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Description	RVBD1186c_(-)_1327695_1329311
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Detailed template information



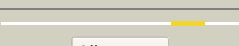
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3onqB_	 Alignment		100.0	16	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: regulator of polyketide synthase expression; PDBTitle: crystal structure of regulator of polyketide synthase expression2 bad_0249 from bifidobacterium adolescentis
2	c5ey0A_	 Alignment		99.8	11	PDB header: transcription Chain: A: PDB Molecule: gtp-sensing transcriptional pleiotropic repressor cody; PDBTitle: crystal structure of cody from staphylococcus aureus with gtp and ile
3	c5ey2A_	 Alignment		99.8	10	PDB header: transcription Chain: A: PDB Molecule: gtp-sensing transcriptional pleiotropic repressor cody; PDBTitle: crystal structure of cody from bacillus cereus
4	c2gx5B_	 Alignment		99.7	15	PDB header: transcription Chain: B: PDB Molecule: gtp-sensing transcriptional pleiotropic repressor cody; PDBTitle: n-terminal gaf domain of transcriptional pleiotropic repressor cody
5	d1ko7a1	 Alignment		99.5	15	Fold: MurF and HprK N-domain-like Superfamily: HprK N-terminal domain-like Family: HPr kinase/phoshatase HprK N-terminal domain
6	c1ko7B_	 Alignment		98.4	15	PDB header: transferase,hydrolase Chain: B: PDB Molecule: hpr kinase/phosphatase; PDBTitle: x-ray structure of the hpr kinase/phosphatase from staphylococcus2 xylosus at 1.95 a resolution
7	c5n0IC_	 Alignment		98.0	15	PDB header: transcription Chain: C: PDB Molecule: gtp-sensing transcriptional pleiotropic repressor cody; PDBTitle: the structure of the cofactor binding gaf domain of the nutrient2 sensor cody from clostridium difficile
8	c1knxF_	 Alignment		97.7	13	PDB header: transferase/hydrolase Chain: F: PDB Molecule: probable hpr(ser) kinase/phosphatase; PDBTitle: hpr kinase/phosphatase from mycoplasma pneumoniae
9	d1knxa1	 Alignment		97.6	13	Fold: MurF and HprK N-domain-like Superfamily: HprK N-terminal domain-like Family: HPr kinase/phoshatase HprK N-terminal domain
10	d2ioja1	 Alignment		97.5	13	Fold: MurF and HprK N-domain-like Superfamily: HprK N-terminal domain-like Family: DRTGG domain
11	d1fipa_	 Alignment		97.4	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like

12	d1ntca_	Alignment		97.4	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
13	c1umqA_	Alignment		97.3	23	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
14	d1umqa_	Alignment		97.3	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
15	d1etxa_	Alignment		97.2	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
16	c2m8gX_	Alignment		97.1	23	PDB header: transcription Chain: X: PDB Molecule: transcriptional regulator; PDBTitle: structure, function, and tethering of dna-binding domains in 542 transcriptional activators
17	d1etob_	Alignment		97.1	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
18	c5fo5A_	Alignment		97.0	26	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
19	c1g2hA_	Alignment		97.0	15	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
20	d1g2ha_	Alignment		97.0	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
21	c5z4yB_	Alignment	not modelled	96.9	17	PDB header: dna binding protein Chain: B: PDB Molecule: cys regulon transcriptional activator; PDBTitle: crystal structure of pacysb ntd domain with space group p4
22	c2esnC_	Alignment	not modelled	96.9	24	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
23	c1iz1B_	Alignment	not modelled	96.8	24	PDB header: dna binding protein Chain: B: PDB Molecule: lysr-type regulatory protein; PDBTitle: crystal structure of cbnr, a lysr family transcriptional2 regulator
24	c5m7nA_	Alignment	not modelled	96.8	10	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
25	c3m1eA_	Alignment	not modelled	96.8	17	PDB header: transcription regulator Chain: A: PDB Molecule: hth-type transcriptional regulator benm; PDBTitle: crystal structure of benm_dbd
26	c3t1bB_	Alignment	not modelled	96.7	17	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator, lysr family; PDBTitle: crystal structure of the full-length aphb n100e variant
27	d2esna1	Alignment	not modelled	96.7	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: LysR-like transcriptional regulators
28	c5y9sD_	Alignment	not modelled	96.7	20	PDB header: transcription Chain: D: PDB Molecule: vv2_1132; PDBTitle: crystal structure of vv2_1132, a lysr family transcriptional regulator

29	c3ispA	Alignment	not modelled	96.7	35	PDB header: transcription Chain: A: PDB Molecule: hth-type transcriptional regulator PDBTitle: crystal structure of argp from mycobacterium tuberculosis
30	c4l5eA	Alignment	not modelled	96.6	13	PDB header: protein binding Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of a. aeolicus ntrc1 dna binding domain
31	c3fzjC	Alignment	not modelled	96.6	30	PDB header: transcription regulator Chain: C: PDB Molecule: lysr type regulator of tsambcd; PDBTitle: tsar low resolution crystal structure, tetragonal form
32	c3e7lD	Alignment	not modelled	96.5	10	PDB header: transcription regulator Chain: D: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigma54 activator ntrc4's dna binding2 domain
33	c5y2vA	Alignment	not modelled	96.4	21	PDB header: transcription Chain: A: PDB Molecule: rubisco operon transcriptional regulator; PDBTitle: strcuture of the full-length ccmr complexed with 2-og from2 synechocystis pcc6803
34	c3k1nB	Alignment	not modelled	96.4	17	PDB header: transcription Chain: B: PDB Molecule: hth-type transcriptional regulator benm; PDBTitle: crystal structure of full-length benm
35	c6g4rE	Alignment	not modelled	96.4	21	PDB header: transcription Chain: E: PDB Molecule: hydrogen peroxide-inducible genes activator; PDBTitle: corynebacterium glutamicum oxyr c206s mutant, h2o2-bound
36	c5ydwB	Alignment	not modelled	96.4	23	PDB header: dna binding protein Chain: B: PDB Molecule: cell density-dependent motility repressor; PDBTitle: full-length structure of pa01 protein, putative lysr family2 typhimuriuma2 (hypochlorite-specific lysr-type transcriptional regulator)
37	c3fzvC	Alignment	not modelled	96.3	16	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
38	d1b9ma1	Alignment	not modelled	96.3	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: N-terminal domain of molybdate-dependent transcriptional regulator ModE
39	c4pzjA	Alignment	not modelled	96.3	20	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
40	d1ixca1	Alignment	not modelled	96.2	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: LysR-like transcriptional regulators
41	c3hhgF	Alignment	not modelled	96.1	20	PDB header: transcription regulator Chain: F: PDB Molecule: transcriptional regulator, lysr family; PDBTitle: structure of crga, a lysr-type transcriptional regulator from2 neisseria meningitidis.
42	c1ojlD	Alignment	not modelled	95.9	27	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
43	c1b9nA	Alignment	not modelled	95.9	22	PDB header: transcription Chain: A: PDB Molecule: protein (mode); PDBTitle: regulator from escherichia coli
44	c2ijjB	Alignment	not modelled	94.7	11	PDB header: transcription Chain: B: PDB Molecule: molybdenum-binding transcriptional repressor; PDBTitle: the structure of a putative mode from agrobacterium tumefaciens.
45	c1zljE	Alignment	not modelled	94.4	15	PDB header: transcription Chain: E: PDB Molecule: dormancy survival regulator; PDBTitle: crystal structure of the mycobacterium tuberculosis hypoxic2 response regulator dosr c-terminal domain
46	c4lfuA	Alignment	not modelled	93.7	14	PDB header: dna binding protein Chain: A: PDB Molecule: regulatory protein sdia; PDBTitle: crystal structure of escherichia coli sdia in the space group c2
47	c4x6gG	Alignment	not modelled	93.4	20	PDB header: dna binding protein Chain: G: PDB Molecule: oxyr; PDBTitle: full-length oxyr c199d from pseudomonas aeruginosa
48	c3qp5C	Alignment	not modelled	93.3	14	PDB header: transcription Chain: C: PDB Molecule: cvir transcriptional regulator; PDBTitle: crystal structure of cvir bound to antagonist chlorolactone (cl)
49	d1a04a1	Alignment	not modelled	93.0	14	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	c2w1tB	Alignment	not modelled	92.8	20	PDB header: transcription Chain: B: PDB Molecule: stage v sporulation protein t; PDBTitle: crystal structure of b. subtilis spovt
51	c2rnjA	Alignment	not modelled	92.6	14	PDB header: transcription Chain: A: PDB Molecule: response regulator protein vrar; PDBTitle: nmr structure of the s. aureus vrar dna binding domain
52	d1p4wa	Alignment	not modelled	92.3	11	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)
53	c3sztB	Alignment	not modelled	92.1	19	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

54	d1l3la1	Alignment	not modelled	91.9	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) PDB header: transcription Chain: G: PDB Molecule: transcriptional regulatory protein rcsb; PDBTitle: conformational dynamism for dna interaction in salmonella typhimurium2 rcsb response regulator.
55	c5o8yG	Alignment	not modelled	91.8	9	PDB header: transcription Chain: A: PDB Molecule: arac family transcriptional regulator; PDBTitle: crystal structure of transcriptional regulator cdpr from pseudomonas2 aeruginosa
56	c5chhA	Alignment	not modelled	91.7	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) PDB header: transcription Chain: A: PDB Molecule: probable transcriptional activator protein trar; PDBTitle: crystal structure of an anti-activation complex in bacterial quorum2 sensing
57	d1yioa1	Alignment	not modelled	91.6	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) PDB header: transcription Chain: A: PDB Molecule: stage v sporulation protein t; PDBTitle: crystal structure of the c-terminal domain of b. subtilis spovt
58	c2q0oA	Alignment	not modelled	91.5	11	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
59	d1fsea	Alignment	not modelled	91.4	25	PDB header: dna binding protein Chain: A: PDB Molecule: dna-binding response regulator; PDBTitle: structure of transcription factor, gere
60	c2w1rA	Alignment	not modelled	91.2	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
61	c1h0mD	Alignment	not modelled	91.2	17	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
62	c6jqsA	Alignment	not modelled	91.1	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain PDB header: transcription Chain: A: PDB Molecule: response regulator protein vrar; PDBTitle: crystal structure of the magnesium and berylliofluoride-activated vrar2 from staphylococcus aureus
63	c2krfB	Alignment	not modelled	91.0	14	PDB header: transcription Chain: A: PDB Molecule: putative rna polymerase ecf-subfamily sigma factor; PDBTitle: the crystal structure streptomyces venezuelae rsbn-bldn complex
64	c6ideA	Alignment	not modelled	89.8	13	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
65	d1rp3a2	Alignment	not modelled	89.7	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Psq domain PDB header: transcription Chain: A: PDB Molecule: ssrb; PDBTitle: ssrb dna binding protein
66	c4if4A	Alignment	not modelled	89.4	14	PDB header: dna binding protein Chain: A: PDB Molecule: ssrb; PDBTitle: ssrb dna binding protein
67	c6c03A	Alignment	not modelled	89.4	11	PDB header: transcription Chain: A: PDB Molecule: lys-r-type regulatory protein; PDBTitle: structures of inactive and activated dntr provide conclusive evidence2 for the mechanism of action of lysr transcription factors
68	c1x3uA	Alignment	not modelled	89.2	18	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
69	d2coba1	Alignment	not modelled	89.1	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Psq domain PDB header: ligase Chain: D: PDB Molecule: udp-n-acetylmuramoyl-l-alanyl-d-glutamate--2,6- PDBTitle: structure of mure from m.tuberculosis with dipeptide and adp
70	d2jn6a1	Alignment	not modelled	88.4	10	PDB header: dna binding protein Chain: A: PDB Molecule: ssrb; PDBTitle: ssrb dna binding protein
71	c2jpcA	Alignment	not modelled	88.3	14	PDB header: transcription Chain: A: PDB Molecule: lys-r-type regulatory protein; PDBTitle: structures of inactive and activated dntr provide conclusive evidence2 for the mechanism of action of lysr transcription factors
72	c5ae5A	Alignment	not modelled	88.1	18	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
73	c3cloC	Alignment	not modelled	88.0	22	PDB header: ligase Chain: D: PDB Molecule: udp-n-acetylmuramoyl-l-alanyl-d-glutamate--2,6- PDBTitle: structure of mure from m.tuberculosis with dipeptide and adp
74	c2xjaD	Alignment	not modelled	88.0	24	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 sigl
75	c3hugA	Alignment	not modelled	87.8	11	PDB header: ligase Chain: C: PDB Molecule: udp-n-acetylmuramoyl-l-alanyl-d-glutamate- PDBTitle: mure ligase of mycobacterium tuberculosis
76	c2wtzC	Alignment	not modelled	87.5	22	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.
77	c4czdA	Alignment	not modelled	87.2	13	

78	c2cfxD	Alignment	not modelled	87.0	24	PDB header: transcription Chain: D: PDB Molecule: hth-type transcriptional regulator lrpc; PDBTitle: structure of b.subtilis lrpc
79	d2cg4a1	Alignment	not modelled	86.1	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
80	c3klnC	Alignment	not modelled	85.9	19	PDB header: transcription Chain: C: PDB Molecule: transcriptional regulator, luxr family; PDBTitle: vibrio cholerae vpst
81	c5f64C	Alignment	not modelled	85.3	16	PDB header: transcription regulator Chain: C: PDB Molecule: positive transcription regulator evga; PDBTitle: putative positive transcription regulator (sensor evgs) from shigella2 flexneri
82	d1or7a1	Alignment	not modelled	85.1	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
83	c2vzbA	Alignment	not modelled	85.1	24	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
84	d2cfxa1	Alignment	not modelled	85.1	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
85	c2e7xA	Alignment	not modelled	84.6	24	PDB header: transcription regulator Chain: A: PDB Molecule: 150aa long hypothetical transcriptional regulator; PDBTitle: structure of the lrp/asnc like transcriptional regulator from2 sulfobolus tokodaii 7 complexed with its cognate ligand
86	c2p6tH	Alignment	not modelled	84.5	12	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
87	c5hevC	Alignment	not modelled	84.2	13	PDB header: transcription Chain: C: PDB Molecule: response regulator protein vrar; PDBTitle: crystal structure of the berylliofluoride-activated liar from2 enterococcus faecium
88	d1ilga1	Alignment	not modelled	83.7	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
89	c2vjwA	Alignment	not modelled	83.6	13	PDB header: hydrolase Chain: A: PDB Molecule: gaf family protein; PDBTitle: crystal structure of the second gaf domain of devs from2 mycobacterium smegmatis
90	d2cyya1	Alignment	not modelled	83.5	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
91	c2l4aA	Alignment	not modelled	83.4	21	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
92	c4g3kB	Alignment	not modelled	83.0	14	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator nh1; PDBTitle: crystal structure of a. aeolicus nh1 gaf domain in an inactive state
93	c1rnlA	Alignment	not modelled	82.8	14	PDB header: signal transduction protein Chain: A: PDB Molecule: nitrate/nitrite response regulator protein narl; PDBTitle: the nitrate/nitrite response regulator protein narl from narl
94	c1zn2A	Alignment	not modelled	82.7	19	PDB header: transcription regulator Chain: A: PDB Molecule: response regulatory protein; PDBTitle: low resolution structure of response regulator styr
95	d1xsva	Alignment	not modelled	82.7	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: YlxM/p13-like
96	d1s7oa	Alignment	not modelled	82.2	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: YlxM/p13-like
97	c2lvsA	Alignment	not modelled	82.1	17	PDB header: dna binding protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: nmr solution structure of a crispr repeat binding protein
98	c5fgmA	Alignment	not modelled	81.6	16	PDB header: hydrolase Chain: A: PDB Molecule: ecf rna polymerase sigma factor sigr; PDBTitle: streptomyces coelicolor sigr region 4
99	c3oovA	Alignment	not modelled	81.3	13	PDB header: signaling protein Chain: A: PDB Molecule: methyl-accepting chemotaxis protein, putative; PDBTitle: crystal structure of a methyl-accepting chemotaxis protein, residues2 122 to 287
100	c5zx3F	Alignment	not modelled	81.3	12	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
101	c2cg4B	Alignment	not modelled	81.2	20	PDB header: transcription Chain: B: PDB Molecule: regulatory protein asnc; PDBTitle: structure of e.coli asnc
102	c6oeiA	Alignment	not modelled	81.1	10	PDB header: structural protein Chain: A: PDB Molecule: spindle pole body component spc42,sigma-54-dependent PDBTitle: yeast spc42 n-terminal coiled-coil fused to pdb: 3k2n
103	c3i4pA	Alignment	not modelled	80.7	15	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, asnc family; PDBTitle: crystal structure of asnc family transcriptional regulator from2 agrobacterium tumefaciens

104	c3k2nB_	 Alignment	not modelled	80.3	10	PDB header: transcription regulator Chain: B: PDB Molecule: sigma-54-dependent transcriptional regulator; PDBTitle: the crystal structure of sigma-54-dependent transcriptional regulator2 domain from chlorobium tepidum t1s
105	c2dbbA_	 Alignment	not modelled	80.2	14	PDB header: transcriptional regulator Chain: A: PDB Molecule: putative hth-type transcriptional regulator ph0061; PDBTitle: crystal structure of ph0061
106	c1rp3G_	 Alignment	not modelled	80.1	10	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
107	c3c3wB_	 Alignment	not modelled	80.1	16	PDB header: transcription Chain: B: PDB Molecule: two component transcriptional regulatory protein devr; PDBTitle: crystal structure of the mycobacterium tuberculosis hypoxic response2 regulator dosr
108	d1ulya_	 Alignment	not modelled	80.0	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Hypothetical protein PH1932
109	c6dvdF_	 Alignment	not modelled	79.7	11	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 I) with 6 nt spacer and bromine3 labelled in position "-11
110	c4pccC_	 Alignment	not modelled	78.8	31	PDB header: transcription Chain: C: PDB Molecule: possible transcriptional regulatory protein (probably PDBTitle: crystal structure of mtbaldr (rv2779c)
111	d1i3ja_	 Alignment	not modelled	78.7	29	Fold: DNA-binding domain of intron-encoded endonucleases Superfamily: DNA-binding domain of intron-encoded endonucleases Family: DNA-binding domain of intron-encoded endonucleases
112	c2e1cA_	 Alignment	not modelled	78.5	17	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
113	c4czdD_	 Alignment	not modelled	78.3	12	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.
114	c4g6qA_	 Alignment	not modelled	77.9	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: the crystal structure of a functionally unknown protein kfla_6221 from2 kribbella flavida dsm 17836
115	c3rqjA_	 Alignment	not modelled	77.4	22	PDB header: transcription Chain: A: PDB Molecule: response regulator protein; PDBTitle: crystal structure of a response regulator protein from burkholderia2 pseudomallei with a phosphorylated aspartic acid, calcium ion and3 citrate
116	c1i1gA_	 Alignment	not modelled	77.4	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
117	c1bl0A_	 Alignment	not modelled	76.9	8	PDB header: transcription/dna Chain: A: PDB Molecule: protein (multiple antibiotic resistance protein); PDBTitle: multiple antibiotic resistance protein (mara)/dna complex
118	c4wxoA_	 Alignment	not modelled	76.7	16	PDB header: transferase Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: sadc (300-487) from pseudomonas aeruginosa pao1
119	c5z7iC_	 Alignment	not modelled	76.6	21	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
120	c1or7A_	 Alignment	not modelled	76.4	18	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