Phyre^2

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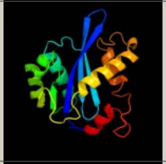
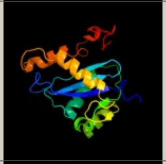
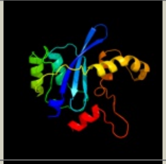
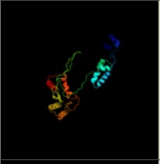
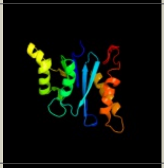
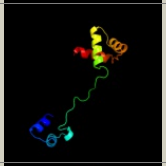
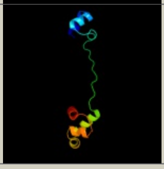
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1bcoa2	Alignment		99.7	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**mu transposase, core domain
2	c3f9kV_	Alignment		99.7	17	**PDB header:**viral protein, recombination **Chain:** V: **PDB Molecule:**integrase; **PDBTitle:** two domain fragment of hiv-2 integrase in complex with ledgf ibd
3	d1c0ma2	Alignment		99.6	22	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Retroviral integrase, catalytic domain
4	c1c0mA_	Alignment		99.6	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein (integrase); **PDBTitle:** crystal structure of rsv two-domain integrase
5	d1asua_	Alignment		99.6	20	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Retroviral integrase, catalytic domain
6	c1bcoA_	Alignment		99.5	15	**PDB header:**transposase **Chain:** A: **PDB Molecule:**bacteriophage mu transposase; **PDBTitle:** bacteriophage mu transposase core domain
7	d1exqa_	Alignment		99.5	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Retroviral integrase, catalytic domain
8	c3nf9A_	Alignment		99.5	20	**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
9	c3hosA_	Alignment		99.4	14	**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
10	c1ex4A_	Alignment		99.4	23	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**integrase; **PDBTitle:** hiv-1 integrase catalytic core and c-terminal domain
11	c3kksB_	Alignment		99.4	17	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**integrase; **PDBTitle:** crystal structure of catalytic core domain of biv integrase in crystal2 form ii

12	d1cxqa_	Alignment		99.3	23	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Retroviral integrase, catalytic domain
13	c1k6yB_	Alignment		99.3	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**integrase; **PDBTitle:** crystal structure of a two-domain fragment of hiv-1 integrase
14	d1c6va_	Alignment		99.2	21	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Retroviral integrase, catalytic domain
15	d1hyva_	Alignment		99.2	23	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Retroviral integrase, catalytic domain
16	c3hpgC_	Alignment		99.2	18	**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
17	c3l2tB_	Alignment		99.0	16	**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)
18	c3dlrA_	Alignment		98.5	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**integrase; **PDBTitle:** crystal structure of the catalytic core domain from pfv2 integrase
19	c6paxA_	Alignment		98.4	14	**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	c1u78A_	Alignment		98.4	15	**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
21	d1pdnc_	Alignment	not modelled	98.2	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
22	c2k27A_	Alignment	not modelled	97.7	10	**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	97.5	16	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**mos1 transposase; **PDBTitle:** crystal structure of the catalytic domain of mos1 mariner2 transposase
24	c3f2kB_	Alignment	not modelled	97.2	11	**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
25	c1hlvA_	Alignment	not modelled	96.9	17	**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
26	d2jn6a1	Alignment	not modelled	96.5	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Cgl2762-like
27	c2elhA_	Alignment	not modelled	96.3	24	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**cg11849-pa; **PDBTitle:** solution structure of the cenp-b n-terminal dna-binding2 domain of fruit fly distal antenna cg11849-pa
28	c3hefB_	Alignment	not modelled	95.8	9	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**gene 1 protein; **PDBTitle:** crystal structure of the bacteriophage sf6 terminase small2 subunit

29	c1umqA_	Alignment	not modelled	95.7	11	**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
30	d1umqa_	Alignment	not modelled	95.7	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
31	d1k78a1	Alignment	not modelled	95.3	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
32	d1ntca_	Alignment	not modelled	94.9	6	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
33	d6paxa1	Alignment	not modelled	94.7	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
34	d1etxa_	Alignment	not modelled	94.5	6	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
35	d1fipa_	Alignment	not modelled	94.4	3	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
36	c3e7lD_	Alignment	not modelled	93.8	15	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** crystal structure of sigma54 activator ntrc4's dna binding2 domain
37	d1hlva1	Alignment	not modelled	93.8	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Centromere-binding
38	d1g2ha_	Alignment	not modelled	93.7	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
39	d1etob_	Alignment	not modelled	93.3	6	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
40	d2coba1	Alignment	not modelled	93.1	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Psq domain
41	c3kjxD_	Alignment	not modelled	92.2	9	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**transcriptional regulator, laci family; **PDBTitle:** crystal structure of a transcriptional regulator, lacl2 family protein from silicibacter pomeroyi
42	c3h5tA_	Alignment	not modelled	92.1	13	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, laci family; **PDBTitle:** crystal structure of a transcriptional regulator, lacl2 family protein from corynebacterium glutamicum
43	c2rn7A_	Alignment	not modelled	91.9	6	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**is629 orfa; **PDBTitle:** nmr solution structure of tnpe protein from shigella2 flexneri. northeast structural genomics target sfr125
44	d2bjca1	Alignment	not modelled	91.9	11	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
45	d1utxa_	Alignment	not modelled	91.0	16	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
46	c3bs3A_	Alignment	not modelled	90.7	14	**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
47	c1z4hA_	Alignment	not modelled	90.5	9	**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
48	c1bdhA_	Alignment	not modelled	90.3	14	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**protein (purine repressor); **PDBTitle:** purine repressor mutant-hypoxanthine-palindromic operator2 complex
49	d2icta1	Alignment	not modelled	90.2	11	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
50	d1adra_	Alignment	not modelled	90.1	14	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
51	d2ao9a1	Alignment	not modelled	89.9	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Nanomeric phage protein-like
52	d1rzsa_	Alignment	not modelled	89.7	15	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
53	d1biaa1	Alignment	not modelled	89.7	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Biotin repressor-like
54	c3cecA_	Alignment	not modelled	89.7	11	**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

55	d1bw6a_	Alignment	not modelled	89.5	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Centromere-binding
56	d1jt6a1	Alignment	not modelled	89.3	5	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
57	c3o60A_	Alignment	not modelled	89.2	36	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lin0861 protein; **PDBTitle:** the crystal structure of lin0861 from listeria innocua to 2.8a
58	c3omtA_	Alignment	not modelled	89.2	11	**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.
59	c1zvvA_	Alignment	not modelled	89.0	13	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**glucose-resistance amylase regulator; **PDBTitle:** crystal structure of a ccpa-crh-dna complex
60	d1y9qa1	Alignment	not modelled	88.8	8	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Probable transcriptional regulator VC1968, N-terminal domain
61	c3f1bA_	Alignment	not modelled	88.8	18	**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.
62	d2hsga1	Alignment	not modelled	88.6	13	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
63	d1t56a1	Alignment	not modelled	88.6	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
64	d1mkma1	Alignment	not modelled	88.5	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Transcriptional regulator IclR, N-terminal domain
65	d1vi0a1	Alignment	not modelled	88.5	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
66	d2fq4a1	Alignment	not modelled	88.5	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
67	c2lcvA_	Alignment	not modelled	88.5	14	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**hth-type transcriptional repressor cytr; **PDBTitle:** structure of the cytidine repressor dna-binding domain; an alternate2 calculation
68	d1lcda_	Alignment	not modelled	88.4	11	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
69	c1vi0B_	Alignment	not modelled	88.4	14	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator; **PDBTitle:** crystal structure of a transcriptional regulator
70	d1jhfa1	Alignment	not modelled	88.3	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**LexA repressor, N-terminal DNA-binding domain
71	d1efaa1	Alignment	not modelled	88.3	11	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
72	d1j5ya1	Alignment	not modelled	88.3	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Biotin repressor-like
73	c2xcjB_	Alignment	not modelled	88.2	16	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**c protein; **PDBTitle:** crystal structure of p2 c, the immunity repressor of2 temperate e. coli phage p2
74	c2l8nA_	Alignment	not modelled	88.1	14	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional repressor cytr; **PDBTitle:** nmr structure of the cytidine repressor dna binding domain in presence2 of operator half-site dna
75	c3gpvA_	Alignment	not modelled	88.1	5	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, merr family; **PDBTitle:** crystal structure of a transcriptional regulator, merr2 family from bacillus thuringiensis
76	c2cg4B_	Alignment	not modelled	88.1	6	**PDB header:**transcription **Chain:** B: **PDB Molecule:**regulatory protein asnc; **PDBTitle:** structure of e.coli asnc
77	d2fbqa1	Alignment	not modelled	88.1	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
78	c2guhA_	Alignment	not modelled	88.0	14	**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
79	c3kkcB_	Alignment	not modelled	88.0	18	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**tetr family transcriptional regulator; **PDBTitle:** the crystal structure of tetr transcriptional regulator from2 streptococcus agalactiae 2603v
80	c2p6tH_	Alignment	not modelled	87.9	6	**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
						Fold: Putative DNA-binding domain

81	d1r8da_	Alignment	not modelled	87.9	5	**Superfamily:**Putative DNA-binding domain **Family:**DNA-binding N-terminal domain of transcription activators
82	c3clcC_	Alignment	not modelled	87.9	9	**PDB header:**transcription regulator/dna **Chain:** C: **PDB Molecule:**regulatory protein; **PDBTitle:** crystal structure of the restriction-modification controller protein2 c.esp1396i tetramer in complex with its natural 35 base-pair operator
83	c2ppxA_	Alignment	not modelled	87.9	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein atu1735; **PDBTitle:** crystal structure of a hth xre-family like protein from agrobacterium2 tumefaciens
84	d2ppxa1	Alignment	not modelled	87.9	11	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
85	c3i4pA_	Alignment	not modelled	87.8	6	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, asnc family; **PDBTitle:** crystal structure of asnc family transcriptional regulator from2 agrobacterium tumefaciens
86	c3ppbB_	Alignment	not modelled	87.7	18	**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
87	c2kpjA_	Alignment	not modelled	87.7	12	**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
88	c3b7hA_	Alignment	not modelled	87.6	12	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**prophage lp1 protein 11; **PDBTitle:** crystal structure of the prophage lp1 protein 11
89	c2ia0A_	Alignment	not modelled	87.5	9	**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)
90	d3c07a1	Alignment	not modelled	87.4	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
91	c3b81A_	Alignment	not modelled	87.4	9	**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
92	c2nx4A_	Alignment	not modelled	87.4	0	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**transcriptional regulator, tetr family protein; **PDBTitle:** the crystal structure of athe putative tetr-family transcriptional2 regulator rha06780 from rhodococcus sp. rha1.
93	c2dg7A_	Alignment	not modelled	87.4	4	**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)
94	c2l0kA_	Alignment	not modelled	87.4	9	**PDB header:**transcription **Chain:** A: **PDB Molecule:**stage iii sporulation protein d; **PDBTitle:** nmr solution structure of a transcription factor spoiiid in complex2 with dna
95	c2e7xA_	Alignment	not modelled	87.3	15	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**150aa long hypothetical transcriptional regulator; **PDBTitle:** structure of the lrp/asnc like transcriptional regulator from2 sulfolobus tokodaii 7 complexed with its cognate ligand
96	c2w48D_	Alignment	not modelled	87.3	14	**PDB header:**transcription **Chain:** D: **PDB Molecule:**sorbitol operon regulator; **PDBTitle:** crystal structure of the full-length sorbitol operon2 regulator sorc from klebsiella pneumoniae
97	d2g3ba1	Alignment	not modelled	87.2	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
98	d1pb6a1	Alignment	not modelled	87.2	5	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
99	c3op9A_	Alignment	not modelled	87.2	8	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**pli0006 protein; **PDBTitle:** crystal structure of transcriptional regulator from listeria innocua
100	d1xsva_	Alignment	not modelled	87.1	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**YlxM/p13-like
101	c2of7A_	Alignment	not modelled	87.1	9	**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
102	c2ebyA_	Alignment	not modelled	87.1	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative hth-type transcriptional regulator ybaq; **PDBTitle:** crystal structure of a hypothetical protein from e. coli
103	d1lmb3_	Alignment	not modelled	87.1	14	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
104	c2vbzA_	Alignment	not modelled	87.0	9	**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

105	d2np5a1	Alignment	not modelled	87.0	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
106	c2eh3A_	Alignment	not modelled	87.0	9	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator; **PDBTitle:** crystal structure of aq_1058, a transcriptional regulator (terr/acrr2 family) from aquifex aeolicus vf5
107	d1ui5a1	Alignment	not modelled	87.0	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
108	c3bcgA_	Alignment	not modelled	86.9	18	**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
109	c2oerA_	Alignment	not modelled	86.8	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**probable transcriptional regulator; **PDBTitle:** probable transcriptional regulator from pseudomonas2 aeruginosa
110	d2vkva1	Alignment	not modelled	86.8	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
111	c3eusB_	Alignment	not modelled	86.8	14	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**dna-binding protein; **PDBTitle:** the crystal structure of the dna binding protein from silicibacter2 pomeroyi
112	c3on4D_	Alignment	not modelled	86.7	14	**PDB header:**transcription **Chain:** D: **PDB Molecule:**transcriptional regulator, tetr family; **PDBTitle:** crystal structure of tetr transcriptional regulator from legionella2 pneumophila
113	d2b5aa1	Alignment	not modelled	86.7	16	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
114	c3cjdB_	Alignment	not modelled	86.6	23	**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
115	c3lwjA_	Alignment	not modelled	86.6	18	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**putative tetr-family transcriptional regulator; **PDBTitle:** crystal structure of putative tetr-family transcriptional regulator2 (yp_752756.1) from syntrophomonas wolfei str. goettingen at 2.07 a3 resolution
116	d2cg4a1	Alignment	not modelled	86.6	6	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
117	c1jumB_	Alignment	not modelled	86.6	5	**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
118	c2f07A_	Alignment	not modelled	86.6	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**yvdt; **PDBTitle:** crystal structure of yvdt from bacillus subtilis
119	c2cfxD_	Alignment	not modelled	86.6	13	**PDB header:**transcription **Chain:** D: **PDB Molecule:**hth-type transcriptional regulator lrpc; **PDBTitle:** structure of b.subtilis lrpc
120	c3dcfB_	Alignment	not modelled	86.6	9	**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