

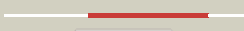


























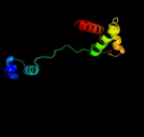



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3f9kV_	 Alignment		99.9	17	PDB header: viral protein, recombination Chain: V: PDB Molecule: integrase; PDBTitle: two domain fragment of hiv-2 integrase in complex with ledgf ibd
2	dlasua_	 Alignment		99.8	16	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
3	c1c0mA_	 Alignment		99.8	17	PDB header: transferase Chain: A: PDB Molecule: protein (integrase); PDBTitle: crystal structure of rsv two-domain integrase
4	d1c0ma2	 Alignment		99.8	17	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
5	c3nf9A_	 Alignment		99.8	16	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: integrase; PDBTitle: structural basis for a new mechanism of inhibition of hiv integrase2 identified by fragment screening and structure based design
6	d1exqa_	 Alignment		99.8	13	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
7	d1bcoa2	 Alignment		99.8	15	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: mu transposase, core domain
8	c1ex4A_	 Alignment		99.8	18	PDB header: viral protein Chain: A: PDB Molecule: integrase; PDBTitle: hiv-1 integrase catalytic core and c-terminal domain
9	c3kksB_	 Alignment		99.7	16	PDB header: dna binding protein Chain: B: PDB Molecule: integrase; PDBTitle: crystal structure of catalytic core domain of biv integrase in crystal2 form ii
10	d1cxqa_	 Alignment		99.7	20	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
11	d1hyva_	 Alignment		99.7	17	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain

12	c1k6yB_	Alignment		99.7	18	PDB header: transferase Chain: B: PDB Molecule: integrase; PDBTitle: crystal structure of a two-domain fragment of hiv-1 integrase
13	c3hpgC_	Alignment		99.6	20	PDB header: transferase Chain: C: PDB Molecule: integrase; PDBTitle: visna virus integrase (residues 1-219) in complex with ledgf2 ibd: examples of open integrase dimer-dimer interfaces
14	c1bcoA_	Alignment		99.6	14	PDB header: transposase Chain: A: PDB Molecule: bacteriophage mu transposase; PDBTitle: bacteriophage mu transposase core domain
15	c3l2tB_	Alignment		99.6	14	PDB header: recombination/dna Chain: B: PDB Molecule: integrase; PDBTitle: crystal structure of the prototype foamy virus (pfv) intasome in2 complex with magnesium and mk0518 (raltegravir)
16	d1c6va_	Alignment		99.6	19	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
17	c3hosA_	Alignment		99.6	13	PDB header: transferase, dna binding protein/dna Chain: A: PDB Molecule: transposable element mariner, complete cds; PDBTitle: crystal structure of the mariner mos1 paired end complex with mg
18	c3dlrA_	Alignment		99.4	14	PDB header: transferase Chain: A: PDB Molecule: integrase; PDBTitle: crystal structure of the catalytic core domain from pfv2 integrase
19	c6paxA_	Alignment		99.0	19	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
20	d1pdnc_	Alignment		98.9	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
21	c1u78A_	Alignment	not modelled	98.6	11	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
22	c2k27A_	Alignment	not modelled	98.6	20	PDB header: transcription regulator Chain: A: PDB Molecule: paired box protein pax-8; PDBTitle: solution structure of human pax8 paired box domain
23	c2f7tA_	Alignment	not modelled	97.8	14	PDB header: dna binding protein Chain: A: PDB Molecule: mos1 transposase; PDBTitle: crystal structure of the catalytic domain of mos1 mariner2 transposase
24	d2jn6a1	Alignment	not modelled	97.8	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Cgl2762-like
25	c3f2kB_	Alignment	not modelled	97.4	18	PDB header: transferase Chain: B: PDB Molecule: histone-lysine n-methyltransferase setmar; PDBTitle: structure of the transposase domain of human histone-lysine2 n-methyltransferase setmar
26	d1k78a1	Alignment	not modelled	96.8	28	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
27	d6paxa1	Alignment	not modelled	96.6	28	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
28	c2rn7A_	Alignment	not modelled	96.6	13	PDB header: unknown function Chain: A: PDB Molecule: is629 orfa; PDBTitle: nmr solution structure of tnpA protein from shigella2 flexneri. northeast structural genomics target sfr125

29	c1hlvA	Alignment	not modelled	96.3	11	PDB header: dna binding protein/dna Chain: A: PDB Molecule: major centromere autoantigen b; PDBTitle: crystal structure of cenp-b(1-129) complexed with the cenp-2 b box dna
30	c1umqA	Alignment	not modelled	96.2	27	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
31	d1umqa	Alignment	not modelled	96.2	27	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
32	c2w48D	Alignment	not modelled	96.1	13	PDB header: transcription Chain: D: PDB Molecule: sorbitol operon regulator; PDBTitle: crystal structure of the full-length sorbitol operon2 regulator sorc from klebsiella pneumoniae
33	d1ntca	Alignment	not modelled	96.0	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
34	c3hefB	Alignment	not modelled	95.9	17	PDB header: viral protein Chain: B: PDB Molecule: gene 1 protein; PDBTitle: crystal structure of the bacteriophage sf6 terminase small2 subunit
35	d1fipa	Alignment	not modelled	95.8	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
36	d1etxa	Alignment	not modelled	95.8	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
37	c3e7lD	Alignment	not modelled	95.4	6	PDB header: transcription regulator Chain: D: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigma54 activator ntrc4's dna binding2 domain
38	c2elhA	Alignment	not modelled	95.3	21	PDB header: dna binding protein Chain: A: PDB Molecule: cgl1849-pa; PDBTitle: solution structure of the cenp-b n-terminal dna-binding2 domain of fruit fly distal antenna cgl1849-pa
39	d1etob	Alignment	not modelled	95.0	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
40	d1g2ha	Alignment	not modelled	94.9	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
41	d2coba1	Alignment	not modelled	94.6	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Psq domain
42	c2x48B	Alignment	not modelled	94.2	26	PDB header: viral protein Chain: B: PDB Molecule: cag38821; PDBTitle: orf 55 from sulfolobus islandicus rudivirus 1
43	c3bs3A	Alignment	not modelled	94.0	9	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
44	c2w7nA	Alignment	not modelled	93.2	11	PDB header: transcription/dna Chain: A: PDB Molecule: trfb transcriptional repressor protein; PDBTitle: crystal structure of kora bound to operator dna: insight2 into repressor cooperation in rp4 gene regulation
45	d1hlva1	Alignment	not modelled	93.0	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Centromere-binding
46	c1r71B	Alignment	not modelled	93.0	16	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
47	d1r71a	Alignment	not modelled	92.5	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: KorB DNA-binding domain-like Family: KorB DNA-binding domain-like
48	c3onqB	Alignment	not modelled	92.5	15	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
49	c1bdhA	Alignment	not modelled	92.3	16	PDB header: transcription/dna Chain: A: PDB Molecule: protein (purine repressor); PDBTitle: purine repressor mutant-hypoxanthine-palindromic operator2 complex
50	c1z4hA	Alignment	not modelled	92.3	4	PDB header: protein binding, dna binding protein Chain: A: PDB Molecule: tor inhibition protein; PDBTitle: the response regulator tori belongs to a new family of2 atypical excisionase
51	d1a04a1	Alignment	not modelled	92.3	24	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)
52	d1ijwc	Alignment	not modelled	92.2	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Recombinase DNA-binding domain
53	d1rzsa	Alignment	not modelled	92.2	20	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
54	d1hcra	Alignment	not modelled	92.2	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Recombinase DNA-binding domain

55	c3t76A	Alignment	not modelled	92.1	17	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator vanug; PDBTitle: crystal structure of transcriptional regulator vanug, form ii
56	d1vz0a1	Alignment	not modelled	92.1	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: KorB DNA-binding domain-like Family: KorB DNA-binding domain-like
57	c3b7hA	Alignment	not modelled	92.0	3	PDB header: structural protein Chain: A: PDB Molecule: prophage lp1 protein 11; PDBTitle: crystal structure of the prophage lp1 protein 11
58	c3cecA	Alignment	not modelled	92.0	10	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
59	c2d6yA	Alignment	not modelled	92.0	19	PDB header: gene regulation Chain: A: PDB Molecule: putative tetr family regulatory protein; PDBTitle: crystal structure of transcriptional factor sco4008 from streptomyces2 coelicolor a3(2)
60	c3h5tA	Alignment	not modelled	91.8	11	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, lacI family; PDBTitle: crystal structure of a transcriptional regulator, lacI2 family protein from corynebacterium glutamicum
61	c2kpiA	Alignment	not modelled	91.8	8	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
62	c3f1bA	Alignment	not modelled	91.7	16	PDB header: transcription regulator Chain: A: PDB Molecule: tetr-like transcriptional regulator; PDBTitle: the crystal structure of a tetr-like transcriptional regulator from2 rhodococcus sp. rha1.
63	d1t56a1	Alignment	not modelled	91.7	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
64	c3omtA	Alignment	not modelled	91.7	8	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.
65	d1gdtA1	Alignment	not modelled	91.7	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Recombinase DNA-binding domain
66	c3gziA	Alignment	not modelled	91.7	13	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, tetr family; PDBTitle: crystal structure of a transcriptional regulator of the tetr family2 (shew_3567) from shewanella loihica pv-4 at 2.05 a resolution
67	c2l0kA	Alignment	not modelled	91.6	13	PDB header: transcription Chain: A: PDB Molecule: stage iii sporulation protein d; PDBTitle: nmr solution structure of a transcription factor spoiiiid in complex2 with dna
68	c1vi0B	Alignment	not modelled	91.5	23	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of a transcriptional regulator
69	c1ui6B	Alignment	not modelled	91.5	23	PDB header: antibiotic Chain: B: PDB Molecule: a-factor receptor homolog; PDBTitle: crystal structure of gamma-butyrolactone receptor (arpa-like protein)
70	d2fq4a1	Alignment	not modelled	91.4	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
71	d1bw6a	Alignment	not modelled	91.4	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Centromere-binding
72	c1zljE	Alignment	not modelled	91.3	10	PDB header: transcription Chain: E: PDB Molecule: dormancy survival regulator; PDBTitle: crystal structure of the mycobacterium tuberculosis hypoxic2 response regulator dosr c-terminal domain
73	c3bjbE	Alignment	not modelled	91.3	16	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
74	d1yioa1	Alignment	not modelled	91.2	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)
75	c2of7A	Alignment	not modelled	91.1	16	PDB header: transcription Chain: A: PDB Molecule: putative tetr-family transcriptional regulator; PDBTitle: structural genomics, the crystal structure of a tetr-family2 transcriptional regulator from streptomyces coelicolor a3
76	c2guhA	Alignment	not modelled	91.1	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
77	c1jumB	Alignment	not modelled	91.1	13	PDB header: transcription Chain: B: PDB Molecule: hypothetical transcriptional regulator in qaca PDBTitle: crystal structure of the multidrug binding transcriptional2 repressor qacr bound to the natural drug berberine
78	c2nx4A	Alignment	not modelled	91.1	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: transcriptional regulator, tetr family protein; PDBTitle: the crystal structure of a the putative tetr-family

					transcriptional2 regulator rha06780 from rhodococcus sp. rha1.
79	c1bjzA_	Alignment	not modelled	91.1	19 PDB header: transcription regulation Chain: A: PDB Molecule: tetracycline repressor; PDBTitle: tetracycline chelated mg2+-ion initiates helix unwinding for tet2 repressor induction
80	d2bjca1	Alignment	not modelled	91.1	16 Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
81	c3mzyA_	Alignment	not modelled	91.0	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
82	c3bcgA_	Alignment	not modelled	91.0	16 PDB header: transcription regulator Chain: A: PDB Molecule: hth-type transcriptional regulator acrr; PDBTitle: conformational changes of the acrr regulator reveal a2 mechanism of induction
83	d1jt6a1	Alignment	not modelled	91.0	13 Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
84	c2genA_	Alignment	not modelled	90.9	13 PDB header: transcription Chain: A: PDB Molecule: probable transcriptional regulator; PDBTitle: structural genomics, the crystal structure of a probable2 transcriptional regulator from pseudomonas aeruginosa pao1
85	c2krfB_	Alignment	not modelled	90.9	14 PDB header: transcription Chain: B: PDB Molecule: transcriptional regulatory protein coma; PDBTitle: nmr solution structure of the dna binding domain of competence protein2 a
86	c1zvvA_	Alignment	not modelled	90.8	18 PDB header: transcription/dna Chain: A: PDB Molecule: glucose-resistance amylase regulator; PDBTitle: crystal structure of a ccpa-crh-dna complex
87	c3cjdB_	Alignment	not modelled	90.7	16 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
88	c3b6aC_	Alignment	not modelled	90.7	13 PDB header: transcription Chain: C: PDB Molecule: actr protein; PDBTitle: crystal structure of the streptomyces coelicolor tetr2 family protein actr in complex with actinorhodin
89	c2rasB_	Alignment	not modelled	90.7	29 PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator, tetr family; PDBTitle: crystal structure of a putative tetr/acrr family transcriptional2 regulator (saro_0558) from novosphingobium aromaticivorans dsm at3 1.80 a resolution
90	c1x3uA_	Alignment	not modelled	90.7	14 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
91	d1uxca_	Alignment	not modelled	90.6	16 Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
92	c3ppbB_	Alignment	not modelled	90.6	19 PDB header: transcription regulator Chain: B: PDB Molecule: putative tetr family transcription regulator; PDBTitle: crystal structure of a putative tetr family transcription regulator2 (shew_3104) from shewanella sp. pv-4 at 2.10 a resolution
93	c2gfnA_	Alignment	not modelled	90.6	29 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
94	c2zcxA_	Alignment	not modelled	90.6	23 PDB header: transcription Chain: A: PDB Molecule: tetr-family transcriptional regulator; PDBTitle: crystal structure of tetr family transcriptional regulator2 sco7815
95	d2hsga1	Alignment	not modelled	90.6	18 Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
96	d1nera_	Alignment	not modelled	90.5	26 Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
97	c2zb9A_	Alignment	not modelled	90.5	19 PDB header: transcription Chain: A: PDB Molecule: putative transcriptional regulator; PDBTitle: crystal structure of tetr family transcription regulator2 sco0332
98	d1lcda_	Alignment	not modelled	90.5	12 Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
99	d1p4wa_	Alignment	not modelled	90.5	21 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)
100	c2wuiA_	Alignment	not modelled	90.4	16 PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of mexz, a key repressor responsible for2 antibiotic resistance in pseudomonas aeruginosa.
101	c2hytA_	Alignment	not modelled	90.4	16 PDB header: transcription Chain: A: PDB Molecule: tetr-family transcriptional regulator; PDBTitle: crystal structure of a tetr-family transcriptional regulator (eca1819)2 from pectobacterium atrosepticum at 1.64 a resolution
102	c2f07A_	Alignment	not modelled	90.4	10 PDB header: transcription Chain: A: PDB Molecule: yvdt; PDBTitle: crystal structure of yvdt from bacillus subtilis
103	d1lutxa_	Alignment	not modelled	90.4	17 Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like

104	c3dewA_	 Alignment	not modelled	90.4	16	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, tetr family; PDBTitle: the structure of a putative tetr family transcriptional regulator from2 geobacter sulfurreducens pca.
105	c3anpD_	 Alignment	not modelled	90.4	19	PDB header: transcription Chain: D: PDB Molecule: transcriptional repressor, tetr family; PDBTitle: crystal structure of thermus thermophilus fadr, a tetr family2 transcriptional repressor, in complex with lauroyl-coa.
106	c2fq4A_	 Alignment	not modelled	90.4	16	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, tetr family; PDBTitle: the crystal structure of the transcriptional regulator (tetr family)2 from bacillus cereus
107	c3on4D_	 Alignment	not modelled	90.4	19	PDB header: transcription Chain: D: PDB Molecule: transcriptional regulator, tetr family; PDBTitle: crystal structure of tetr transcriptional regulator from legionella2 pneumophila
108	c2dg7A_	 Alignment	not modelled	90.4	13	PDB header: gene regulation Chain: A: PDB Molecule: putative transcriptional regulator; PDBTitle: crystal structure of the putative transcriptional regulator sco03372 from streptomyces coelicolor a3(2)
109	c2cg4B_	 Alignment	not modelled	90.3	19	PDB header: transcription Chain: B: PDB Molecule: regulatory protein asnc; PDBTitle: structure of e.coli asnc
110	c3c2bA_	 Alignment	not modelled	90.3	23	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, tetr family; PDBTitle: crystal structure of tetr transcriptional regulator from agrobacterium2 tumefaciens
111	c2qtqB_	 Alignment	not modelled	90.3	13	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator, tetr family; PDBTitle: crystal structure of a predicted dna-binding transcriptional regulator2 (saro_1072) from novosphingobium aromaticivorans dsm at 1.85 a3 resolution
112	d3c07a1	 Alignment	not modelled	90.3	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
113	c3c07B_	 Alignment	not modelled	90.3	16	PDB header: transcription regulator Chain: B: PDB Molecule: putative tetr-family transcriptional regulator; PDBTitle: crystal structure of a tetr family transcriptional regulator from2 streptomyces coelicolor a3(2)
114	c3b81A_	 Alignment	not modelled	90.3	10	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, acrr family; PDBTitle: crystal structure of predicted dna-binding transcriptional regulator2 of tetr/acrr family (np_350189.1) from clostridium acetobutylicum at3 2.10 a resolution
115	c2o7tA_	 Alignment	not modelled	90.3	13	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of a tetr family transcriptional regulator2 (ncgl1578, cgl1640) from corynebacterium glutamicum at 2.10 a3 resolution
116	c3dcfB_	 Alignment	not modelled	90.2	6	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator of the tetr/acrr PDBTitle: crystal structure of transcriptional regulator of the2 tetr/acrr family (yp_290855.1) from thermobifida fusca yx-3 er1 at 2.50 a resolution
117	c3fiwB_	 Alignment	not modelled	90.2	19	PDB header: transcription regulator Chain: B: PDB Molecule: putative tetr-family transcriptional regulator; PDBTitle: structure of sco0253, a tetr-family transcriptional regulator from2 streptomyces coelicolor
118	d1ui5a1	 Alignment	not modelled	90.1	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
119	c2jpcA_	 Alignment	not modelled	90.1	21	PDB header: dna binding protein Chain: A: PDB Molecule: ssrb; PDBTitle: ssrb dna binding protein
120	c3fmyA_	 Alignment	not modelled	90.1	3	PDB header: dna binding protein Chain: A: PDB Molecule: hth-type transcriptional regulator mqsa PDBTitle: structure of the c-terminal domain of the e. coli protein2 mqsa (ygit/b3021)