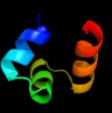
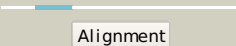
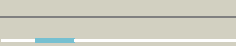
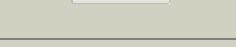
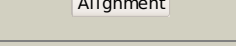
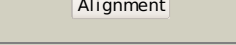
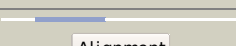
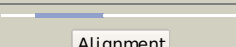
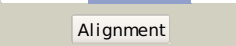
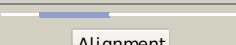
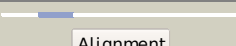
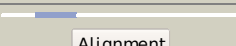
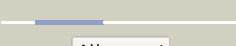


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1rzsa_	 Alignment		89.1	16	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
2	d1fipa_	 Alignment		88.7	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
3	c3bd1B_	 Alignment		87.8	20	PDB header: transcription Chain: B: PDB Molecule: cro protein; PDBTitle: structure of the cro protein from putative prophage element xfaso 1 in2 xylella fastidiosa strain ann-1
4	d1etxa_	 Alignment		86.7	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
5	c3e7ID_	 Alignment		84.3	6	PDB header: transcription regulator Chain: D: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigma54 activator ntrc4's dna binding2 domain
6	d1g2ha_	 Alignment		83.4	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
7	d1etob_	 Alignment		83.2	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
8	c3trbA_	 Alignment		82.8	17	PDB header: dna binding protein Chain: A: PDB Molecule: virulence-associated protein i; PDBTitle: structure of an addiction module antidote protein of a higa (higa)2 family from coxiella burnetii
9	d1umqa_	 Alignment		82.8	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
10	c1umqA_	 Alignment		82.8	13	PDB header: dna-binding protein Chain: A: PDB Molecule: photosynthetic apparatus regulatory protein; PDBTitle: solution structure and dna binding of the effector domain2 from the global regulator prra(rega) from r. sphaeroides:3 insights into dna binding specificity
11	c2fjrB_	 Alignment		82.2	21	PDB header: transcription regulator Chain: B: PDB Molecule: repressor protein ci; PDBTitle: crystal structure of bacteriophage 186

12	d1ntca_	Alignment		81.1	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
13	c3cecA_	Alignment		80.3	17	PDB header: transcription Chain: A: PDB Molecule: putative antidote protein of plasmid maintenance system; PDBTitle: crystal structure of a putative antidote protein of plasmid2 maintenance system (npun_f2943) from nostoc punctiforme pcc 73102 at3 1.60 a resolution
14	d2ou3a1	Alignment		74.8	21	Fold: TerB-like Superfamily: TerB-like Family: COG3793-like
15	c3onqB_	Alignment		70.1	21	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
16	c3omtA_	Alignment		66.3	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: putative antitoxin component, chu_2935 protein, from xre family from2 prevotella buccae.
17	d1vz0a1	Alignment		61.2	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: KorB DNA-binding domain-like Family: KorB DNA-binding domain-like
18	c2jxuA_	Alignment		58.9	22	PDB header: unknown function Chain: A: PDB Molecule: terb; PDBTitle: nmr solution structure of kp-terb, a tellurite resistance2 protein from klebsiella pneumoniae
19	c3mn2B_	Alignment		58.3	14	PDB header: transcription regulator Chain: B: PDB Molecule: probable arac family transcriptional regulator; PDBTitle: the crystal structure of a probable arac family transcriptional2 regulator from rhodopseudomonas palustris cga009
20	c3bdnB_	Alignment		57.7	12	PDB header: transcription/dna Chain: B: PDB Molecule: lambda repressor; PDBTitle: crystal structure of the lambda repressor
21	d1utxa_	Alignment	not modelled	57.4	14	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
22	c3bs3A_	Alignment	not modelled	56.8	10	PDB header: dna binding protein Chain: A: PDB Molecule: putative dna-binding protein; PDBTitle: crystal structure of a putative dna-binding protein from bacteroides2 fragilis
23	c3mklB_	Alignment	not modelled	55.3	22	PDB header: transcription regulator Chain: B: PDB Molecule: hth-type transcriptional regulator gadx; PDBTitle: crystal structure of dna-binding transcriptional dual regulator from2 escherichia coli k-12
24	d2cg4a1	Alignment	not modelled	54.8	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
25	d2icta1	Alignment	not modelled	54.8	14	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
26	d1ctda_	Alignment	not modelled	54.4	24	Fold: EF Hand-like Superfamily: EF-hand Family: Calmodulin-like
27	d2a61a1	Alignment		54.0	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
						PDB header: dna binding protein/dna

28	c3mkyP_	Alignment	not modelled	53.5	7	Chain: P: PDB Molecule: protein sobp; PDBTitle: structure of sobp(155-323)-18mer dna complex, i23 form
29	c3eusB_	Alignment	not modelled	51.8	15	PDB header: dna binding protein Chain: B: PDB Molecule: dna-binding protein; PDBTitle: the crystal structure of the dna binding protein from silicibacter2 pomeroyi
30	d2cfxa1	Alignment	not modelled	51.4	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
31	d2cyya1	Alignment	not modelled	50.4	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
32	c3lisB_	Alignment	not modelled	50.4	12	PDB header: transcription Chain: B: PDB Molecule: csp231i c protein; PDBTitle: crystal structure of the restriction-modification controller protein2 c.csp231i (monoclinic form)
33	c1nh2D_	Alignment	not modelled	49.0	12	PDB header: transcription/dna Chain: D: PDB Molecule: transcription initiation factor iia small chain; PDBTitle: crystal structure of a yeast tfiia/tpb/dna complex
34	c3op9A_	Alignment	not modelled	47.7	13	PDB header: transcription regulator Chain: A: PDB Molecule: pli0006 protein; PDBTitle: crystal structure of transcriptional regulator from listeria innocua
35	c2l4aA_	Alignment	not modelled	47.6	9	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
36	d1l1ga1	Alignment	not modelled	45.8	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
37	c3f6wE_	Alignment	not modelled	44.3	15	PDB header: dna binding protein Chain: E: PDB Molecule: xre-family like protein; PDBTitle: xre-family like protein from pseudomonas syringae pv. tomato str.2 dc3000
38	d2p12a1	Alignment	not modelled	44.1	12	Fold: FomD barrel-like Superfamily: FomD-like Family: FomD-like
39	d1y9qa1	Alignment	not modelled	43.5	7	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Probable transcriptional regulator VC1968, N-terminal domain
40	c2o38A_	Alignment	not modelled	43.5	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: putative xre family transcriptional regulator
41	d2o38a1	Alignment	not modelled	43.5	16	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE1354
42	c2kpiA_	Alignment	not modelled	43.2	18	PDB header: transcription regulator Chain: A: PDB Molecule: sos-response transcriptional repressor, lexa; PDBTitle: solution structure of protein sos-response transcriptional2 repressor, lexa from eubacterium rectale. northeast3 structural genomics consortium target err9a
43	c3mkzU_	Alignment	not modelled	43.1	6	PDB header: dna-binding protein/dna Chain: U: PDB Molecule: protein sobp; PDBTitle: structure of sobp(155-272)-18mer complex, p21 form
44	c1vkoA_	Alignment	not modelled	42.2	21	PDB header: isomerase Chain: A: PDB Molecule: inositol-3-phosphate synthase; PDBTitle: crystal structure of inositol-3-phosphate synthase (ce21227) from2 caenorhabditis elegans at 2.30 a resolution
45	c3b7hA_	Alignment	not modelled	40.8	7	PDB header: structural protein Chain: A: PDB Molecule: prophage lp1 protein 11; PDBTitle: crystal structure of the prophage lp1 protein 11
46	c2dbbA_	Alignment	not modelled	40.4	24	PDB header: transcriptional regulator Chain: A: PDB Molecule: putative hth-type transcriptional regulator ph0061; PDBTitle: crystal structure of ph0061
47	c3lsgD_	Alignment	not modelled	39.8	9	PDB header: transcription regulator Chain: D: PDB Molecule: two-component response regulator yesn; PDBTitle: the crystal structure of the c-terminal domain of the two-2 component response regulator yesn from fusobacterium3 nucleatum subsp. nucleatum atcc 25586
48	d1rp3a1	Alignment	not modelled	39.0	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma3 domain
49	c2ebyA_	Alignment	not modelled	38.9	16	PDB header: transcription Chain: A: PDB Molecule: putative hth-type transcriptional regulator ybaq; PDBTitle: crystal structure of a hypothetical protein from e. coli
50	c3f52A_	Alignment	not modelled	38.4	20	PDB header: transcription activator Chain: A: PDB Molecule: clp gene regulator (clgr); PDBTitle: crystal structure of the clp gene regulator clgr from c. glutamicum
51	d1e6yb1	Alignment	not modelled	35.9	27	Fold: Methyl-coenzyme M reductase alpha and beta chain C-terminal domain Superfamily: Methyl-coenzyme M reductase alpha and beta chain C-terminal domain Family: Methyl-coenzyme M reductase alpha and beta chain C-terminal domain
52	c3oi0A_	Alignment	not modelled	35.9	15	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator (arac-type dna-binding domain- PDBTitle: crystal structure of transcriptional regulator (arac-type dna-binding2 domain-containing proteins) from chromobacterium violaceum

53	c3k2zA	 Alignment	not modelled	35.5	18	PDB header: hydrolase Chain: A: PDB Molecule: lexa repressor; PDBTitle: crystal structure of a lexa protein from thermotoga maritima
54	c1r71B	 Alignment	not modelled	35.2	6	PDB header: transcription/dna Chain: B: PDB Molecule: transcriptional repressor protein korb; PDBTitle: crystal structure of the dna binding domain of korb in2 complex with the operator dna
55	d1ttya	 Alignment	not modelled	35.2	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
56	c2e1cA	 Alignment	not modelled	34.3	15	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
57	c3exmA	 Alignment	not modelled	33.4	11	PDB header: hydrolase Chain: A: PDB Molecule: phosphatase sc4828; PDBTitle: crystal structure of the phosphatase sc4828 with the non-hydrolyzable2 nucleotide gpcp
58	d2r1jl1	 Alignment	not modelled	32.5	13	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
59	d3ygsP	 Alignment	not modelled	32.4	13	Fold: DEATH domain Superfamily: DEATH domain Family: Caspase recruitment domain, CARD
60	c2p6tH	 Alignment	not modelled	30.8	12	PDB header: transcription Chain: H: PDB Molecule: transcriptional regulator, Irp/asnc family; PDBTitle: crystal structure of transcriptional regulator nmb0573 and l-leucine2 complex from neisseria meningitidis
61	c2q9lA	 Alignment	not modelled	30.0	21	PDB header: hydrolase Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of imazg from vibrio dat 722: ctag-imazg (p43212)
62	c2vbzA	 Alignment	not modelled	28.8	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
63	d1e6vb1	 Alignment	not modelled	28.3	22	Fold: Methyl-coenzyme M reductase alpha and beta chain C-terminal domain Superfamily: Methyl-coenzyme M reductase alpha and beta chain C-terminal domain Family: Methyl-coenzyme M reductase alpha and beta chain C-terminal domain
64	d1llib	 Alignment	not modelled	27.3	12	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
65	d2b5aa1	 Alignment	not modelled	26.5	16	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
66	d2f2ea1	 Alignment	not modelled	26.5	28	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Hxlr-like
67	d1z0xa1	 Alignment	not modelled	26.3	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
68	d1ui5a1	 Alignment	not modelled	26.3	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
69	d2vcha1	 Alignment	not modelled	25.9	6	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDPGT-like
70	d1r71a	 Alignment	not modelled	25.7	6	Fold: DNA/RNA-binding 3-helical bundle Superfamily: KorB DNA-binding domain-like Family: KorB DNA-binding domain-like
71	c3hugl	 Alignment	not modelled	25.7	10	PDB header: transcription/membrane protein Chain: J: PDB Molecule: probable conserved membrane protein; PDBTitle: crystal structure of mycobacterium tuberculosis anti-sigma factor rslA2 in complex with -35 promoter binding domain of sigl
72	c3kxaD	 Alignment	not modelled	25.5	15	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of ngo0477 from neisseria gonorrhoeae
73	d1or7a1	 Alignment	not modelled	25.3	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
74	d2jn6a1	 Alignment	not modelled	25.1	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Cgl2762-like
75	c3clcC	 Alignment	not modelled	25.0	4	PDB header: transcription regulator/dna Chain: C: PDB Molecule: regulatory protein; PDBTitle: crystal structure of the restriction-modification controller protein2 c.esp13961 tetramer in complex with its natural 35 base-pair operator
76	c3bhqB	 Alignment	not modelled	24.8	10	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of a putative tetr-family transcriptional regulator2 (mlr_4833) from mesorhizobium loti maff303099 at 1.54 a resolution
77	c1nvpD	 Alignment	not modelled	24.8	9	PDB header: transcription/dna Chain: D: PDB Molecule: transcription initiation factor iia gamma chain;

						PDBTitle: human tfiia/tbp/dna complex
78	d1adra_	Alignment	not modelled	24.6	15	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
79	c3k0lA_	Alignment	not modelled	24.6	15	PDB header: transcription regulator Chain: A: PDB Molecule: repressor protein; PDBTitle: crystal structure of putative marr family transcriptional2 regulator from acinetobacter sp. adp
80	c3m1fC_	Alignment	not modelled	24.3	12	PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulator; PDBTitle: putative transcriptional regulator from staphylococcus aureus.
81	d1kl7a_	Alignment	not modelled	23.8	16	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
82	c1e6yE_	Alignment	not modelled	23.7	29	PDB header: oxidoreductase Chain: E: PDB Molecule: methyl-coenzyme m reductase i beta subunit; PDBTitle: methyl-coenzyme m reductase from methanosarcina barkeri
83	d1nh2d1	Alignment	not modelled	23.7	12	Fold: Transcription factor IIA (TFIIA), alpha-helical domain Superfamily: Transcription factor IIA (TFIIA), alpha-helical domain Family: Transcription factor IIA (TFIIA), alpha-helical domain
84	d1lmb3_	Alignment	not modelled	23.6	11	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
85	c2cfxD_	Alignment	not modelled	23.6	9	PDB header: transcription Chain: D: PDB Molecule: hth-type transcriptional regulator lrpc; PDBTitle: structure of b.subtilis lrpc
86	c2k9sA_	Alignment	not modelled	23.4	10	PDB header: transcription Chain: A: PDB Molecule: arabinose operon regulatory protein; PDBTitle: solution structure of dna binding domain of e. coli arac
87	c2ia0A_	Alignment	not modelled	23.1	15	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)
88	c2gqQB_	Alignment	not modelled	22.9	9	PDB header: transcription Chain: B: PDB Molecule: leucine-responsive regulatory protein; PDBTitle: crystal structure of e. coli leucine-responsive regulatory protein2 (lrp)
89	c1i1gA_	Alignment	not modelled	22.8	18	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator lrpa; PDBTitle: crystal structure of the lrp-like transcriptional regulator from the2 archaeon pyrococcus furiosus
90	c2p8tA_	Alignment	not modelled	22.3	26	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein ph0730; PDBTitle: hypothetical protein ph0730 from pyrococcus horikoshii ot3
91	d2h5na1	Alignment	not modelled	22.2	26	Fold: TerB-like Superfamily: TerB-like Family: PG1108-like
92	c3mzyA_	Alignment	not modelled	22.2	25	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
93	d1in4a1	Alignment	not modelled	22.1	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Helicase DNA-binding domain
94	c3oouA_	Alignment	not modelled	22.1	10	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lin2118 protein; PDBTitle: the structure of a protein with unkown function from listeria innocua
95	d1sq8a_	Alignment	not modelled	22.0	20	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
96	c2nz7A_	Alignment	not modelled	21.9	8	PDB header: apoptosis Chain: A: PDB Molecule: caspase recruitment domain-containing protein 4; PDBTitle: crystal structure analysis of caspase-recruitment domain2 (card) of nod1
97	d1b0na2	Alignment	not modelled	21.8	9	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
98	c1bl0A_	Alignment	not modelled	21.7	6	PDB header: transcription/dna Chain: A: PDB Molecule: protein (multiple antibiotic resistance protein); PDBTitle: multiple antibiotic resistance protein (mara)/dna complex
99	d1r69a_	Alignment	not modelled	21.7	17	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
100	c3katA_	Alignment	not modelled	21.6	7	PDB header: apoptosis Chain: A: PDB Molecule: nacht, lrr and pyd domains-containing protein 1; PDBTitle: crystal structure of the card domain of the human nlrp12 protein, northeast structural genomics consortium target3 hr3486e
101	c3b6aC_	Alignment	not modelled	21.5	15	PDB header: transcription Chain: C: PDB Molecule: actr protein; PDBTitle: crystal structure of the streptomyces coelicolor tetr2 family protein actr in complex with actinorhodin
102	d2fq4a1	Alignment	not modelled	21.4	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like

						Family: Tetracyclin repressor-like, N-terminal domain
103	c2b1wA_	Alignment	not modelled	20.9	8	PDB header: apoptosis Chain: A: PDB Molecule: caspase recruitment domain protein 4; PDBTitle: solution structure of the nod1 caspase activating and recruitment2 domain
104	d1luxca_	Alignment	not modelled	20.3	8	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
105	c1zljE_	Alignment	not modelled	20.3	20	PDB header: transcription Chain: E: PDB Molecule: dormancy survival regulator; PDBTitle: crystal structure of the mycobacterium tuberculosis hypoxic2 response regulator dosr c-terminal domain
106	c4a5mH_	Alignment	not modelled	20.2	19	PDB header: transcription Chain: H: PDB Molecule: uncharacterized hth-type transcriptional regulator yybr; PDBTitle: redox regulator hypr in its oxidized form
107	d1ixrc1	Alignment	not modelled	20.1	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Helicase DNA-binding domain
108	c3t76A_	Alignment	not modelled	20.1	8	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator vanug; PDBTitle: crystal structure of transcriptional regulator vanug, form ii