarboxylase2 (yp_555818.1) from burkholderia xenovorans lb400 at 1.65 a resolution
57	c2kfsA_	Alignment	not modelled	62.1	16	PDB header: dna-binding protein Chain: A: PDB Molecule: conserved hypothetical regulatory protein; PDBTitle: nmr structure of rv2175c
58	c4ch7A_	Alignment	not modelled	61.9	10	PDB header: transcription Chain: A: PDB Molecule: nird-like protein; PDBTitle: crystal structure of the siroheme decarboxylase nirdl
59	c5ojyA_	Alignment	not modelled	61.6	15	PDB header: transcription Chain: A: PDB Molecule: tetr family transcription regulator; PDBTitle: co-complex structure of regulator protein 2 (pamr2) with pamamycin 6072 from streptomyces alboniger
60	c5xe7A_	Alignment	not modelled	60.9	25	PDB header: dna binding protein Chain: A: PDB Molecule: ecf rna polymerase sigma factor sigj; PDBTitle: crystal structure of mycobacterium tuberculosis extracytoplasmic2 function sigma factor sigj
61	c3v6gA_	Alignment	not modelled	60.6	15	PDB header: transcription Chain: A: PDB Molecule: probable transcriptional regulatory protein (probably deor- PDBTitle: crystal structure of transcriptional regulator
62	c5vl9D_	Alignment	not modelled	60.4	26	PDB header: transcription/dna Chain: D: PDB Molecule: regulatory protein tetr; PDBTitle: crystal structure of eilr in complex with eilo dna element
63	c5dipB_	Alignment	not modelled	60.1	11	PDB header: oxidoreductase Chain: B: PDB Molecule: alkyl hydroperoxide reductase ahpd; PDBTitle: crystal structure of lpg0406 in reduced form from legionella2 pneumophila
64	d1vkea_	Alignment	not modelled	59.9	12	Fold: AhpD-like Superfamily: AhpD-like Family: CMD-like
65	c3cjdB_	Alignment	not modelled	59.4	15	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, tetr family; PDBTitle: crystal structure of putative tetr transcriptional regulator2 (yp_510936.1) from jannaschia sp. ccs1 at 1.79 a resolution
66	c2g7IA_	Alignment	not modelled	59.3	18	PDB header: transcription Chain: A: PDB Molecule: tetr-family transcriptional regulator; PDBTitle: crystal structure of putative transcription regulator sco7704 from2 streptomyces coelicor
67	c2w7nA_	Alignment	not modelled	58.6	38	PDB header: transcription/dna Chain: A: PDB Molecule: trfb transcriptional repressor protein; PDBTitle: crystal structure of kora bound to operator dna: insight into2 repressor cooperation in rp4 gene regulation
68	c1zx4B_	Alignment	not modelled	58.2	11	PDB header: cell cycle Chain: B: PDB Molecule: plasmid partition par b protein; PDBTitle: structure of parb bound to dna
69	d1k78a1	Alignment	not modelled	58.0	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
70	d1adra_	Alignment	not modelled	57.5	26	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
71	c2g7gA_	Alignment	not modelled	57.5	14	PDB header: transcription Chain: A: PDB Molecule: rha04620, putative transcriptional regulator; PDBTitle: the crystal structure of the putative transcriptional regulator2 rha04620 from rhodococcus sp. rha1
72	c5ipmF_	Alignment	not modelled	57.3	27	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
73	c2llkA_	Alignment	not modelled	57.2	30	PDB header: cell cycle, transcription Chain: A: PDB Molecule: cyclin-d-binding myb-like transcription factor 1; PDBTitle: solution nmr structure of the n-terminal myb-like 1 domain of the2 human cyclin-d-binding transcription factor 1 (hdmp1), northeast3 structural genomics consortium (nesg) target id hr8011a
74	c2gfnA_	Alignment	not modelled	57.0	17	PDB header: transcription Chain: A: PDB Molecule: hth-type transcriptional regulator pksa related protein; PDBTitle: crystal structure of hth-type transcriptional regulator pksa related2 protein from rhodococcus sp. rha1
75	d1smyf2	Alignment	not modelled	56.4	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
76	c4pu4C_	Alignment	not modelled	56.1	17	PDB header: toxin/antitoxin/dna Chain: C: PDB Molecule: toxin-antitoxin system antidote transcriptional repressor PDBTitle: shewanella oneidensis mr-1 toxin antitoxin system hipa, hipb and its2 operator dna complex (space group p21)
77	c5z7iC_	Alignment	not modelled	55.8	30	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
						PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator, tetr family;

78	c2qtqB_	Alignment	not modelled	55.7	18	PDBTitle: crystal structure of a predicted dna-binding transcriptional regulator2 (saro_1072) from novosphingobium aromaticivorans dsm at 1.85 a3 resolution
79	d1nr3a_	Alignment	not modelled	55.1	37	Fold: DNA-binding protein Tfx Superfamily: DNA-binding protein Tfx Family: DNA-binding protein Tfx
80	d2cwqa1	Alignment	not modelled	55.1	20	Fold: AhpD-like Superfamily: AhpD-like Family: TTHA0727-like
81	d2ouwa1	Alignment	not modelled	54.4	20	Fold: AhpD-like Superfamily: AhpD-like Family: TTHA0727-like
82	c5eybB_	Alignment	not modelled	54.1	27	PDB header: dna binding protein/dna Chain: B: PDB Molecule: dna-binding protein reb1; PDBTitle: x-ray structure of reb1-ter complex
83	c5e57B_	Alignment	not modelled	53.8	21	PDB header: translation Chain: B: PDB Molecule: transcription regulator amtr; PDBTitle: crystal structure of mycobacterium smegmatis amtr
84	c2raeA_	Alignment	not modelled	53.8	18	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, acrr family protein; PDBTitle: crystal structure of a tetr/acrr family transcriptional regulator from2 rhodococcus sp. rha1
85	c2ewnA_	Alignment	not modelled	53.7	30	PDB header: ligase, transcription Chain: A: PDB Molecule: bira bifunctional protein; PDBTitle: ecoli biotin repressor with co-repressor analog
86	c2auwB_	Alignment	not modelled	53.0	21	PDB header: unknown function Chain: B: PDB Molecule: hypothetical protein ne0471; PDBTitle: crystal structure of putative dna binding protein ne0471 from2 nitrosomonas europaea atcc 19718
87	c2guhA_	Alignment	not modelled	52.1	23	PDB header: transcription Chain: A: PDB Molecule: putative tetr-family transcriptional regulator; PDBTitle: crystal structure of the putative tetr-family transcriptional2 regulator from rhodococcus sp. rha1
88	c3vdoA_	Alignment	not modelled	51.9	17	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
89	c5mwrB_	Alignment	not modelled	51.8	17	PDB header: transcription Chain: B: PDB Molecule: tetr family transcriptional regulator; PDBTitle: the fadr transcription regulator from sulfobolus acidocaldarius
90	c2q1za_	Alignment	not modelled	50.4	14	PDB header: transcription Chain: A: PDB Molecule: rpoe, ecf sige; PDBTitle: crystal structure of rhodobacter sphaeroides sige in complex with the2 anti-sigma chrr
91	c3bjbE_	Alignment	not modelled	50.3	15	PDB header: transcription regulator Chain: E: PDB Molecule: probable transcriptional regulator, tetr family protein; PDBTitle: crystal structure of a tetr transcriptional regulator from rhodococcus2 sp. rha1
92	c3t76A_	Alignment	not modelled	49.6	9	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator vanug; PDBTitle: crystal structure of transcriptional regulator vanug, form ii
93	c5ydpC_	Alignment	not modelled	49.5	21	PDB header: gene regulation Chain: C: PDB Molecule: tetr transcriptional regulatory protein; PDBTitle: crystal structure of tetr family repressor alkx from dietzia sp.2 strain dq12-45-1b implicated in biodegradation of n-alkanes
94	c6paxA_	Alignment	not modelled	49.3	13	PDB header: gene regulation/dna Chain: A: PDB Molecule: homeobox protein pax-6; PDBTitle: crystal structure of the human pax-6 paired domain-dna2 complex reveals a general model for pax protein-dna3 interactions
95	c5d1rA_	Alignment	not modelled	48.9	19	PDB header: transcription Chain: A: PDB Molecule: rv1816 transcriptional regulator; PDBTitle: crystal structure of mycobacterium tuberculosis rv1816 transcriptional2 regulator.
96	d1i5za1	Alignment	not modelled	48.8	26	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: CAP C-terminal domain-like
97	c3b6aC_	Alignment	not modelled	48.6	15	PDB header: transcription Chain: C: PDB Molecule: actr protein; PDBTitle: crystal structure of the streptomyces coelicolor tetr family protein2 actr in complex with actinorhodin
98	c3mnlA_	Alignment	not modelled	48.3	13	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulatory protein (probably tetr-family); PDBTitle: the crystal structure of kstr (rv3574) from mycobacterium tuberculosis2 h37rv
99	c1l9uH_	Alignment	not modelled	48.3	29	PDB header: transcription Chain: H: PDB Molecule: sigma factor siga; PDBTitle: thermus aquaticus rna polymerase holoenzyme at 4 a2 resolution
100	d2oz6a1	Alignment	not modelled	48.2	26	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: CAP C-terminal domain-like
101	c6g8hC_	Alignment	not modelled	48.2	23	PDB header: transcription Chain: C: PDB Molecule: tetr/acrr family transcriptional regulator; PDBTitle: flavonoid-responsive regulator frra in complex with naringenin
102	c3m1fC_	Alignment	not modelled	47.5	13	PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulator; PDBTitle: putative transcriptional regulator from staphylococcus aureus.
						PDB header: structural genomics, unknown function

103	c3beyC_	Alignment	not modelled	47.4	12	Chain: C; PDB Molecule: conserved protein o27018; PDBTitle: crystal structure of the protein o27018 from methanobacterium2 thermoautotrophicum. northeast structural genomics consortium target3 tt217
104	c2o38A_	Alignment	not modelled	47.4	24	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: hypothetical protein; PDBTitle: putative xre family transcriptional regulator
105	d2o38a1	Alignment	not modelled	47.4	24	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE1354
106	c2fd5A_	Alignment	not modelled	47.3	24	PDB header: transcription regulator Chain: A; PDB Molecule: transcriptional regulator; PDBTitle: the crystal structure of a transcriptional regulator from pseudomonas2 aeruginosa pao1
107	c3iuvA_	Alignment	not modelled	47.0	13	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: uncharacterized tetr family protein; PDBTitle: the structure of a member of tetr family (sco1917) from2 streptomyces coelicolor a3
108	c3dcfB_	Alignment	not modelled	46.5	19	PDB header: transcription regulator Chain: B; PDB Molecule: transcriptional regulator of the tetr/acrr family; PDBTitle: crystal structure of transcriptional regulator of the tetr/acrr family2 (yp_290855.1) from thermobifida fusca yx-er1 at 2.50 a resolution
109	c3mzyA_	Alignment	not modelled	46.3	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
110	c1bjzA_	Alignment	not modelled	46.1	26	PDB header: transcription regulation Chain: A; PDB Molecule: tetracycline repressor; PDBTitle: tetracycline chelated mg2+-ion initiates helix unwinding for tet2 repressor induction
111	c6dvdF_	Alignment	not modelled	45.9	18	PDB header: transferase/dna Chain: F; PDB Molecule: ecf rna polymerase sigma factor sigl; PDBTitle: crystal structure of mycobacterium tuberculosis transcription2 initiation complex(ecf sigma factor l) with 6 nt spacer and bromine3 labelled in position "-11
112	d1vkeb_	Alignment	not modelled	45.5	15	Fold: AhpD-like Superfamily: AhpD-like Family: CMD-like
113	c2m8gX_	Alignment	not modelled	44.9	18	PDB header: transcription Chain: X; PDB Molecule: transcriptional regulator; PDBTitle: structure, function, and tethering of dna-binding domains in 542 transcriptional activators
114	c3egqB_	Alignment	not modelled	44.0	12	PDB header: transcription Chain: B; PDB Molecule: tetr family transcriptional regulator; PDBTitle: crystal structure of a tetr-family transcriptional regulator (af_1817)2 from archaeoglobus fulgidus at 2.55 a resolution
115	c1rktA_	Alignment	not modelled	44.0	17	PDB header: transcription Chain: A; PDB Molecule: protein yfir; PDBTitle: crystal structure of yfir, a putative transcriptional regulator from2 bacillus subtilis
116	c2jvA_	Alignment	not modelled	43.9	24	PDB header: transcription Chain: A; PDB Molecule: trmbf1; PDBTitle: nmr structure of the c-terminal domain of mbf1 of trichoderma reesei
117	c2y31A_	Alignment	not modelled	43.9	21	PDB header: transcription Chain: A; PDB Molecule: putative repressor simreg2; PDBTitle: simocyclinone c4 bound form of tetr-like repressor simr
118	c3korD_	Alignment	not modelled	43.8	18	PDB header: transcription Chain: D; PDB Molecule: possible trp repressor; PDBTitle: crystal structure of a putative trp repressor from staphylococcus2 aureus
119	c2r0qF_	Alignment	not modelled	43.7	21	PDB header: recombination/dna Chain: F; PDB Molecule: putative transposon tn552 dna-invertase bin3; PDBTitle: crystal structure of a serine recombinase- dna regulatory2 complex
120	c5uxxC_	Alignment	not modelled	43.6	17	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